

OK nucleic - nucleic search, using SW model

Run on: October 14, 2004, 09:12:14 ; Search time 3341.74 Seconds
(without alignments) 8443.595 Million cell updates/sec

Title: US-09-407-804A-5

Perfect score: 651
Sequence: 1 atgaacagagcaataatag.....acaagagagagattcaatga 651

Scoring table: IDENTITY_NUC

Gapop 10.0 / Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_hg: +
3: gb_in: +
4: gb_cm: +
5: gb_ov: +
6: gb_pac: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_scs: +
12: gb_sy: +
13: gb_un: +
14: gb_vl: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
23: em_pac: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_scs: +

28: em_un: +
29: em_vl: +
30: em_hg_hum: +
31: em_hg_inv: +
32: em_hg_other: +
33: em_hg_mus: +
34: em_hg_pin: +
35: em_hg_rnd: +
36: em_hg_mam: +
37: em_hg_vrt: +
38: em_sy: +
39: em_hgco_hum: +
40: em_hgco_mus: +
41: em_hgco_other: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				ID	Description
	Score	Match	Length	DB		
1	651	100.0	651	6	BD245276	BD245276 Developme
2	651	100.0	41401	7	AB009866	AB009866 Bacterioph
3	651	100.0	41708	6	BD245281	BD245281 Developme
4	651	100.0	41708	6	AR368770	AR368770 Sequence
5	651	100.0	272850	1	AP004828	AP004828 Staphyloc
6	175.6	27.0	222887	1	AB063171	AB063171 Staphyloc
7	103.4	16.2	165118	2	AC119033	AC119033 Danio rer
8	103.4	15.9	155204	2	AC007926	AC007926 Trypanoso
9	102.2	15.7	110000	2	AL954295_2	Continuation (3 of
10	102.2	15.7	122838	2	BK248494	BK248494 Danio rer
11	99	15.2	146275	2	AL935272	AL935272 Danio rer
12	98.8	15.2	151802	3	AC114263	AC114263 Dictyoste
13	98.2	15.1	153751	3	AC116531	AC116531 Dictyoste
14	98	15.1	333321	3	AC116986	AC116986 Dictyoste
15	97.8	15.0	250029	2	AE014820	AE014820 Plasmodiu
16	96.2	14.8	116807	2	BK890614	BK890614 Danio rer
17	95.2	14.6	94534	5	AL929250	AL929250 Zebrafish
18	94.8	14.6	151341	5	AL929536	AL929536 Zebrafish
19	94.6	14.5	177595	2	AL933867	AL933867 Danio rer
20	94.4	14.5	349751	3	PFMAL4P3	PFMAL4P3 Plasmodiu
21	94.2	14.5	225581	2	BK537105	BK537105 Danio rer
22	93.6	14.4	171798	2	AC084397	AC084397 Trypanoso
23	93.6	14.4	198743	2	BK530070	BK530070 Danio rer
24	92.8	14.3	183584	9	AC012492	AC012492 Homo sapi
25	92	14.1	110000	3	AC116957_2	Continuation (3 of
26	91.8	14.1	169841	9	AL607043	AL607043 Human DNA
27	91.6	14.1	245802	2	AC006279	AC006279 Plasmodiu
28	91.6	14.1	260929	3	AE014852	AE014852 Plasmodiu
29	91.2	14.0	4865	3	AF364131	AF364131 Anopholes
30	91.2	14.0	199347	2	BK321884	BK321884 Danio rer
31	91.2	14.0	203204	2	AC092052	AC092052 Homo sapi
32	91	14.0	8056	6	AX599046	AX599046 Sequence
33	91	14.0	180023	2	BK897685	BK897685 Danio rer

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c 36 89.6 13.8 384 3 AF201315 Digesta p
c 37 89.6 13.8 8056 6 AX599046 Sequence
c 38 89.4 13.7 349980 6 AX344555 Sequence
c 39 88.6 13.6 183357 2 BX569779 Danto rer
c 40 88.2 13.5 17443 3 AC024806 Ctenorhab
c 41 88.2 13.5 111882 3 AC115612 Dictyoste
c 42 88 13.5 104992 2 AC005504 Plasmodu
c 43 88 13.5 169546 2 AC004157 Plasmodu
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ALIGNMENTS

RESULT 1
BD245276 651 bp DNA linear PAT 17-JUL-2003
LOCUS BD245276
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245276
VERSION BD245276.1 GI:33055046
KEYWORDS JP 2002531107-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 651)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 11 24-SEP-2002;
PHARTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/11
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454232 PT JERRY
PELLETIER, PHILLIPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K45/00, A61P31/04, C07K14/005,
PC C12N15/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FH Key
FT source
FT aureus bacteriophage 77'

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ORIGIN

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Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GTTAAAGAGATTTTATAGTATTTTACGAGTCTTAACTTACAGTAAATCAATTTA 120
QY 121 GACAAATATATCCGATATATTTAGATGTTTAAAAAGGCTAAAAAGATGATTGAGCT 180
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QY 361 AGTACAAATCAATTTTATATCTCTTTGTTATGGAACAAATGCTATTATTAAT 420
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QY 601 TCGATTAAGAAAGATATATTTATTTAAACAGAGAGATTAATGA 651
DB 601 TCGATTAAGAAAGATATATTTATTTAAACAGAGAGATTTAATGA 651

RESULT 2
AB009866 41401 bp DNA linear PHG 23-MAY-2000
LOCUS AB009866
DEFINITION Bacteriophage phi PVL proviral DNA, complete sequence.
ACCESSION AB009866
VERSION AB009866.2 GI:8051688
KEYWORDS dutPase; ssDNA binding protein; anti repressor; repressor;

integrases; LukF-PV; LukS-PV; holin; amidase (peptidoglycan hydrolase); cepcid protein; portal protein.
SOURCE
ORGANISM
Staphylococcus aureus bacteriophage PV1
Staphylococcus aureus bacteriophage PV1
Virus(es) dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
REFERENCE
AUTHORS
TITLE
1 (sites)
Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775) Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
JOURNAL
MEDLINE
98067870
PUBMED
940084
REFERENCE
AUTHORS
TITLE
2 (sites)
Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPV1 carrying Panton-Valentine leukocidin genes
JOURNAL
Gene 215 (1), 57-67 (1998)
MEDLINE
98332719
PUBMED
9666077
REFERENCE
AUTHORS
TITLE
3 (bases 1 to 41401)
Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
Direct Submision
Submitted (17-DEC-1997) Jun Kaneko, Tohoku University, Dept. Appl. Biol. Chem., Faculty of Agriculture; 1-1 Tsurumi-dori Aamajiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan (E-mail:j.kaneko@biochem.tohoku.ac.jp, tel:81-22-717-8781, Fax:81-22-717-8780)
COMMENT
On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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RESULT 3
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patient: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 P1 JERRY
PELLETIER,PHILLIPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage 77.
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ORIGIN

Query Match 100.0%; Score 651; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 8-66-73;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACGACCAATATATAGGACATATATATCTTATGACGAGAGGTGTGCTTTATTTCA 60
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61 GTTAAAGATTTTATGATTTTATGAGATCTTAACCTTAACGTAACCAATTTA 120
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Db 39911 GTTAAAGATTTTATGATTTTATGAGATCTTAACCTTAACGTAACCAATTTA 39970
121 GACCAATATATCCGATATATTTAGATTTTAAAGAGCTTAAAGATTTGAGCT 180
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Db 39971 GACCAATATATCCGATATATTTAGATTTTAAAGAGCTTAAAGATTTGAGCT 40030
181 TATATTTATCCAGACGACGATGAAATTTTATGATTTTATGATGAAATTTTAT 240
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Db 40031 TATATTTATCCAGACGACGATGAAATTTTATGATTTTATGATGAAATTTTAT 40090
241 AATTATGATTAAGCAAGTAAAAAGCTATGAAATGTTATGATTTATGACCAATGAT 300
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Db 40091 AATTATGATTAAGCAAGTAAAAAGCTATGAAATGTTATGATTTATGACCAATGAT 40150
301 AATTATCAATATAGGATTAAGCAATGAAATTTTAAAGATGATTTCAACATGATTT 360
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Db 40151 AATTATCAATATAGGATTAAGCAATGAAATTTTAAAGATGATTTCAACATGATTT 40210
361 AGTACCAATGATTTTATATCTCTCTTTGTTATGAAACATGCTATTATTAAT 420
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Db 40211 AGTACCAATGATTTTATATCTCTCTTTGTTATGAAACATGCTATTATTAAT 40270
421 GAATATCAAAAAGATATCTTATTTAAAAATATATTAATGATGAAATGAA 480
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Db 40271 GAATATCAAAAAGATATCTTATTTAAAAATATATTAATGATGAAATGAA 40330
481 GCTTATATCATATGATAGTTTATATCATCTGACGACGACGAAAAATTAACGATAT 540
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Db 40331 GCTTATATCATATGATAGTTTATATCATCTGACGACGACGAAAAATTAACGATAT 40390
541 AATCTTATCTTGATTAATTTGAGACAGTTTATGTCAGAAAGTTTAAATTAACAGACT 600
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Db 40391 AATCTTATCTTGATTAATTTGAGACAGTTTATGTCAGAAAGTTTAAATTAACAGACT 40450
601 TCGATTAAGAAAGATATATTTAAATTAACAGAGAGATTTAAATGA 651
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Db 40451 TCGATTAAGAAAGATATATTTAAATTAACAGAGAGATTTAAATGA 40501

RESULT 4
AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS

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 KHEDDKLSVYNNVANDTQILVCGAPVYEAQKVVAVGAVWPSGAVIKQALRGV
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 complement(8279. .9136)
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 /note="ORFID:MM1686"
 /codon_start=1
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 /protein_id="BAB95551.1"
 /db_xref="GI:21204856"
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 LNAIVAKYEDKEKIVDEIVYVYDEALAQMDKLTLESISSQINPVIKATSFQDKRQ
 GVFETIDETRAETAVYVADLQKSYRLIDSNLEDKLTBOQIREKSLNPKRKNISY
 KTDVEKNGKTFYFINSDGQDASRLINTAFINELIACQCGEALVAVPHQVLIADIRN
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 /codon_start=1
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 /db_xref="GI:21204857"
 /translation="MKQLCSQFESLQGVYFETAMQPCDQRYTEPDLPELARY
 PMEDVYSDNDKQKELINGINGIPSELYVKNGELLSQYIGKRRKSLQIDAFQAY
 V"
 complement(9612. .10688)

gene
CDS
/gene="NM1688"
complement(9612..10688)
/gene="NM1688"
/note="ORFID:NM1688
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/codon_start=1
/transl_table=11
/protein_id="BAB9553.1"
/db_xref="GI:21204858"
/translation="MNINKKVTLLQRIQLTEHGAPGEFEENKYNVQQMAPYVDEFI
ENRMGFFGVKSKRNPNKRNVMIAHMEIGFMTNTKNGIQFTNLGVANDIMWG
ORLVIKRNNGDKTIGVSNIPKHFRTGEGAPETKDLTDIGANDDEVREBERGDIQD
TIVPTPTQLSHRYSKAKMDRKGCLAEILELTKRIELDPDLVGVANVGEVEL
RKAKSABMIDPDAFVVDSPANDKSGPLSGELKGTFLRKIDGTMLKPVFRDY
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/translation="MTKLKTIPTIIYAVIISTISIIQYINRKNPNVNLNWK
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R"
complement(11211..12053)
/gene="NM1690"
complement(11211..12053)
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/note="ORFID:NM1690"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
Query Match 100.0%; Score 651; DB 1; Length 272850;
Best Local Similarity 100.0%; Pred. No. 4,5e-73;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGAGAAATATAGAGCATATATACCTTAGAGAGAGGTGTGCTTTATCA 60
DB 250006 ATGAAGAGAAATATAGAGCATATATACCTTAGAGAGAGGTGTGCTTTATCA 249947
QY 61 GTTAAAGATTTTATGATTTTACGATTTCACTTACACGCTTAAAAATCAATTA 120
DB 249946 GTTAAAGATTTTATGATTTTACGATTTCACTTACACGCTTAAAAATCAATTA 249887
QY 121 GAACAATATATCCGATATATTTAGATTTTAAAAAGCTAAAAAGATTTGAGCT 180
DB 249886 GAACAATATATCCGATATATTTAGATTTTAAAAAGCTAAAAAGATTTGAGCT 249827

QY 181 TATATTATCCAGACAGATGAAATTTTATGATTTTGAATGAGTCTTTAT 240
DB 249826 TATATTATCCAGACAGATGAAATTTTATGATTTTGAATGAGTCTTTAT 249767
QY 241 AATTGATTAAGCAAGTAAAAAGCGTATGAAAATGTTTGGATTTAGCAAAATGAT 300
DB 249766 AATTGATTAAGCAAGTAAAAAGCGTATGAAAATGTTTGGATTTAGCAAAATGAT 249707
QY 301 AATTATCAAAATGAGTAAAGCAATGGAATTTTAAAGTATGATTTCAACATGATTT 360
DB 249706 AATTATCAAAATGAGTAAAGCAATGGAATTTTAAAGTATGATTTCAACATGATTT 249647
QY 361 AGTACAAATGAGATTTTATATCGTCTTTGTTATGGAACAAATGCTATTAAT 420
DB 249646 AGTACAAATGAGATTTTATATCGTCTTTGTTATGGAACAAATGCTATTAAT 249587
QY 421 GAATATCAAAAGATATATCTTATTTAAAAATATATATTAATGAATGAATAGA 480
DB 249586 GAATATCAAAAGATATATCTTATTTAAAAATATATTAATGAATGAATAGA 249527
QY 481 GCTTATATCATATATGATTTTATCATCTCAGATGACGAGAAAAATTAACGATTA 540
DB 249526 GCTTATATCATATATGATTTTATCATCTCAGATGACGAGAAAAATTAACGATTA 249467
QY 541 AATCTTATCTGATTAATTTGAAGAACGTTAGTCAAAAAGTTTAAATTAACGAAT 600
DB 249466 AATCTTATCTGATTAATTTGAAGAACGTTAGTCAAAAAGTTTAAATTAACGAAT 249407
QY 601 TCGATTAAGAAAGATATATTTATTTAAACAAGAGATTTAAATGA 651
DB 249406 TCGATTAAGAAAGATATATTTATTTAAACAAGAGATTTAAATGA 249356
Search completed: October 14, 2004, 16:00:24
Job time : 3346.74 secs

OM nucleic - nucleic search, using mw model

Run on: October 14, 2004, 07:30:59 ; Search time 434 Seconds
(without alignments)

6372.297 Million cell updates/sec

Title: US-09-407-804a-5

Perfect score: 651
Sequence: 1 atgaacagagacataatagg.....acaaagagagatttaataga 651

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N_Geneseq_29Jan04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2003as:*\n8: geneseqn2003bs:*\n9: geneseqn2003cs:*\n10: geneseqn2004as:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	651	100.0	651	3	AAA68249
2	651	100.0	41708	3	AA68247 Bacterioph
3	651	100.0	41708	4	AA68247 Bacterioph
4	91.2	14.0	4985	6	AB075107 Complete
5	91.2	14.0	4985	9	ACF79720 Mosquito
6	91	14.0	8056	7	AB210246 Haematopo
7	89.6	13.8	8056	7	AB210246 Haematopo

8	83.2	12.8	8056	7	AB210100	Ab210100 Haematopo
9	82	12.6	8056	7	AB210100	Ab210100 Haematopo
10	80.2	12.3	1830	6	AB156243	AB156243 AmePV met
11	80.2	12.3	32392	6	AB156203	AB156203 AmePV gen
12	79.6	12.2	7892	6	ABK40056	ABK40056 Human che
13	78.6	12.1	50000	6	AB135643	AB135643 AmePV gen
14	78	12.0	7695	6	AB133536	AB133536 Human imm
15	78	12.0	7695	6	AB192258	AB192258 Chemical1
16	77.4	11.9	11143	4	AB112834	AB112834 Drosophila
17	77.2	11.9	34688	6	AB067060	AB067060 Human ang
18	76.2	11.7	6437	6	AB133261	AB133261 Human imm
19	76	11.7	7171	6	ABN80217	ABN80217 Human che
20	75.8	11.6	15743	6	ABK28395	ABK28395 DNA trans
21	75.4	11.6	6106	4	AA546429	AA546429 Tumour su
22	75.4	11.6	6106	6	ABK40031	ABK40031 Human che
23	75.4	11.6	6106	6	AB133472	AB133472 Human imm
24	75.4	11.6	15548	6	AB134155	AB134155 Human imm
25	75.2	11.6	9810	6	AB132426	AB132426 Human imm
26	74.8	11.5	6106	4	AA546429	AA546429 Tumour su
27	74.8	11.5	6106	6	ABK40031	ABK40031 Human che
28	74.8	11.5	6106	6	AB133472	AB133472 Human imm
29	74.8	11.5	19124	2	AA772882	AA772882 Plasmodiu
30	74.8	11.5	19124	2	AA772882	AA772882 Plasmodiu
31	74.8	11.5	50000	6	AB156202	AB156202 AmePV gen
32	74.6	11.5	6106	4	AA546430	AA546430 Tumour su
33	74.6	11.5	6106	6	ABK40032	ABK40032 Human che
34	74.6	11.5	6106	6	AB133473	AB133473 Human imm
35	74.6	11.5	7722	3	AA470168	AA470168 Plasmodiu
36	73.6	11.3	3255	2	AA598608	AA598608 Nucleic a
37	73.6	11.3	9810	6	AB132427	AB132427 Human imm
38	73.4	11.3	3567	3	AA470117	AA470117 Plasmodiu
39	73.4	11.3	110000	6	ABK2787_3	ABK2787_3 Continuati
40	73.2	11.2	7597	6	AB133013	AB133013 Human imm
41	73.2	11.2	15548	6	AB134155	AB134155 Human imm
42	72.8	11.2	969	6	AB039490	AB039490 Oligonuc
43	72.8	11.2	969	6	AB039491	AB039491 Oligonuc
44	72.4	11.1	831	6	AB156245	AB156245 AmePV NTP
45	72.4	11.1	50000	6	AB15644	AB15644 AmePV gen

ALIGNMENTS

RESULT 1	AAA68249	standard; DNA; 651 BP.
ID	AAA68249	
XX	AC	AAA68249;
XX	AC	AAA68249;
DT	15-SEP-2003	(revised)
DT	06-AUG-2003	(revised)
DT	27-OCT-2000	(first entry)
XX	XX	
DE	Bacteriophage 77	77ORF019 nucleotide sequence.
XX	XX	
RW	Bacteriophage; antimicrobial; genome; identification; antibacterial;	
RW	Bacterial growth inhibition; bacterial infection; ds.	

XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by *Staphylococcus*
PT aureus.
PS
XX
XX Disclosure: Fig 2, 107pp; English.

CC This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from *S.*
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially *Staphylococcus*, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX

SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 other;

Query Match 100.0%; Score 651; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACGACAAATATAGAGCATATATACCTTACGAGAGGTGTGCTTTATTC 60
DB 39851 ATGAACGACAAATATAGAGCATATATACCTTACGAGAGGTGTGCTTTATTC 39910
QY 61 GTAAAGAGATTTTAGGATTTTACAGATTCTACAGCTAAAGTAAATCAATT 120
DB 39911 GTAAAGAGATTTTAGGATTTTACAGATTCTACAGCTAAAGTAAATCAATT 39970
QY 121 GAACAAATATATCGATATATTTAGATTGTTTAAAGGCTAAAGATGATGGAGCT 180
DB 39971 GAACAAATATATCGATATATTTAGATTGTTTAAAGGCTAAAGATGATGGAGCT 40030
QY 181 TATATTATTCACAGAACGATGATTTTGAATTTTGAATTTGATGAGCTTTAT 240
DB 40031 TATATTATTCACAGAACGATGATTTTGAATTTTGAATTTGATGAGCTTTAT 40090
QY 241 AATTAGATACGAAAGTAAAGGCTATGAAATGTTATGGATTAGCAAAATGAT 300
DB 40091 AATTAGATACGAAAGTAAAGGCTATGAAATGTTATGGATTAGCAAAATGAT 40150
QY 301 AATTATCAAAATAGGTTAAGGCAATGAAAGATTTAAGATGATTCACATGATTT 360
DB 40151 AATTATCAAAATAGGTTAAGGCAATGAAAGATTTAAGATGATTCACATGATTT 40210
QY 361 AGTCAAAATCAGATTTTAACTCTTTGTTATGAAACAATGCTATTATTAAT 420
DB 40211 AGTCAAAATCAGATTTTAACTCTTTGTTATGAAACAATGCTATTATTAAT 40270
QY 421 GAATATCAAAAGATATATCTTATTTAAATATATTAATGAATGAATTAAGA 480
DB 40271 GAATATCAAAAGATATATCTTATTTAAATATATTAATGAATGAATTAAGA 40330
QY 481 GCTTATATCATATTGATGATTTTATCATCTGAGTACGAGGAAAAATAAAGATTAT 540
DB 40331 GCTTATATCATATTGATGATTTTATCATCTGAGTACGAGGAAAAATAAAGATTAT 40390

DB 40331 GCTTATATCATATTGATGATTTTATCATCTGAGTACGAGGAAAAATAAAGATTAT 40390
QY 541 AATCTTATCTGTAAATTTGAGAACAGTTTACGAAAGTTTAAATTAACAGACT 600
DB 40391 AATCTTATCTGTAAATTTGAGAACAGTTTACGAAAGTTTAAATTAACAGACT 40450
QY 601 TCGATTAAGAAAGATATTTATTTAATTTAAACAGAGATTTAAATGA 651
DB 40451 TCGATTAAGAAAGATATTTATTTAATTTAAACAGAGATTTAAATGA 40501
Search completed: October 14, 2004, 12:48:12
Job time : 436 secs

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 3040.61 Seconds

(without alignments)
6393.544 Million cell updates/sec

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

28: gb_gss1:.*
29: gb_gss2:.*

Title: US-09-407-804A-5
Perfect score: 651
Sequence: 1 atgacagcagcacaataag.....acaagagagagattcaatga 651
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_gssba:.*
2: em_gssbun:.*
3: em_gsscln:.*
4: em_gsscmu:.*
5: em_gsscov:.*
6: em_gsscp1:.*
7: em_gsscp2:.*
8: em_gsscp3:.*
9: gb_gsscl:.*
10: gb_gsscl2:.*
11: gb_gsscl3:.*
12: gb_gsscl4:.*
13: gb_gsscl5:.*
14: gb_gsscl6:.*
15: em_gssclun:.*
16: em_gssclun2:.*
17: em_gssclun3:.*
18: em_gssclun4:.*
19: em_gssclun5:.*
20: em_gssclun6:.*
21: em_gssclun7:.*
22: em_gssclun8:.*
23: em_gssclun9:.*
24: em_gssclun10:.*
25: em_gssclun11:.*
26: em_gssclun12:.*
27: em_gssclun13:.*

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	121.6	18.7	1101	29	CNS00EVL
2	105.2	16.2	1201	9	AL536104
3	104.8	16.1	1200	13	BK437758
4	102	15.7	1200	13	BK415878
5	100.8	15.5	1201	13	BK443774
6	100	15.4	1201	13	BK439779
7	99.2	15.2	1101	29	CNS003BD
8	98.8	15.2	1200	13	BK415878
9	98.6	15.1	1101	29	CNS00E07
10	98	15.1	1056	13	BK415058
11	98	15.1	1201	9	AL536104
12	97.4	15.0	999	13	BK380865
13	97.2	14.9	1201	13	BK420717
14	97	14.9	1201	13	BK426629
15	97	14.9	1277	28	CC253231
16	96.6	14.8	781	29	BK145762
17	96.2	14.8	1064	13	BK361825
18	94.2	14.5	1101	29	CNS00E07
19	93.8	14.4	1201	13	BK458623
20	93.6	14.4	964	13	BK341256
21	92.2	14.2	1098	13	BK377526
22	91.2	14.0	1348	29	CG749499
23	91	14.0	829	29	BK173672
24	90.8	13.9	641	28	AQ946120
25	90.6	13.9	707	29	CG403361
26	90.2	13.9	893	12	BP507314
27	90.2	13.9	1092	29	CNS020K7
28	90	13.8	886	28	BH177277
29	89.6	13.8	1056	13	BK415058
30	89.6	13.8	886	29	CNS07JUX
31	89.6	13.8	1201	13	BK462660
32	89.4	13.7	1201	9	AL565455
33	89.4	13.7	1201	13	BK340226
34	89.4	13.7	1272	28	CC264939
35	89.4	13.7	1392	29	CG757503
36	89	13.7	1200	13	BK437739
37	88.8	13.6	660	28	BH183498
38	88.8	13.6	660	29	CNS070NJ
39	88.8	13.6	670	28	B2388480
40	88.8	13.6	975	13	BK414927
41	88.8	13.6	1201	13	BK366070
42	88.4	13.6	1101	29	CNS003BD
43	88.4	13.6	1133	13	BK444099
44	88.2	13.5	700	28	AQ940248
45	87.4	13.4	1206	28	B2695529

Search completed: October 14, 2004, 18:55:08
Job time : 3043.61 secs

OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 09:12:14 ; Search time 1339.78 Seconds
(without alignments)

8443.595 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: 261
Sequence: 1 atgtatttcgaatacagcga.....acttgatcatgaattgtag 261

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: 1: gb_ba: 2: gb_hvg: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_ey: 12: gb_ay: 13: gb_un: 14: gb_vl: 15: em_da: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_cm: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_ey:

28: em_un: 29: em_vl: 30: em_hvg_hum: 31: em_hvg_inv: 32: em_hvg_other: 33: em_hvg_mus: 34: em_hvg_pin: 35: em_hvg_rtd: 36: em_hvg_mam: 37: em_hvg_vrt: 38: em_ey: 39: em_hvg_hum: 40: em_hvg_mus: 41: em_hvg_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	261	100.0	261	6	BD245277
2	261	100.0	297	6	BD245280
3	261	100.0	41708	6	BD245281
4	261	100.0	41708	6	AR368770
5	257.8	98.8	41401	7	AB009866
6	256.2	98.2	42942	7	AB045978
7	256.2	98.2	348527	1	AP003360
8	254.6	97.3	45636	7	AB044534
9	253	96.9	43081	7	AP001553
10	133	51.0	348650	1	AP003364
11	131.4	50.3	580	6	AR355085
12	131.4	50.3	43594	6	BD245634
13	131.4	50.3	43604	7	AR424781
14	128.4	49.2	258	6	AK618548
15	121.8	46.7	42722	7	AF424783
16	121.8	46.7	272850	1	AP004828
17	118.8	45.5	267	6	AK618246
18	101	38.7	291150	1	AP003135
19	47.4	18.2	82281	8	AC025295
20	47.4	18.2	192780	9	AL162723
21	45.8	17.5	207726	2	AC024953
22	45.8	17.5	209287	9	AC012077
23	45.2	17.3	200473	2	AC133762
24	45.2	17.3	254977	2	AC117353
25	45	17.2	110000	2	AC112311_2
26	45	17.2	175406	5	BX000522
27	45	17.2	241807	2	AC126077
28	44.5	17.2	248933	2	AC109773
29	44.4	17.0	156060	2	AC004153
30	44.4	17.0	184090	10	AC122304
31	44.4	17.0	250707	3	AE014848
32	44.2	16.9	138807	9	AL161650
33	44	16.9	238646	2	AC099463

ALIGNMENTS

RESULT 1

COMMENT

C12N15/00
PC A61K31/00

FEATURES	Location/Qualifiers
SOURCE	1. .261

ORIGIN

QY 1 ATGTATTTACGAAATAGCGGAATCATACGCAAAAATATTCATGTTAACGATTCAATTTT 60
|||||

0
1
2
3
4
5
6

VERSION BD245280.1 GI:33055050
KEYWORDS JP 2002531107-A/15.

FT aureus bacteriophage 77' /organism='Staphylococcus aureus bacteriophage 77'

FEATURES source Location/Qualifiers 1..297 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"

Query Match 100.0%; Score 261; DB 6; Length 297; Best Local Similarity 100.0%; Pred. No. 6.7e-45; Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTACGAAATAGCGCAATCATACGCAAAATATTCATGTAAAGGATTCGATTT 60
DB 37 ATGATTACGAAATAGCGCAATCATACGCAAAATATTCATGTAAAGGATTCGATTT 96
QY 61 AAGCTATTCATTTAAAGGTCATATGGCATATCATACAGTTAAAGATGAAAC 120
DB 97 AAGCTATTCATTTAAAGGTCATATGGCATATCATACAGTTAAAGATGAAAC 156
QY 121 GTACCAATTAAACATGCTTATGTCTAGATGAGATGACTTAAGTGGCATCACTTA 180
DB 157 GTACCAATTAAACATGCTTATGTCTAGATGAGATGACTTAAGTGGCATCACTTA 216
QY 181 TTTAACCAAGCATAGATGATGATGAAAGAAACAGACAGACAGACACTAAT 240
DB 217 TTTAACCAAGCATAGATGATGATGAAAGAAACAGACAGACAGACACTAAT 276
QY 241 AACTAGTCATGAATGGTAG 261
DB 277 AACTAGTCATGAATGGTAG 297

RESULT 3
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS Development of novel antibiotics based on bacteriophage genomics.
DEFINITION
ACCESSION BD245281 GI:33055051
VERSION BD245281.1
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL PHAGE TECH INC Patent: JP 2002531107-A 16 24-SEP-2002;
COMMENT 05 Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY

PELLETIER, PHILIPPE, GROS, MICHAEL, DUBOW
PC C12N13/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
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CC Genome Sequence
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FT source Location/Qualifiers
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LOCUS AR368770
DEFINITION Sequence 3 from patent US 637652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus

aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-APR-2002;
FEATURES Location/Qualifiers

source 1..41708
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Best Local Similarity 100.0%; Pred. No. 3,88-45;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTACGAAATGAGCGAAATCATACGAAATATCATGTACGATTCGATTTT 60
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RESULT 5
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LOCUS Bacteriophage phi PVL proviral DNA, complete sequence.
DEFINITION AB009866
ACCESSION AB009866
VERSION AB009866.2 GI:8031688
KEYWORDS dUTPase; ssDNA binding protein; anti repressor; repressor; integrase; LukF-PV; LukS-PV; holin; amidase (peptidoglycan hydrolase); capsid protein; portal protein.
SOURCE Staphylococcus aureus bacteriophage PVL
ORGANISM Staphylococcus aureus bacteriophage PVL
REFERENCE 1 Vituase; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
AUTHORS Kaneo, Y., Kimura, T., Kawakami, Y., Tomita, T. and Kamio, Y.
TITLE Pantom-valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (sites)
AUTHORS Kaneo, Y., Kimura, T., Narita, S., Tomita, T. and Kamio, Y.
TITLE Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPVL carrying Pantom-Valentine leukocidin genes

JOURNAL Gene 215 (1), 57-67 (1998)
MEDLINE 98332719
PUBMED 9666077
REFERENCE 3 (bases 1 to 41401)
AUTHORS Kaneo, Y., Kimura, T., Narita, S., Tomita, T. and Kamio, Y.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1997) Jun Kaneo, Tohoku University, Dept. Appl. Biol. Chem., Faculty of Agriculture, 1-1 Tsurumi-dori, Aomiyamaechi, Aoba-ku, Sendai, Miyagi 981, Japan (E-mail: jkaneob@biochem.tohoku.ac.jp, Tel: 81-22-717-8781, Fax: 81-22-717-8780)

COMMENT On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
FEATURES Location/Qualifiers

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```

FEATURES
  SOURCE
    Sendai, Miyagi 981-5555, Japan
    (E-mail: j.kaneko@ci.ochim.tohoku.ac.jp, Tel: 81-22-717-8761,
    Fax: 81-22-747-8780)
    location/Qualifiers
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RESULT 7
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AP003360.2 GI:14246388
VERSION
AP003360.2 GI:14246388
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Staphylococcus aureus subsp. aureus Mu50
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Staphylococcus aureus subsp. aureus Mu50
REFERENCE
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1
Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Imai, J., Ito, T., Kanamori, M.,
Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A.,
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Sekimizu, K., Hiraoka, H., Kuwano, S., Goto, S., Yabuzaki, J.,
Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiratake, K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
JOURNAL
Lancet 357 (9264), 1225-1240 (2001)
MEDLINE
2131952
PUBMED
11418146

REFERENCE
2 (bases 1 to 348527)
Ohta, T.
Direct Submission
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology, 1-1-1 Ten-noda, Tsukuba, Ibaraki 305-8577, Japan
(E-mail: tohta@tsukuba.ac.jp, Tel: 81-298-53-3454,
Fax: 81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13874937.
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Query Match 98.2%; Score 256.2; DB 1; Length 348527;
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Matches 258; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 230674 ATGATTACGAATAGCGCAATCTACGCAAAATATCATGTACGATTCGATTT 230733
OY 61 AACCTATTCATTTAAAGGTCAATGCGCATATCATACATAGCTTAAAGATGAAAC 120
DB 230734 AACCTATTCATTTAAAGGTCAATGCGCATATCATACATAGCTTAAAGATGAAAC 230793
OY 121 GACCAATTAAACGCTTATGTCGTAGATGAGAAATGACTTATGATGGCATCACTTA 180
DB 230794 GACCAATTAAACGCTTATGTCGTAGATGAGAAATGACTTATGATGGCATCACTTA 230853
OY 181 TTAAACCAAGCATATGATGATTTGAAAGAAACAGACAGACAGACAGATTA 240
DB 230854 TTAAACCAAGCATATGATGATTTGAAAGAAACAGACAGACAGACAGATTA 230913
OY 241 AACTTAGTCATGAATGCTAG 261
DB 230914 AACTTAGTCATGAATGCTAG 230934

RESULT 8
LOCUS AB044554 45636 bp DNA linear PHG 04-JUL-2000
DEFINITION *Staphylococcus aureus* prophage phiPV83 proviral DNA, complete
sequence.
AB044554
ACCESSION AB044554.1 GI:8918747
VERSION
KEYWORDS
SOURCE *Staphylococcus aureus* prophage phiPV83
ORGANISM *Staphylococcus aureus* prophage phiPV83
1 (ntes)
REFERENCE
AUTHORS Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
TITLE Pantom-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated *Staphylococcus aureus* V8 (ATCC 49775)
JOURNAL Biorat. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE
AUTHORS Zou,D., Kaneko,J., Narita,S. and Kamio,Y.

TITLE Complete nucleotide sequence and molecular characterization of
prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in
Staphylococcus aureus strain P83
Unpublished
JOURNAL 3 (bases 1 to 45636)
REFERENCE
AUTHORS Kaneko,J., Zou,D. and Kamio,Y.
TITLE Direct Submission
Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural Science, 1-1 Tsutsumi-dori Aamamach,1,
Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail:jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-717-8780)

FEATURES
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Location/Qualifiers
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CDS
CDS

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Best Local Similarity 96.5%; Pred. No. 8.2e-44;
Matches 257; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 61 AAGCATTCATTTAAAGGTCAATGGCATTCATCAAGTTAAAGATGAAAC 120
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DB 7035 AAGCATTCATTTAAAGGTCAATGGCATTCATCAAGTTAAAGATGAAAC 7094
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QY 121 GTACCAATTAAACATGCTATGTGTGATGATGAGATGACTAGATATGGCATCACTTA 180
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DB 7095 GTACCAATTAAACATGCTATGTGTGATGATGAGATGACTAGATATGGCATCACTTA 7154
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QY 181 TTACCAAGCATAGATGATGATGAGCAACACAGACAGACAGACTAAT 240
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DB 7155 TTACCAAGCATAGATGATGATGAGCAACACAGACAGACAGACTAAT 7214
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QY 241 AACTAGTCATGAATGCTAG 261
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DB 7215 AACTAGTCATGAATGCTAG 7235
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RESULT 9
LOCUS AP001553 43081 bp DNA circular PHG 14-MAR-2001
DEFINITION Bacteriophage phi ETA DNA, complete genome.
ACCESSION AP001553
VERSION AP001553.1 GI:8918415
KEYWORDS
SOURCE Bacteriophage phi ETA
ORGANISM Bacteriophage phi ETA
REFERENCE 1 (sites)
Yamaguchi, T., Hayashi, T., Takami, H., Nakasone, K., Ohnishi, M.,
Nakayama, K., Yamada, S., Komatsu, H., and Sugai, M.,
Phage conversion of exfoliative toxin A production in
Staphylococcus aureus
JOURNAL Mol. Microbiol. 38 (4), 694-705 (2000)
MEDLINE 20566787
PUBMED 1115106
REFERENCE 2 (bases 1 to 43081)
Sugai, M., Yamaguchi, T., Hayashi, T., Nakasone, K. and Takami, H.

CDS

TITLE Direct Submission
JOURNAL Submitted (28-Mar-2000) Motoyuki Sugai, Hiroshima University
Faculty of Dentistry, Microbiology/ Kaasumi 1-2-3, Hiroshima,
Hiroshima 734-8553, Japan (E-mail: sugai@hiroshima-u.ac.jp,
Tel:81-82-257-5637, Fax:81-82-257-5639)
FEATURES
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 FPRMLKGFEEENTDYTAIAGKRAITAGQNMHHYIDHALTIDPAKETAMQREBGRKAR
 QYFQVQKMANSPENIQRAKIANNTINGLETIERDKRTYFADAVATKTSILVG
 ELAKTIKQNGINIQQRLFEWLNQNGELIRKGVDPNPTQYSMEHELFEIKETSITH
 SDGHTSISKTPVTKGQGVFNKFLQTYT"
 complement(5731..6396)
 CDS
 /note="ORF12
 unknown
 /codon_start=1
 /transl_table=11
 /protein_id="BA97598.1"
 /db_xref="GI:8918427"
 /translation="MNNINFTORQDLIKKQQAISKLPEYEAAYAKAATNANSYVANA
 LEIQSTVNNVANSIRINOSKLSDMASYHQVTKNHPMKNTLSEKTIDEFISNSFP
 DDEVKRYSTHLKSPVDTPVDPVLEKTVNSAPIDNNVTESDKTFYISINQFIAPS
 SSFVHDSITLVAKSYAVNPFRTANDDYVNFSTAVIAVAVASCLNNAFDLNNRK
 DK"
 6467..6688
 CDS
 /note="ORF13
 unknown
 /codon_start=1
 /transl_table=11
 /protein_id="BA97599.1"
 /db_xref="GI:8918428"
 /translation="MINSIQAKELAVLISVSKSAQGITREINKLEDEGYIAINGR
 IPVQLARKKFPYHDSQRIAMELKKENE"
 6681..6842
 CDS
 /note="ORF14
 similar to phage phi PVL ORF38"
 /codon_start=1
 /transl_table=11
 /protein_id="BA97600.1"
 /db_xref="GI:8918429"
 /translation="MSRTKSYLAVLCTVIAIVLWPEFLYFTTANSTAGASIAITFI
 FYKIFYEE"
 6936..7196
 CDS
 /note="ORF15
 similar to phage phi PVL ORF39"
 /codon_start=1
 /transl_table=11
 /protein_id="BA97601.1"
 /db_xref="GI:8918430"
 /translation="MYYEIGEIIIRKIHVNGDFDKIFILKGHGKISIQVKDNNVPIK
 HAYVDDNDLMAASDLNQALDEWIEENTDEQDRILINLNNRW"
 7206..7427
 CDS
 /note="ORF16
 unknown
 /codon_start=1
 /transl_table=11

/protein_id="BA97602.1"
/db_xref="GI:8918431"
/translation="MNOVTYII RHNDPIYINKPTINNDSVSYSTNNRAREFNGM
EEASINDYHKAI KKTVEITEYEVEHD"
7420..8199
/note="ORF17
unknown"
/codon_start=1
/transl_table=11
/protein_id="BA97603.1"
/db_xref="GI:8918432"

Query Match 96.9%; Score 253; DB 7; Length 43081;
Basic Similarity 98.1%; Pred. No. 1.8e-43;
Matches 256; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGATTACGAATAGCGAAATCATACGCAAAATATTCATGTACGATTCGATTT 60
|||||
DB 6936 ATGATTACGAATAGCGAAATCATACGCAAAATATTCATGTACGATTCGATTT 6995
|||||
QY 61 AAGCTATTCATTTAAAGGTCATATGGGCATATCATACAGTTAAAGATGAAAC 120
|||||
DB 6996 AAATATTCATTTAAAGGTCATATGGGCATATCATACAGTTAAAGATGAAAC 7055
|||||
QY 121 GTACCAATTAAACATGCTATGTCCTATGATGAGATGCTTATGCTATGCTT 180
|||||
DB 7056 GTACCAATTAAACATGCTATGTCCTATGATGAGATGCTTATGCTATGCTT 7115
|||||
QY 181 TTAAACCAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 240
|||||
DB 7116 TTAAACCAAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 7175
|||||
QY 241 AACTTAGTCATGAATGCTAG 261
|||||
DB 7176 AACTTAGTCATGAATGCTAG 7196
|||||

Search completed: October 14, 2004, 16:00:28
Job time : 1343.78 secs

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OM nucleole - nucleole search, using sw model

Run on: October 14, 2004, 07:30:59 ; Search time 174 Seconds
(without alignments)
6372.297 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: 261
Sequence: 1 atgattacgaatagcgaa.....acttagcatgaatgctag 261

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04: +
1: geneseqn1980s: +
2: geneseqn1990s: +
3: geneseqn2000s: +
4: geneseqn2001s: +
5: geneseqn2001bs: +
6: geneseqn2002s: +
7: geneseqn2003s: +
8: geneseqn2003bs: +
9: geneseqn2003cs: +
10: geneseqn2004s: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	100.0	261	3	AAA68250 Bacterioph
2	261	100.0	297	3	AAA68253 Bacterioph
3	261	100.0	41708	3	AAA68247 Bacterioph
4	261	100.0	41708	4	AA086106 Complete
5	131.4	50.3	380	2	AAV75514 Staphyloc
6	131.4	50.3	43576	3	AAA68609 Bacterioph
7	128.4	49.2	258	7	ACF73076 Staphyloc

8	118.8	45.5	267	ACF72925	AcF72925 Staphyloc
c	9	41.4	15.9	ABIS5563	AbI55563 AmePV gen
10	38.6	14.8	3365	ABLO6224	AbI06224 Drosophil
11	38.4	14.7	110000	ABA90521_07	Continuation (8 of
12	38.4	14.7	110000	ABA90521_08	Continuation (9 of
c	13	37.8	14.5	AA661395	AA661395 Human gen
c	14	37.8	14.5	AA646588	AA646588 Human gen
c	15	37.8	14.5	AB133841	AbI33841 Human imm
16	37.8	14.5	32392	ABIS6203	AbI56203 AmePV gen
17	37.6	14.4	2685	ACA28606	ACA28606 Prokaryot
c	18	37.4	14.3	ACA52799	ACA52799 Prokaryot
c	19	37.4	14.3	AA791010	AA791010 Full-10ng
c	20	37.4	14.3	ABX14745	AbI14745 cDNA enco
21	37.2	14.3	6835	AA13141	AA13141 Enterococ
22	37.2	14.3	6835	AB598936	Ab598936 Enterococ
c	23	37	14.2	AA792531	AA792531 Rat T2R04
c	24	37	14.2	AB132991	AbI32991 Human imm
c	25	37	14.2	AB149302	AbI49302 Human imm
c	26	36.8	14.1	7319	AB134044 Human imm
c	27	36.6	14.0	3534	ACA28380 Prokaryot
28	36.6	14.0	5686	AA646462	AA646462 Tumour su
c	29	36.6	14.0	AAV74570	AAV74570 Staphyloc
c	30	36.4	13.9	AA546613	AA546613 Tumour su
31	36.2	13.9	924	AAA70276	AAA70276 Plasmodiu
c	32	36.2	13.9	7158	ABLO6684 Drosophil
c	33	36.2	13.9	17594	AbI34027 Human imm
c	34	36.2	13.9	50000	AbI55644 AmePV gen
35	36	13.8	17848	AA545322	AA545322 Chemicall
36	36	13.8	17848	ABK39975	AbK39975 Human che
37	36	13.8	17848	ABK28163	AbK28163 DNA trans
38	35.8	13.7	994	AAV27429	AAV27429 streptoco
39	35.8	13.7	994	AB084897	Ab084897 S. pneumo
40	35.8	13.7	994	ADC45392	ADC45392 S. pneumo
41	35.8	13.7	1033	AAV27419	AAV27419 Streptoco
42	35.8	13.7	1033	AB084887	Ab084887 S. pneumo
43	35.8	13.7	1033	ADC45272	ADC45272 S. pneumo
44	35.8	13.7	1110	ABX06325	Abx06325 S. pneumo
45	35.8	13.7	1112	AAA05427	AA05427 Streptoco

ALIGNMENTS

RESULT 1
 ID AAA68250 standard; DNA; 261 BP.
 AC AAA68250;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 77ORF043 nucleotide sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.

XX	Staphylococcus aureus; bacteriophage 77.
OS	WO200032825-A2.
XX	
PN	08-JUN-2000.
XX	
PD	
XX	
PF	03-DEC-1999; 99WO-1B002040.
XX	
PR	03-DEC-1998; 98US-0110992P.
PR	03-JUN-1999; 99US-00326144.
PR	28-SEP-1999; 99US-00407804.
PR	30-SEP-1999; 99US-0157218P.
PR	01-DEC-1999; 99US-0168777P.
PR	02-DEC-1999; 99US-00454252.
PA	(PHAG-) PHAGEGEN INC.
XX	
PI	Pelletier J, Gros P, Dubow M,
XX	WPI; 2000-412361/35.
DR	P-PSDB; AAB16525.
XX	
PT	Identifying a bacteriophage coding region for treating bacterial
PT	infections comprises identifying a nucleic acid encoding a product that
XX	inhibits bacteria when a bacteriophage infects a bacterium.
XX	
PS	Disclosure; Page 157; 456pp; English.
XX	
CC	The present invention describes a method for identifying a bacteriophage
CC	coding region encoding a product active on an essential bacterial target.
CC	The method comprises identifying a nucleic acid sequence encoding a gene
CC	product that provides a bacteria-inhibiting function when an
CC	uncharacterized bacteriophage infects a pathogenic bacterium. The
CC	compound active on a target of a bacteriophage inhibitor protein in a
CC	bacteria is used to treat or prevent a bacterial infection in an animal.
CC	AA68243 to AA69442 and AAB16923 to AAB16954 represent bacteriophage
CC	nucleotide and protein sequences which are used in the exemplification of
CC	the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC	(Updated on 15-SEP-2003 to standardise OS field)
XX	
SQ	Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
XX	
QY	Query Match 100.0%; Score 261; DB 3; Length 261;
Db	Best Local Similarity 100.0%; Pred. No. 9.2e-57;
QY	Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	ATGATATACGAAATAGCGAAATATCGAAATATTCATGTTAAGGATTCATTTT 60
1	ATGATATACGAAATAGCGAAATATCGAAATATTCATGTTAAGGATTCATTTT 60
61	AAGCTATTCATTTTAAAGGTCATATGGGCATATCAATCAAGTAAGATGAACAC 120
61	AAGCTATTCATTTTAAAGGTCATATGGGCATATCAATCAAGTAAGATGAACAC 120
121	GTACCAATTAACATGCTATGCTAGATGAGATGACTAGATGATGATGATGATGAT 180

Db 121 GTACCAATTAACGCTATGTGCTAGATGGAATGACTAGATGGCATCAGACTTA 180

Qy 181 TTAAACCAAGCATATGATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 240

Db 181 TTAAACCAAGCATATGATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 240

Qy 241 AACTTAGTCATGAATGGTAG 261

Db 241 AACTTAGTCATGAATGGTAG 261

RESULT 2

AAA68253

ID AAA68253 standard; DNA; 297 BP.

XX

AC AAA68253;

XX

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX

DE Bacteriophage 77 77ORF182 nucleotide sequence.

XX

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; ds.

XX

OS Staphylococcus aureus; bacteriophage 77.

XX

PN WO200032825-A2.

PD 08-JUN-2000.

XX

PF 03-DEC-1999; 99WO-1B002040.

XX

PR 03-DEC-1999; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00454252.

XX

PA (PHAG-) PHAGETECH INC.

XX

PI Polletier J, Gros P, Dubow M;

XX

DR WPI, 2000-412361/35.

DR P-PSDB; AAB16528.

XX

XX Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

XX

PS Disclosure; Page 165; 456pp; English.

XX

CC The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a

CC bacteria is used to treat or prevent a bacterial infection in an animal.

CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

CC nucleotide and protein sequences which are used in the exemplification of

CC the present invention. (updated on 06-AUG-2003 to correct OS field.)

CC (updated on 15-SEP-2003 to standardise OS field)

XX

SQ Sequence 297 BP; 123 A; 40 C; 57 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 261; DB 3; Length 297;

Best Local Similarity 100.0%; Pred. No. 9.5e-57;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTTACGAATATAGCGAATCATACGCAAAATATCATGTTAAGGATTCATTT 60

Db 37 ATGATTTACGAATATAGCGAATCATACGCAAAATATCATGTTAAGGATTCATTT 96

Qy 61 AAGCTATTCATTTTAAAGGTCATATGGCATATCAATACAGTTAAAGATGAAACAC 120

Db 97 AAGCTATTCATTTTAAAGGTCATATGGCATATCAATACAGTTAAAGATGAAACAC 156

Qy 121 GTACCAATTAACGCTATGTGCTAGATGGAATGACTAGATGGCATCAGACTTA 180

Db 157 GTACCAATTAACGCTATGTGCTAGATGGAATGACTAGATGGCATCAGACTTA 216

Qy 181 TTAAACCAAGCATATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 240

Db 217 TTAAACCAAGCATATGATGATTTGAAGAAACACAGACAGACAGACTTAAT 276

Qy 241 AACTTAGTCATGAATGGTAG 261

Db 277 AACTTAGTCATGAATGGTAG 297

RESULT 3

AAA68247

ID AAA68247 standard; DNA; 41708 BP.

XX

AC AAA68247;

XX

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX

DE Bacteriophage 77 complete genome sequence.

XX

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; ds.

XX

OS Staphylococcus aureus; bacteriophage 77.

XX

PN WO200032825-A2.

PD 08-JUN-2000.

XX

PF 03-DEC-1999; 99WO-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGE TECH INC.
XX
PI Pelletier J, Gros P, Dubow M;
XX
DR WPI, 2000-412361/35.
XX
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS Example 3; Page 141-151; 456pp; English.
XX
CC The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 261; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2,5e-56;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTATTACGAATAGCGAATCATACGCAAAATATTATGTTAGAGATTGATTTT 60
DB 29304 ATGTATTACGAATAGCGAATCATACGCAAAATATTATGTTAGAGATTGATTTT 29363
OY 61 AAGCTATTCATTTTAAAGGTCATATGGCATATCATACAAGTTAAAGATATGAACAC 120
DB 29364 AAGCTATTCATTTTAAAGGTCATATGGCATATCATACAAGTTAAAGATATGAACAC 29423
OY 121 GTACCAATTAAACATGCTATATGCTAGATGAGATGACTTATGATGGCATCAAGCTTA 180.
DB 29424 GTACCAATTAAACATGCTATATGCTAGATGAGATGACTTATGATGGCATCAAGCTTA 29483
OY 181 TTACCAAGCAATAGATGATGATGAGAGAACAGACAGACAGACAGACATAT 240
DB 29484 TTACCAAGCAATAGATGATGATGAGAGAACAGACAGACAGACAGACATAT 29543
OY 241 AACTTAGTCATGAATGCTAG 261
|||||

DB 29544 AACTTAGTCATGAATGCTAG 29564
RESULT 4
AAC86106
ID AAC86106 standard; cDNA; 41708 BP.
XX
XX AAC86106;
AC
XX
DT 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
XX Complete genome of bacteriophage 77.
XX
XX DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
XX screening assay; ss.
XX
OS Bacteriophage.
XX
XX WO200146383-A2.
XX
XX 28-JUN-2001.
XX
XX 21-DEC-2000; 2000WO-US035180.
XX
XX 22-DEC-1999; 99US-00470512.
XX 12-OCT-2000; 2000US-00689952.
XX
XX (PHAG-) PHAGE TECH INC.
XX (WILL/) WILLIAMS K M.
XX
XX Pelletier J, Gros P, Dubow M;
XX
XX WPI, 2001-418052/44.
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
XX preferably bacterial, diseases such as those caused by *Staphylococcus*
XX *aureus*.
XX
XX Disclosure; Fig 2; 107pp; English.
XX
XX This sequence represents the genome of Bacteriophage 77. The growth
XX inhibitory gene product of ORF 104 interacts with DnaI derived from *S.*
XX *aureus*, to form the basis of a screening assay. DnaI polypeptides and
XX polynucleotides are useful for treating microbial, preferably bacterial,
XX especially *Staphylococcus*, infections. DnaI polypeptides and
XX polynucleotides are useful for biological, diagnostic, prophylactic,
XX clinical and therapeutic use, and as components in databases useful for
XX search analyses as well as in sequence analysis algorithms. (Updated on
XX 06-AUG-2003 to correct OS field.)
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 261; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2,5e-56;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTATTACGAAATAGCGAAATCATACGAAATATTCATGTACGATTCATTTT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29304 ATGTATTACGAAATAGCGAAATCATACGAAATATTCATGTACGATTCATTTT 29363
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 AAGCTATTCATTTTAAAGGTCATATGGCATTCATACAGTTAAAGATATGACAC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29364 AAGCTATTCATTTTAAAGGTCATATGGCATTCATACAGTTAAAGATATGACAC 29423
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTAAATGGCATCACTTA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29424 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTAAATGGCATCACTTA 29483
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 TTAAACCAAGCAATAGTGAATGATTTGAAAGACACACACACACACACACACTAAT 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29484 TTAAACCAAGCAATAGTGAATGATTTGAAAGACACACACACACACACACTAAT 29543
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 AACTTAGTCATGAATGCTAG 261
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29544 AACTTAGTCATGAATGCTAG 29564
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: October 14, 2004, 12:48:14
 Job time : 176 secs

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OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 12:03:47 ; Search time 1219.05 Seconds
 (without alignments)
 6393.544 Million cell updates/sec

Title: US-09-407-804A-6

Perfect score: .261

Sequence: 1 atgattacgaataagcgga.....acttagcatgaatgtag 261

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vr1:*

28: gb_gsa1:++
29: gb_gsa2:++

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	46.4	17.8	1083	29	CNS009YQ	A054505	Drosophila
2	45.6	17.5	328	28	AZ923265	AZ923265	4908.gf205
3	43.6	16.7	700	28	BH371930	BH371930	AG-ND-1320
4	42.6	16.3	1101	29	CNS001FB	AL060732	Drosophila
5	42.4	16.2	509	28	BZ842685	BZ842685	CH240.276
6	42.2	16.2	1044	13	BK415231	BK415231	BK415231
7	41.8	16.0	519	28	AZ525518	AZ525518	244PBH11
8	41.8	16.0	571	28	AZ526884	AZ526884	260PB612
9	41.6	15.9	706	28	BH954338	BH954338	cdh21b04
10	41.6	15.9	924	28	AZ674753	AZ674753	ENTHU31TR
11	41.4	15.9	988	13	BK410403	BK410403	BK410403
12	41.4	15.9	1101	29	CNS00HOT	AL072991	Drosophila
13	41.2	15.8	801	14	CA508813	CA508813	UT-R-F50-
14	41	15.7	1097	29	CNS01235	AL101650	Drosophila
15	40.8	15.6	561	14	CD526186	CD526186	kw31f06.y
16	40.6	15.6	523	14	CF263276	CF263276	AUA IPTes
17	40.6	15.6	954	14	CA788983	CA788983	AGENCOURT
18	40.4	15.5	538	28	BH296850	BH296850	CH230-13P
19	40.4	15.5	592	12	BJ368128	BJ368128	BJ368128
20	40.4	15.5	692	28	BZ011251	BZ011251	oel12a10
21	40.2	15.4	1453	28	CC294053	CC294053	CH261-175
22	39.8	15.2	284	10	BB381549	BB381549	BB381549
23	39.8	15.2	523	28	AA550417	AA550417	1568m3 gm
24	39.8	15.2	737	12	BM160122	BM160122	EST562645
25	39.8	15.2	759	29	CNS060XY	AL411257	T7 end of
26	39.6	15.2	621	28	AZ178178	AZ178178	SP_0149.A
27	39.6	15.2	948	12	BG286502	BG286502	602382994
28	39.6	15.2	1101	29	CNS007AB	AL066914	Drosophila
29	39.4	15.1	549	9	AL388772	AL388772	MBEC50F05
30	39.4	15.1	880	13	BK464942	BK464942	BK464942
31	39.4	15.1	926	28	AZ137368	AZ137368	SP_0175.F
32	39.4	15.1	1287	14	CF222655	CF222655	AGENCOURT
33	39.2	15.0	425	13	BU496326	BU496326	PESTOac0
34	39.2	15.0	430	9	AV879351	AV879351	AV879351
35	39.2	15.0	623	29	CE633602	CE633602	tigr-gas-
36	39.2	15.0	644	29	DR28C4T	AL984585	Danio rerio
37	39.2	15.0	661	29	AG153453	AG153453	Pan troglodytes
38	39.2	15.0	849	14	CB943202	CB943202	AGENCOURT
39	39	14.9	286	10	BB514506	BB514506	BB514506
40	39	14.9	292	10	BB065040	BB065040	BB065040
41	39	14.9	296	10	BB156700	BB156700	BB156700
42	39	14.9	297	10	BB485740	BB485740	BB485740
43	39	14.9	318	10	BB273660	BB273660	BB273660
44	39	14.9	369	9	AU270532	AU270532	AU270532
45	39	14.9	588	29	AG238463	AG238463	Lotus corniculatus

Search completed: October 14, 2004, 18:55:12
Job time : 1223.05 secs

OW nucleic - nucleic search, using sw model

Run on: October 14, 2004, 19:00:14 ; Search time 831.658 seconds
(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-7

Perfect score: 162
Sequence: 1 atgagcaacattatataaag.....aatgctttctcaagaactaa 162

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167131695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:
1: gb_ba:.*
2: gb_hvg:.*
3: gb_in:.*
4: gb_cm:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sta:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_de:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_om:.*
21: em_or:.*
22: em_ov:.*
23: em_pat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sta:.*

28: em_un:.*
29: em_vl:.*
30: em_hvg_hum:.*
31: em_hvg_inv:.*
32: em_hvg_other:.*
33: em_hvg_mus:.*
34: em_hvg_pin:.*
35: em_hvg_rod:.*
36: em_hvg_mam:.*
37: em_hvg_vrt:.*
38: em_sy:.*
39: em_hvgc_hum:.*
40: em_hvgc_mus:.*
41: em_hvgc_other:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	162	100.0	162	6	BD245278
2	162	100.0	41708	6	BD245281
3	162	100.0	41708	6	AR368770
4	74	45.7	159	6	AX583668
5	67	41.4	159	6	AX618544
6	67	41.4	1408	6	AR354422
7	67	41.4	43604	7	AF424781
8	67	41.4	291150	1	AP003135
9	65	40.1	43095	6	BD245282
10	55	34.0	43594	6	BD245634
11	50	30.9	45636	7	AB044554
12	41	25.3	348527	1	AP003360
13	36	22.2	42722	7	AF424783
14	36	22.2	27850	1	AP004828
15	36	22.2	348650	1	AP003364
16	35	21.6	41401	7	AB009866
17	32	19.8	333750	1	AP004827
18	28	17.3	43081	7	AP001553
19	26	16.0	2049	6	AR354173
20	26	16.0	27650	1	AC090967
21	26	16.0	42942	7	AB045978
22	26	16.0	44970	7	AF424782
23	23	14.2	25	6	BD245934
24	21	13.0	25	6	BD245869
25	20	12.3	195607	2	AC117567
26	20	12.3	222621	2	AC119890
27	19	11.7	4279	9	BC035013
28	19	11.7	4725	9	BC028603
29	19	11.7	4983	6	AX056364
30	19	11.7	5181	9	AB023182
31	19	11.7	13484	1	AF400047
32	19	11.7	13484	1	AY044156
33	19	11.7	110283	9	AC093245

34	c	19	11.7	116783	9	AC092829	AC092829 Homo sapi	91	18	11.1	173359	2	AC021536	AC021536 Homo sapi
35	c	19	11.7	132775	10	AL671899	AL671899 Mouse DNA	92	18	11.1	173746	2	AC024040	AC024040 Homo sapi
36	c	19	11.7	141819	5	AL935063	AL935063 Zebrafish	93	18	11.1	176046	2	BX601643	BX601643 Homo sapi
37	c	19	11.7	145021	2	AC093257	AC093257 Homo sapi	94	18	11.1	176048	5	AL929314	AL929314 Zebrafish
38	c	19	11.7	158588	2	AC092273	AC092273 Homo sapi	95	18	11.1	182297	2	BX571738	BX571738 Homo sapi
39	c	19	11.7	160984	9	AC092453	AC092453 Homo sapi	96	18	11.1	188848	10	AC116709	AC116709 Homo sapi
40	c	19	11.7	161823	2	AC136947	AC136947 Homo sapi	97	18	11.1	190732	2	AC142150	AC142150 Homo sapi
41	c	19	11.7	161970	2	AC021737	AC021737 Homo sapi	98	18	11.1	194170	2	AC138401	AC138401 Homo sapi
42	c	19	11.7	163693	9	AC087879	AC087879 Homo sapi	99	18	11.1	202438	2	AC116145	AC116145 Homo sapi
43	c	19	11.7	168434	2	BX294123	BX294123 Dantio rer	100	18	11.1	203212	2	AC122469	AC122469 Homo sapi
44	c	19	11.7	192400	2	AC022712	AC022712 Homo sapi	101	18	11.1	206470	2	AC135811	AC135811 Homo sapi
45	c	19	11.7	201437	2	AC015981	AC015981 Homo sapi	102	18	11.1	206966	9	AC021850	AC021850 Homo sapi
46	c	19	11.7	221526	10	AC117668	AC117668 Mus muscu	103	18	11.1	210998	2	AC101667	AC101667 Homo sapi
47	c	19	11.7	235320	2	AC106175	AC106175 Rattus no	104	18	11.1	211465	2	AC103070	AC103070 Rattus no
48	c	19	11.7	235327	2	AC093463	AC093463 Rattus no	105	18	11.1	212455	10	AC108419	AC108419 Mus muscu
49	c	19	11.7	239624	2	AC093365	AC093365 Mus muscu	106	18	11.1	212445	2	AC108419	AC108419 Mus muscu
50	c	19	11.7	245146	2	AC130643	AC130643 Rattus no	107	18	11.1	214256	10	AC123108	AC123108 Mus muscu
51	c	19	11.7	245323	2	AC111925	AC111925 Rattus no	108	18	11.1	214468	2	AC123108	AC123108 Mus muscu
52	c	19	11.7	248333	2	AC097869	AC097869 Rattus no	109	18	11.1	220495	10	AL732525	AL732525 Homo sapi
53	c	19	11.7	253903	2	AC121208	AC121208 Rattus no	110	18	11.1	228355	10	AL731839	AL731839 Homo sapi
54	c	19	11.7	254875	2	AC095125	AC095125 Rattus no	111	18	11.1	234595	2	AC110204	AC110204 Homo sapi
55	c	19	11.7	254975	2	AC095125	AC095125 Rattus no	112	18	11.1	234950	2	AC109079	AC109079 Homo sapi
56	c	19	11.7	262183	1	CJ11168X4	AF315795 Paplo ham	113	18	11.1	237754	10	AC125576	AC125576 Homo sapi
57	c	18	11.1	538	8	AY189701	AY189701 Pheillus	114	18	11.1	241610	2	AC093465	AC093465 Homo sapi
58	c	18	11.1	33498	3	CEZK593	CEZK593 Homo sapi	115	18	11.1	247108	2	AC123333	AC123333 Homo sapi
59	c	18	11.1	57578	9	AL589825	AL589825 Human DNA	116	18	11.1	252283	2	AC126977	AC126977 Homo sapi
60	c	18	11.1	59441	9	AC109588	AC109588 Homo sapi	117	18	11.1	254844	2	AC125555	AC125555 Homo sapi
61	c	18	11.1	60791	9	AC004749	AC004749 Homo sapi	118	18	11.1	262050	2	AC105575	AC105575 Homo sapi
62	c	18	11.1	79041	9	AC009016	AC009016 Homo sapi	119	18	11.1	265423	2	AC128960	AC128960 Homo sapi
63	c	18	11.1	79851	9	AC034252	AC034252 Homo sapi	120	18	11.1	272677	2	AC097289	AC097289 Homo sapi
64	c	18	11.1	80402	8	AB025636	AB025636 Arabidops	121	18	11.1	281660	2	AC127837	AC127837 Homo sapi
65	c	18	11.1	89017	2	AC135193	AC135193 Rattus no	122	18	11.1	281957	2	AC095956	AC095956 Homo sapi
66	c	18	11.1	111701	2	AC144405	AC144405 Medicago	123	18	11.1	318115	2	AC098550	AC098550 Homo sapi
67	c	18	11.1	11367	8	AF058826	AF058826 Arabidops	124	17	10.5	546	11	BV067122	BV067122 Homo sapi
68	c	18	11.1	11367	10	AL596447	AL596447 Mouse DNA	125	17	10.5	609	11	G91194	G91194 Homo sapi
69	c	18	11.1	116261	9	AL555357	AL555357 Human DNA	126	17	10.5	674	14	AB057066	AB057066 Homo sapi
70	c	18	11.1	122557	2	AC011429	AC011429 Homo sapi	127	17	10.5	834	1	AB086272	AB086272 Homo sapi
71	c	18	11.1	129608	8	OSJN00214	AL663013 Oryza sat	128	17	10.5	835	14	AB086272	AB086272 Homo sapi
72	c	18	11.1	132119	9	AC008497	AC008497 Homo sapi	129	17	10.5	1067	3	AF438039	AF438039 Homo sapi
73	c	18	11.1	133345	9	AL356294	AL356294 Human DNA	130	17	10.5	1379	6	BD249104	BD249104 Homo sapi
74	c	18	11.1	138094	8	AC141113	AC141113 Medicago	131	17	10.5	1529	5	BC054177	BC054177 Homo sapi
75	c	18	11.1	138224	9	AC096562	AC096562 Homo sapi	132	17	10.5	1923	8	AK064446	AK064446 Homo sapi
76	c	18	11.1	139401	2	AC124406	AC124406 Mus muscu	133	17	10.5	3000	1	AP525506	AP525506 Homo sapi
77	c	18	11.1	139490	2	BX640536	BX640536 Dantio rer	134	17	10.5	6477	6	AK653060	AK653060 Homo sapi
78	c	18	11.1	145115	8	AC096690	AC096690 Oryza sat	135	17	10.5	10410	1	AE010782	AE010782 Homo sapi
79	c	18	11.1	148088	4	AC096883	AC096883 Sus scrofa	136	17	10.5	10717	1	AE010553	AE010553 Homo sapi
80	c	18	11.1	149273	10	AL928732	AL928732 Mouse DNA	137	17	10.5	11730	1	AE010579	AE010579 Homo sapi
81	c	18	11.1	158472	9	AC146247	AC146247 Pan trogl	138	17	10.5	11815	1	AE001262	AE001262 Homo sapi
82	c	18	11.1	158472	9	AC146247	AC146247 Homo sapi	139	17	10.5	12500	1	AE001261	AE001261 Homo sapi
83	c	18	11.1	161341	2	AL929055	AL929055 Mus muscu	140	17	10.5	16341	1	AF178757	AF178757 Homo sapi
84	c	18	11.1	163828	8	AC104433	AC104433 Oryza sat	141	17	10.5	18092	9	AL590874	AL590874 Homo sapi
85	c	18	11.1	166074	5	AL645307	AL645307 Zebrafish	142	17	10.5	38231	8	AB072893	AB072893 Homo sapi
86	c	18	11.1	167168	2	AC115907	AC115907 Mus muscu	143	17	10.5	39709	2	AC145431	AC145431 Homo sapi
87	c	18	11.1	168049	2	AC022830	AC022830 Homo sapi	144	17	10.5	50737	2	AC020294	AC020294 Homo sapi
88	c	18	11.1	168353	2	AC146598	AC146598 Mus muscu	145	17	10.5	54355	6	AK695644	AK695644 Homo sapi
89	c	18	11.1	168527	2	AC040993	AC040993 Homo sapi	146	17	10.5	62464	9	AL139164	AL139164 Homo sapi
90	c	18	11.1	172337	8	AC133007	AC133007 Oryza sat	147	17	10.5	68273	9	AL138695	AL138695 Homo sapi

c 148	17	10.5	68678	2	AC126334	Homo sapi	c 205	17	10.5	152309	9	AC138185	AC138185 Homo sapi
c 149	17	10.5	70282	2	AC091141	Homo sapi	c 206	17	10.5	152905	2	AC104480	AC104480 Sus scrofa
c 150	17	10.5	70983	2	AC134259	Rattus no	c 207	17	10.5	153472	9	AC011179	AC011179 Homo sapi
c 151	17	10.5	90440	2	AC123574	Medicago	c 208	17	10.5	153814	9	AC095063	AC095063 Homo sapi
c 152	17	10.5	90657	2	AC131755	Homo sapi	c 209	17	10.5	154055	9	AC157774	AC157774 Homo sapi
c 153	17	10.5	90696	2	AC017624	Drosophila	c 210	17	10.5	155348	5	AL1928820	AL1928820 Zebrafish
c 154	17	10.5	91155	2	AC026450	Homo sapi	c 211	17	10.5	156466	2	AL139181	AL139181 Homo sapi
c 155	17	10.5	95553	4	AC124804	Equus cab	c 212	17	10.5	157023	9	AL165360	AL165360 Homo sapi
c 156	17	10.5	96396	6	AC093595	Sequence	c 213	17	10.5	157306	9	AL161417	AL161417 Human DNA
c 157	17	10.5	101098	8	AC002427	Arabidops	c 214	17	10.5	157534	2	AC090100	AC090100 Homo sapi
c 158	17	10.5	107271	8	ATT0416	Arabidops	c 215	17	10.5	157706	5	AL1928936	AL1928936 Homo sapi
c 159	17	10.5	109476	6	AL133548	Human DNA	c 216	17	10.5	158213	2	AC016865	AC016865 Homo sapi
c 160	17	10.5	110000	2	AC098456	Rattus no	c 217	17	10.5	158486	2	BX649350	BX649350 Dario rer
c 161	17	10.5	110000	2	AC129939	Mus muscu	c 218	17	10.5	159565	9	AP001318	AP001318 Homo sapi
c 162	17	10.5	110000	2	AC143189	Continuation (3 of	c 219	17	10.5	160004	9	AL139318	AL139318 Homo sapi
c 163	17	10.5	110000	2	AY294423	Continuation (2 of	c 220	17	10.5	160013	9	AL133325	AL133325 Human DNA
c 164	17	10.5	110000	9	AY129465	Continuation (3 of	c 221	17	10.5	160180	10	AL129016	AL129016 Homo sapi
c 165	17	10.5	111876	8	ATF4110	Arabidops	c 222	17	10.5	160502	2	AC139369	AC139369 Homo sapi
c 166	17	10.5	113148	8	HSBG54N10	Human DNA	c 223	17	10.5	160612	9	AP005856	AP005856 Homo sapi
c 167	17	10.5	113266	8	AC092262	Oryza sat	c 224	17	10.5	160739	9	AP001092	AP001092 Homo sapi
c 168	17	10.5	115224	9	AL356234	Human DNA	c 225	17	10.5	160922	2	AC104848	AC104848 Homo sapi
c 169	17	10.5	115306	9	AC008615	Homo sapi	c 226	17	10.5	162246	10	BX000428	BX000428 Mouse DNA
c 170	17	10.5	119374	9	AC018763	Homo sapi	c 227	17	10.5	162739	9	AL353788	AL353788 Human DNA
c 171	17	10.5	122630	2	AC012434	Homo sapi	c 228	17	10.5	162976	9	AC114301	AC114301 Homo sapi
c 172	17	10.5	123109	2	AC007149	Drosophila	c 229	17	10.5	164117	5	ALB44513	ALB44513 Zebrafish
c 173	17	10.5	123889	2	AC115872	Mus muscu	c 230	17	10.5	164404	2	AC027149	AC027149 Homo sapi
c 174	17	10.5	124786	8	AC115285	Homo sapi	c 231	17	10.5	164620	9	AC110721	AC110721 Homo sapi
c 175	17	10.5	126323	8	AC132215	Genomic s	c 232	17	10.5	164735	2	AC090475	AC090475 Homo sapi
c 176	17	10.5	128749	2	AC145811	Oryza sat	c 233	17	10.5	164907	3	AC007146	AC007146 Drosophila
c 177	17	10.5	129167	8	AC113433	Oryza sat	c 234	17	10.5	165178	2	AC025355	AC025355 Homo sapi
c 178	17	10.5	129398	6	AL596276	Human DNA	c 235	17	10.5	165236	9	AC024255	AC024255 Homo sapi
c 179	17	10.5	130218	2	CNS08C81	Oryza sat	c 236	17	10.5	165644	9	AC011352	AC011352 Homo sapi
c 180	17	10.5	130372	2	CNS08C92	Rattus no	c 237	17	10.5	166653	2	AC115862	AC115862 Homo sapi
c 181	17	10.5	130801	2	AC141188	Rattus no	c 238	17	10.5	167099	2	AC104486	AC104486 Sus scrofa
c 182	17	10.5	131042	10	AC110166	Mus muscu	c 239	17	10.5	167604	2	AC084017	AC084017 Homo sapi
c 183	17	10.5	131577	2	AC146333	Medicago	c 240	17	10.5	167629	9	AL353595	AL353595 Human DNA
c 184	17	10.5	131577	2	AC146333	Medicago	c 241	17	10.5	168010	2	AC132984	AC132984 Rattus no
c 185	17	10.5	133028	8	AP003447	Oryza sat	c 242	17	10.5	168259	2	AC009936	AC009936 Homo sapi
c 186	17	10.5	133400	2	AC134521	Medicago	c 243	17	10.5	168484	9	AC113366	AC113366 Homo sapi
c 187	17	10.5	134725	2	AC091852	Homo sapi	c 244	17	10.5	168728	2	AC026183	AC026183 Homo sapi
c 188	17	10.5	139754	2	AC124322	Mus muscu	c 245	17	10.5	169891	2	AC114479	AC114479 Homo sapi
c 189	17	10.5	140597	9	AC074270	Homo sapi	c 246	17	10.5	169988	2	BX321875	BX321875 Dario rer
c 190	17	10.5	140934	9	AC009491	Homo sapi	c 247	17	10.5	170114	9	AC044790	AC044790 Homo sapi
c 191	17	10.5	141459	2	BX539347	Dario rer	c 248	17	10.5	171127	2	AC024527	AC024527 Homo sapi
c 192	17	10.5	141834	8	AP003445	Oryza sat	c 249	17	10.5	171744	9	CNS01D99	CNS01D99 Homo sapi
c 193	17	10.5	145009	2	AC141949	Rattus no	c 250	17	10.5	172061	2	AC027156	AC027156 Homo sapi
c 194	17	10.5	145122	9	AC025588	Homo sapi	c 251	17	10.5	172366	9	AC004949	AC004949 Homo sapi
c 195	17	10.5	146368	2	AC022651	Medicago	c 252	17	10.5	172618	2	AC144822	AC144822 Dario rer
c 196	17	10.5	148247	10	AL935057	Mouse DNA	c 253	17	10.5	173154	2	AC019132	AC019132 Homo sapi
c 197	17	10.5	148841	9	AC110794	Homo sapi	c 254	17	10.5	173383	5	AL929216	AL929216 Zebrafish
c 198	17	10.5	149391	9	AC093825	Homo sapi	c 255	17	10.5	173520	9	AL732423	AL732423 Homo sapi
c 199	17	10.5	149646	10	AC122482	Mus muscu	c 256	17	10.5	174383	5	AL929216	AL929216 Zebrafish
c 200	17	10.5	149849	9	AL190678	Human DNA	c 257	17	10.5	175100	2	AC132241	AC132241 Mus muscu
c 201	17	10.5	150547	2	AC102787	Mus muscu	c 258	17	10.5	175100	2	AC132241	AC132241 Mus muscu
c 202	17	10.5	150934	2	AC022252	Homo sapi	c 259	17	10.5	175100	2	AC132241	AC132241 Mus muscu
c 203	17	10.5	150955	2	AL356111	Human DNA	c 260	17	10.5	175100	2	AC132241	AC132241 Mus muscu
c 204	17	10.5	151682	2	AC147146	Mus muscu	c 261	17	10.5	175100	2	AC132241	AC132241 Mus muscu

262	17	10.5	175158	2	AC120531	Oryza sat
263	17	10.5	175483	9	AL445258	Human DNA
264	17	10.5	175965	10	AC121921	Mus muscu
265	17	10.5	175977	3	AC007470	Drosophill
266	17	10.5	177662	2	AC013665	Homo sapi
267	17	10.5	178273	2	AC099620	Mus muscu
268	17	10.5	178414	2	AC025341	Homo sapi
269	17	10.5	178448	2	AC134419	Mus muscu
270	17	10.5	179138	9	CNS0786V	Human chr
271	17	10.5	179798	9	AL359532	Human DNA
272	17	10.5	179862	9	CNS05TEE	Human chr
273	17	10.5	180192	2	AC058810	Homo sapi
274	17	10.5	180213	3	AC010847	Drosophill
275	17	10.5	181058	2	AC068118	Homo sapi
276	17	10.5	181463	10	AC122452	Mus muscu
277	17	10.5	181852	2	AC120866	Mus muscu
278	17	10.5	183619	2	AC104485	Sus scrof
279	17	10.5	183976	9	AC100821	Homo sapi
280	17	10.5	184032	9	AC079926	Homo sapi
281	17	10.5	184701	2	AC136630	Homo sapi
282	17	10.5	184752	2	AC125845	Homo sapi
283	17	10.5	185212	2	BX572088	Mus muscu
284	17	10.5	185324	2	AC026265	Homo sapi
285	17	10.5	186321	2	AC134738	Rattus no
286	17	10.5	191081	2	AC023143	Homo sapi
287	17	10.5	191634	2	AC112755	Rattus no
288	17	10.5	192651	2	AC142465	Rattus no
289	17	10.5	193826	9	AL131379	Human DNA
290	17	10.5	194808	2	AC120857	Mus muscu
291	17	10.5	194869	5	AL954136	Zebrafish
292	17	10.5	196591	2	AC091082	Homo sapi
293	17	10.5	196617	2	AC115134	Rattus no
294	17	10.5	198190	2	AC136446	Homo sapi
295	17	10.5	198386	9	AC079789	Homo sapi
296	17	10.5	199280	2	AC079364	Mus muscu
297	17	10.5	199536	8	ATGRI179	Arabidops
298	17	10.5	199913	2	AC121308	Mus muscu
299	17	10.5	200512	2	AC135358	Mus muscu
300	17	10.5	201429	2	AC109375	Rattus no
301	17	10.5	202229	2	AC128611	Rattus no
302	17	10.5	202774	2	AC108851	Rattus no
303	17	10.5	202915	10	AC116703	Mus muscu
304	17	10.5	203047	10	AL928922	Mouse DNA
305	17	10.5	203326	9	AC105479	Rattus no
306	17	10.5	203300	9	AC000134	Homo sapi
307	17	10.5	207050	2	AC123667	Mus muscu
308	17	10.5	207304	4	AC125499	Equus cab
309	17	10.5	207411	2	AC084746	Mus muscu
310	17	10.5	207625	2	AC140270	Mus muscu
311	17	10.5	208670	9	AC103588	Homo sapi
312	17	10.5	209003	2	AC073724	Mus muscu
313	17	10.5	211041	2	AC116413	Mus muscu
314	17	10.5	212246	10	AC123686	Mus muscu
315	17	10.5	212253	2	AC140184	Mus muscu
316	17	10.5	213375	2	AC129581	Mus muscu
317	17	10.5	213721	9	HS172820	Human DNA
318	17	10.5	215435	10	AC124752	Mus muscu
319	17	10.5	215850	2	AC138285	Mus muscu
320	17	10.5	216386	2	AC113795	Rattus no
321	17	10.5	217097	2	AC112080	Rattus no
322	17	10.5	218131	2	AC105635	Rattus no
323	17	10.5	222964	2	AC117649	Mus muscu
324	17	10.5	223711	2	AC112697	Rattus no
325	17	10.5	223794	2	AC145076	Mus muscu
326	17	10.5	224044	10	AL935326	Mouse DNA
327	17	10.5	224346	2	BX530018	Dentio rex
328	17	10.5	225490	2	AC140213	Mus muscu
329	17	10.5	225538	2	AC108577	Rattus no
330	17	10.5	225648	2	AC133459	Mus muscu
331	17	10.5	225782	2	AC109529	Rattus no
332	17	10.5	227459	2	AC127039	Rattus no
333	17	10.5	227682	2	AC131460	Rattus no
334	17	10.5	228080	2	AC134938	Rattus no
335	17	10.5	230127	10	AL691481	Mouse DNA
336	17	10.5	230567	2	AC111696	Rattus no
337	17	10.5	232842	2	AC109880	Rattus no
338	17	10.5	235024	2	AC120681	Rattus no
339	17	10.5	235129	2	AC130145	Rattus no
340	17	10.5	236237	2	AC106297	Rattus no
341	17	10.5	238543	2	AC133701	Rattus no
342	17	10.5	238560	2	AC114016	Rattus no
343	17	10.5	239475	2	AC122116	Rattus no
344	17	10.5	240181	2	AC098105	Rattus no
345	17	10.5	240272	2	AC097809	Rattus no
346	17	10.5	241100	2	AC095453	Rattus no
347	17	10.5	243613	2	AC105517	Rattus no
348	17	10.5	243822	2	AC094751	Rattus no
349	17	10.5	244866	2	AC097571	Rattus no
350	17	10.5	246401	2	AC094195	Rattus no
351	17	10.5	248835	2	AC097256	Rattus no
352	17	10.5	249181	2	AC130997	Rattus no
353	17	10.5	249995	3	AE014840	Plasmodiu
354	17	10.5	250360	2	AC106965	Rattus no
355	17	10.5	250586	2	AC094879	Rattus no
356	17	10.5	252230	2	AC114944	Homo sapi
357	17	10.5	252374	2	AC105618	Rattus no
358	17	10.5	254366	2	AC125987	Rattus no
359	17	10.5	254578	10	AC109253	Mus muscu
360	17	10.5	258545	2	AC136666	Rattus no
361	17	10.5	259790	2	AC106956	Rattus no
362	17	10.5	261236	2	AC119381	Rattus no
363	17	10.5	262718	2	AC106366	Rattus no
364	17	10.5	265750	2	BX539323	Dentio rex
365	17	10.5	266175	3	AE003633	Drosophill
366	17	10.5	266188	2	AC103296	Rattus no
367	17	10.5	268342	2	AC144457	Homo sapi
368	17	10.5	273959	2	AC11814	Rattus no
369	17	10.5	281085	2	AC123455	Rattus no
370	17	10.5	281926	2	AC094818	Rattus no
371	17	10.5	283769	2	AC094777	Rattus no
372	17	10.5	285841	2	AC126476	Rattus no
373	17	10.5	302529	1	AE016851	Tropheym
374	17	10.5	324050	1	BX251410	Tropheym

c 375	17	10.5	332889	2	AC098450	AC098450 Rattus no	432	16	9.9	1354	3	DAM538207	AJ538207 Drosophila
376	17	10.5	334120	2	AC114017	AC114017 Rattus no	433	16	9.9	1354	3	DAM538211	AJ538211 Drosophila
377	17	10.5	339193	2	AC098394	AC098394 Rattus no	434	16	9.9	1354	3	DAM538213	AJ538213 Drosophila
378	17	10.5	342650	1	AP003582	AP003582 Neotoma sp	435	16	9.9	1354	3	DAM538216	AJ538216 Drosophila
379	17	10.5	346474	3	AE003512	AE003512 Drosophila	436	16	9.9	1354	3	DAM538219	AJ538219 Drosophila
380	16	9.9	25	6	BD45696	BD45696 Drosophila	437	16	9.9	1354	3	DAM538225	AJ538225 Drosophila
381	16	9.9	149	9	565841S04	565844 gamma-actin	438	16	9.9	1354	3	DAM538201	AJ538201 Drosophila
382	16	9.9	250	11	GJ5137	GJ5137 human STS S	439	16	9.9	1355	3	DAM538204	AJ538204 Drosophila
c 383	16	9.9	253	11	BK276154	BK276154 Arabidopsis	440	16	9.9	1355	3	DAM538205	AJ538205 Drosophila
384	16	9.9	284	11	GJ5786	GJ5786 human STS C	441	16	9.9	1355	3	DAM538208	AJ538208 Drosophila
c 386	16	9.9	302	11	BY072730	BY072730 S208P6815	442	16	9.9	1355	3	DAM538209	AJ538209 Drosophila
c 387	16	9.9	334	8	AY199611	AY199611 Arabidopsis	443	16	9.9	1355	3	DAM538210	AJ538210 Drosophila
c 388	16	9.9	361	11	BK663978	BK663978 Arabidopsis	444	16	9.9	1355	3	DAM538218	AJ538218 Drosophila
c 389	16	9.9	400	6	AR356817	AR356817 Sequence	445	16	9.9	1355	3	DAM538228	AJ538228 Drosophila
390	16	9.9	403	1	MGU01787	U01787 Mycoplasma	446	16	9.9	1355	3	DAM538230	AJ538230 Drosophila
391	16	9.9	427	6	AR427627	AR427627 Sequence	447	16	9.9	1356	3	DAM538212	AJ538212 Drosophila
392	16	9.9	427	6	BD123180	BD123180 EST and e	448	16	9.9	1356	3	DAM538214	AJ538214 Drosophila
393	16	9.9	468	1	UPR318208	AJ318208 Unculture	449	16	9.9	1356	3	DAM538215	AJ538215 Drosophila
394	16	9.9	495	6	AK874669	AK874669 Sequence	450	16	9.9	1356	3	DAM538222	AJ538222 Drosophila
395	16	9.9	495	6	BD154731	BD154731 Primer fo	451	16	9.9	1360	3	DAM538227	AJ538227 Drosophila
396	16	9.9	592	8	AJ586321	AJ586321 Fagus cre	452	16	9.9	1367	3	DAM538224	AJ538224 Drosophila
c 397	16	9.9	649	11	G66008	G66008 sy885 Mlase	453	16	9.9	1489	6	AX882999	AX882999 Sequence
c 398	16	9.9	660	11	G67144	G67144 233F8-R Hum	454	16	9.9	1489	6	BD160056	BD160056 Primer fo
c 399	16	9.9	684	11	BY064590	BY064590 S212P6035	455	16	9.9	1489	6	AK023592	AK023592 Homo sapi
400	16	9.9	702	3	AB107990	AB107990 Polyandro	456	16	9.9	1515	5	AF201348	AF201348 Oreochrom
401	16	9.9	753	9	AY459026	AY459026 Pan trogl	457	16	9.9	1722	6	AR379576	AR379576 Sequence
402	16	9.9	755	9	AY459027	AY459027 Pan trogl	458	16	9.9	1782	8	AK071245	AK071245 Oryza sat
403	16	9.9	755	9	AY459028	AY459028 Pan trogl	459	16	9.9	1794	8	AK102584	AK102584 Oryza sat
404	16	9.9	755	9	AY459029	AY459029 Pan trogl	460	16	9.9	1814	1	AF190223	AF190223 Polimetel
405	16	9.9	755	9	AY459030	AY459030 Pan trogl	461	16	9.9	1896	6	AX618652	AX618652 Sequence
406	16	9.9	755	9	AY459031	AY459031 Pan trogl	462	16	9.9	2046	9	AK094627	AK094627 Homo sapi
407	16	9.9	755	9	AY459032	AY459032 Pan trogl	463	16	9.9	2212	6	AX881562	AX881562 Sequence
408	16	9.9	755	9	AY459033	AY459033 Pan trogl	464	16	9.9	2212	6	BD159124	BD159124 Primer fo
409	16	9.9	755	9	AY459034	AY459034 Pan trogl	465	16	9.9	2212	9	AK021757	AK021757 Homo sapi
410	16	9.9	755	9	AY459035	AY459035 Pan trogl	466	16	9.9	2269	8	SCESBP6	SCESBP6 S. cerevisia
411	16	9.9	755	9	AY459036	AY459036 Pan trogl	467	16	9.9	2298	9	HSGAT1MR	HSGAT1MR H. sapiens G
412	16	9.9	755	9	AY459037	AY459037 Pan trogl	468	16	9.9	2349	3	560739	560739 cEGRHecdy
413	16	9.9	755	9	AY459038	AY459038 Pan trogl	469	16	9.9	2366	10	BC014810	BC014810 Mus muscu
414	16	9.9	755	9	AY459039	AY459039 Pan trogl	470	16	9.9	2394	2	AC019569	AC019569 Drosophila
415	16	9.9	795	6	AX434330	AX434330 Sequence	471	16	9.9	2407	5	BC057507	BC057507 Dario rer
c 416	16	9.9	837	11	BY039632	BY039632 S212P6009	472	16	9.9	2630	1	AY036014	AY036014 Bacillus
c 417	16	9.9	846	11	BY035787	BY035787 S212P6046	473	16	9.9	2744	9	BC063868	BC063868 Homo sapi
418	16	9.9	1084	3	AF438064	AF438064 Dypca sp	474	16	9.9	2915	5	BC060000	BC060000 Xenopus 1
c 419	16	9.9	1091	3	AF398659	AF398659 Desera au	475	16	9.9	3027	3	AY061587	AY061587 Drosophila
c 420	16	9.9	1198	3	AF129083	AF129083 Drosophila	476	16	9.9	3124	8	SCN125C	SCN125C BC029230
c 421	16	9.9	1201	3	AF132563	AF132563 Drosophila	477	16	9.9	3322	10	BC029230	BC029230 Mus muscu
422	16	9.9	1349	3	DAM538226	AJ538226 Drosophila	478	16	9.9	3327	1	CCPLASPC1	CCPLASPC1 X62019 C.coli plas
423	16	9.9	1350	3	DAM538221	AJ538221 Drosophila	479	16	9.9	3330	3	AT298857S1	AT298857 Xiphophor
424	16	9.9	1350	3	DAM538229	AJ538229 Drosophila	480	16	9.9	3344	1	CCPLAPCC2	CCPLAPCC2 X62080 C.coli plas
425	16	9.9	1352	3	DAM538206	AJ538206 Drosophila	481	16	9.9	3571	1	PHU07788	PHU07788 Pasteurella
426	16	9.9	1352	3	DAM538220	AJ538220 Drosophila	482	16	9.9	3628	1	PASSAIA	PASSAIA M62363 P.haemolyti
427	16	9.9	1353	3	DAM538200	AJ538200 Drosophila	483	16	9.9	3779	9	BC009650	BC009650 Homo sapi
428	16	9.9	1353	3	DAM538217	AJ538217 Drosophila	484	16	9.9	3920	3	AY119444	AY119444 Drosophila
429	16	9.9	1353	3	DAM538223	AJ538223 Drosophila	485	16	9.9	4438	10	PMU300673	PMU300673 Mus muscu
430	16	9.9	1354	3	DAM538202	AJ538202 Drosophila	486	16	9.9	4455	5	XLCFTRM	X65256 X.laevis CF
431	16	9.9	1354	3	DAM538203	AJ538203 Drosophila	487	16	9.9	4455	5	XLU60209	X60209 Xenopus lae

489	16	9.9	4470	3	AF001796	AF001796 Drosophila	c 546	16	9.9	43081	7	AP001553	AP001553 Bacterioph
490	16	9.9	4493	9	BC033904	BC033904 Homo sapi	c 547	16	9.9	43331	9	HSX297824	AJ297824 Homo sapi
c 491	16	9.9	4467	9	AF513856	AF513856 Stephyloc	c 548	16	9.9	43481	8	SCCKXIV43	Z46843 S. cerevisiae
c 492	16	9.9	5177	9	AB014548	AB014548 Homo sapi	c 549	16	9.9	43594	6	BD245634	BD245634 Drosophila
c 493	16	9.9	5561	9	HUMIL2B	K02056 Human Inter	c 550	16	9.9	43604	7	AF424781	AF424781 Stephyloc
c 494	16	9.9	5693	8	AF533704	AF533704 Pyrenoph	c 551	16	9.9	43927	9	HS0244610	HS0244610 Stephyloc
c 495	16	9.9	5742	7	PIHORS	L77215 Bacterioph	c 552	16	9.9	45878	9	AP003773	AP003773 Human DNA
c 496	16	9.9	6086	8	SCNLI26W	Z77402 S. cerevisiae	c 553	16	9.9	46508	1	AP005352	AP005352 Vibrio vu
c 497	16	9.9	6103	8	AF533703	AF533703 Pyrenoph	c 554	16	9.9	48940	5	AY298859	AY298859 Xiphophor
c 498	16	9.9	6684	9	HSIL105	X00699 Human Inter	c 555	16	9.9	53336	9	AC092600	AC092600 Homo sapi
c 499	16	9.9	6744	9	AF294791	AF294791 Homo sapi	c 556	16	9.9	54874	2	AC139691	AC139691 Homo sapi
c 500	16	9.9	6752	9	AF359939	AF359939 Homo sapi	c 557	16	9.9	55021	6	AC025815	AC025815 Arabidops
c 501	16	9.9	7035	1	LIU60336	LIU60336 Lactococcus	c 558	16	9.9	55417	2	AL390919	AL390919 Homo sapi
c 502	16	9.9	7120	7	AF195902	AF195902 Lactobaci	c 559	16	9.9	55564	3	AB000109	AB000109 Dicyoste
c 503	16	9.9	7608	3	PFA51DN	X85133 P. tetraurel	c 560	16	9.9	55741	2	AC135912	AC135912 Homo sapi
c 504	16	9.9	8154	3	PFA51A	M65163 P. tetraurel	c 561	16	9.9	55741	2	AC008293	AC008293 Drosophila
c 505	16	9.9	8115	8	OSAS35044	AJ35044 Oryza sat	c 562	16	9.9	56328	2	AC068514	AC068514 Homo sapi
c 506	16	9.9	8850	12	AF292555	AF292555 Gfp marke	c 563	16	9.9	58333	2	AC020257	AC020257 Homo sapi
c 507	16	9.9	8850	12	AF292559	AF292559 Yfp marke	c 564	16	9.9	58970	2	AC101231	AC101231 Mus muscu
c 508	16	9.9	8950	12	AF292560	AF292560 Gfp marke	c 565	16	9.9	59356	9	AC115109	AC115109 Homo sapi
c 509	16	9.9	8974	12	AF292556	AF292556 Gfp marke	c 566	16	9.9	59463	9	AC107486	AC107486 Homo sapi
c 510	16	9.9	8974	12	AF292557	AF292557 Yfp marke	c 567	16	9.9	59800	2	AC100183	AC100183 Mus muscu
c 511	16	9.9	8974	12	AF292558	AF292558 Gfp marke	c 568	16	9.9	59800	2	AC100183	AC100183 Mus muscu
c 512	16	9.9	9330	5	AY298856	AY298856 Xiphophor	c 569	16	9.9	61199	2	AC100497	AC100497 Mus muscu
c 513	16	9.9	9621	2	AC020370	AC020370 Drosophila	c 570	16	9.9	61419	2	AC014418	AC014418 Drosophila
c 514	16	9.9	10210	1	AE000558	AE000558 Helicobac	c 571	16	9.9	61550	2	AC069038	AC069038 Homo sapi
c 515	16	9.9	10266	12	CCSHUTVEC	AR353902 Sequence	c 572	16	9.9	62892	2	AC092282	AC092282 Homo sapi
c 516	16	9.9	10470	6	AR353902	AR353902 Sequence	c 573	16	9.9	64074	2	AC130374	AC130374 Homo sapi
c 517	16	9.9	10823	1	AE000641	AE000641 Helicobac	c 574	16	9.9	65181	2	AC087443	AC087443 Homo sapi
c 518	16	9.9	11135	3	PARI1DNA	L26124 Parametium	c 575	16	9.9	65866	2	AC116462	AC116462 Homo sapi
c 519	16	9.9	11743	1	U67495	U67495 Methanococ	c 576	16	9.9	67124	9	AC026415	AC026415 Homo sapi
c 520	16	9.9	12119	1	AE007316	AE007316 Clostridi	c 577	16	9.9	67497	4	BX649310	BX649310 Smilthops
c 521	16	9.9	12285	1	U39689	U39689 Mycoplasma	c 578	16	9.9	68196	2	AC108407	AC108407 Homo sapi
c 522	16	9.9	12752	1	AE011441	AE011441 Leptospir	c 579	16	9.9	69146	9	AC068668	AC068668 Homo sapi
c 523	16	9.9	13322	3	DDID16466	DI6466 Dicyostel	c 580	16	9.9	69749	9	AY341031	AY341031 Homo sapi
c 524	16	9.9	13320	3	PTALPHA51	X96400 P. tetraurel	c 581	16	9.9	70564	9	HS0334662	HS0334662 Homo sapi
c 525	16	9.9	15561	6	AX076016	AX076016 Sequence	c 582	16	9.9	72030	2	AC083987	AC083987 Homo sapi
c 526	16	9.9	22212	9	AC015979	AC015979 Homo sapi	c 583	16	9.9	72576	10	BX005243	BX005243 Mus muscu
c 527	16	9.9	24342	3	CEFA9A5	Z81542 Caenorhabd	c 584	16	9.9	73397	2	AC101427	AC101427 Homo sapi
c 528	16	9.9	24686	2	CEFA9A5	AL117199 Caenorhab	c 585	16	9.9	73427	9	HS324L9	HS324L9 Homo sapi
c 529	16	9.9	24766	2	AC014976	AC014976 Drosophila	c 586	16	9.9	73908	9	AL596112	AL596112 Human DNA
c 530	16	9.9	24874	8	AY101381	AY101381 Cryptococ	c 587	16	9.9	74315	2	AC136287	AC136287 Homo sapi
c 531	16	9.9	29657	6	AX695329	AX695329 Sequence	c 588	16	9.9	74315	2	AC136287	AC136287 Homo sapi
c 532	16	9.9	32767	6	AX695329	Z82262 Caenorhabd	c 589	16	9.9	74560	9	HS433B8	HS433B8 Homo sapi
c 533	16	9.9	32873	3	CECA359	AC091830 Homo sapi	c 590	16	9.9	76568	3	MSREV	MSREV Homo sapi
c 534	16	9.9	33565	2	AC091830	AC139089 Homo sapi	c 591	16	9.9	76568	3	MSREV	MSREV Homo sapi
c 535	16	9.9	36160	2	AC139089	AL358774 Mouse DNA	c 592	16	9.9	78170	2	AC015396	AC015396 Homo sapi
c 536	16	9.9	36971	10	AL358774	Z69382 S. cerevisiae	c 593	16	9.9	78260	2	AC015438	AC015438 Homo sapi
c 537	16	9.9	37860	8	SCCKXIV38K	AL512375 Human DNA	c 594	16	9.9	78746	9	AC024289	AC024289 Homo sapi
c 538	16	9.9	37897	9	AL512375	AC138922 Homo sapi	c 595	16	9.9	78874	2	AL355521	AL355521 Homo sapi
c 539	16	9.9	38735	9	AC138922	AC025155 Homo sapi	c 596	16	9.9	79418	2	AC005429	AC005429 Drosophila
c 540	16	9.9	40307	9	AC025155	AC138921 Homo sapi	c 597	16	9.9	79718	8	AFAL2H2	AFAL2H2 Homo sapi
c 541	16	9.9	40307	9	AC138921	AC138921 Homo sapi	c 598	16	9.9	79867	8	ATT18N14	ATT18N14 Homo sapi
c 542	16	9.9	40307	9	AC138921	AC139074 Homo sapi	c 599	16	9.9	80514	9	AC004454	AC004454 Homo sapi
c 543	16	9.9	41733	2	AC139074	AC084425 Caenorhab	c 600	16	9.9	80845	9	AC090821	AC090821 Homo sapi
c 544	16	9.9	42310	3	CBRC01B5	BX324221 Mouse DNA	c 601	16	9.9	81056	2	AC096441	AC096441 Homo sapi
c 545	16	9.9	42786	10	BX324221		c 602	16	9.9	81580	8	AP000736	AP000736 Arabidops

603	16	9.9	81835	8	ATTC8	297344 Arabidopsis	660	16	9.9	110000	2	BK64394_2	Continuation (3 of
604	16	9.9	82061	9	AC025180	AC025180 Homo sapi	c 661	16	9.9	110000	6	AR271569_10	Continuation (11 o
605	16	9.9	83385	2	AL590104	AL590104 Homo sapi	c 662	16	9.9	110000	6	AR300198_1	Continuation (2 of
c 606	16	9.9	85710	8	AL137809	AL137809 Arabidops	663	16	9.9	110394	8	AC130808	AC130808 Medicago
607	16	9.9	86358	2	AP003739	AP003739 Oryza sat	664	16	9.9	110855	2	AC142095	AC142095 Medicago
608	16	9.9	87095	10	AL928770	AL928770 Mouse DNA	c 665	16	9.9	111075	2	AC114337	AC114337 Medicago
c 609	16	9.9	87350	10	BK284690	BK284690 Mouse DNA	666	16	9.9	112171	10	ALB37306	ALB37306 Mouse DNA
c 610	16	9.9	88871	10	MM58105	U88105 Mus musculus	667	16	9.9	112268	9	AC118653	AC118653 Homo sapi
c 611	16	9.9	90688	9	AC119732	AC119732 Homo sapi	c 668	16	9.9	112780	2	AC027274	AC027274 Homo sapi
c 612	16	9.9	90840	8	AC091913	AC091913 Homo sapi	c 669	16	9.9	112864	2	AC024127	AC024127 Homo sapi
613	16	9.9	90923	8	AF527808	AF527808 Sorghum b	c 670	16	9.9	113167	8	AC144539	AC144539 Arabidops
614	16	9.9	91883	8	CNS08CDY	BX000508 Oryza sat	c 671	16	9.9	113284	9	AP003382	AP003382 Medicago
615	16	9.9	92809	9	AC073618	AC073618 Homo sapi	c 672	16	9.9	113733	9	AP003139	AP003139 Homo sapi
c 616	16	9.9	93476	2	AC112352_3	Continuation (4 of	c 673	16	9.9	114620	2	AC009628	AC009628 Homo sapi
c 617	16	9.9	94349	8	ATFE6013	AL133452 Arabidops	c 674	16	9.9	115281	9	AC013815	AC013815 Homo sapi
618	16	9.9	95107	9	AL591242	AL591242 Human DNA	c 675	16	9.9	115304	2	BK548251	BK548251 Homo sapi
619	16	9.9	95214	9	AC012457	AC012457 Homo sapi	c 676	16	9.9	116275	2	AP003993	AP003993 Dario rer
620	16	9.9	95643	8	FGN15	AF069299 Arabidops	c 677	16	9.9	116772	2	AC141229	AC141229 Oryza sat
621	16	9.9	95692	2	AC015534	AC015534 Homo sapi	c 678	16	9.9	116793	10	AC079990	AC079990 Homo sapi
c 622	16	9.9	95786	2	BX571801	BX571801 Homo sapi	c 679	16	9.9	117824	9	ALB89886	ALB89886 Human DNA
c 623	16	9.9	95921	9	AC004141	AC004141 Homo sapi	c 680	16	9.9	119377	2	AC133691	AC133691 Rattus no
624	16	9.9	96618	9	HS34781	AL035670 Human DNA	c 681	16	9.9	120187	9	AC005884	AC005884 Homo sapi
625	16	9.9	98017	8	AC027033	AC027033 Arabidops	c 682	16	9.9	120538	9	AC004815	AC004815 Homo sapi
626	16	9.9	98109	9	AC025777	AC025777 Homo sapi	c 683	16	9.9	120709	9	AL445123	AL445123 Human DNA
627	16	9.9	98190	2	AC125738_3	Continuation (4 of	c 684	16	9.9	121436	2	AC142023	AC142023 Rattus no
c 628	16	9.9	98345	2	BK64394_3	Continuation (4 of	c 685	16	9.9	121799	8	OSN00064	OSN00064 Oryza sat
c 629	16	9.9	98461	8	ATFEH20	AL066609 Oryza sat	c 686	16	9.9	121848	9	AC109456	AC109456 Homo sapi
c 630	16	9.9	99661	2	AC137530	AL037530 Takifugu	c 687	16	9.9	121902	9	AC008386	AC008386 Homo sapi
c 631	16	9.9	100443	9	AL731532	AL731532 Human DNA	c 688	16	9.9	123023	9	AC104788	AC104788 Homo sapi
632	16	9.9	101270	9	HS483K16	AL034374 Human DNA	c 689	16	9.9	123169	9	AC008871	AC008871 Homo sapi
633	16	9.9	102146	2	AC133396	AC133396 Felle cat	c 690	16	9.9	123551	9	AC026361	AC026361 Homo sapi
634	16	9.9	103181	9	HS97P20	AL031397 Human DNA	c 691	16	9.9	123567	9	AC091958	AC091958 Homo sapi
635	16	9.9	103216	9	HS093P18	AL080251 Human DNA	c 692	16	9.9	123925	9	AC003976	AC003976 Homo sapi
c 636	16	9.9	103366	9	AL029560	AL029560 Zebrafish	c 693	16	9.9	124170	8	AC135501	AC135501 Oryza sat
637	16	9.9	104307	8	CNS08CDU	BX000504 Oryza sat	c 694	16	9.9	124582	8	AC114828	AC114828 Homo sapi
638	16	9.9	104307	8	CNS08CDU	BX000504 Oryza sat	c 695	16	9.9	125147	2	AC074081	AC074081 Homo sapi
639	16	9.9	105001	9	AC105287	AC105287 Homo sapi	c 696	16	9.9	125693	9	AL354774	AL354774 Homo sapi
640	16	9.9	106123	9	AC109821	AC109821 Homo sapi	c 697	16	9.9	125766	2	AC013137	AC013137 Homo sapi
641	16	9.9	106420	9	AC002546	AC002546 Homo sapi	c 698	16	9.9	126052	9	AC018764	AC018764 Homo sapi
c 642	16	9.9	106795	9	AC004864	AC004864 Homo sapi	c 699	16	9.9	126349	2	AC101076	AC101076 Mus muscu
c 643	16	9.9	107027	8	ATF14L2	AL353818 Arabidops	c 700	16	9.9	126838	9	AC125609	AC125609 Homo sapi
c 644	16	9.9	107826	2	AC124968	AC124968 Medicago	c 701	16	9.9	127514	9	AC004417	AC004417 Homo sapi
645	16	9.9	109431	8	AC035249	AC035249 Arabidops	c 702	16	9.9	127587	9	AC006448	AC006448 Homo sapi
646	16	9.9	109887	10	ALB45169	ALB45169 Mouse DNA	c 703	16	9.9	127833	9	AC009358	AC009358 Homo sapi
647	16	9.9	110000	2	AC09180_5	Continuation (6 of	c 704	16	9.9	127997	2	AC143890	AC143890 Macaca mu
c 648	16	9.9	110000	2	AC096441_2	Continuation (3 of	c 705	16	9.9	128622	2	AC114968	AC114968 Homo sapi
c 649	16	9.9	110000	2	AC098250_2	Continuation (3 of	c 706	16	9.9	128945	9	AL449083	AL449083 Human DNA
c 650	16	9.9	110000	2	AC106549_3	Continuation (4 of	c 707	16	9.9	129575	9	AL160159	AL160159 Human DNA
651	16	9.9	110000	2	AC112373_08	Continuation (9 of	c 708	16	9.9	129626	2	AC040929	AC040929 Homo sapi
652	16	9.9	110000	2	AC121462_3	Continuation (4 of	c 709	16	9.9	129638	9	AC094083	AC094083 Homo sapi
c 653	16	9.9	110000	2	AC125156_0	AC125156 Mus muscu	c 710	16	9.9	129638	9	AC094083	AC094083 Homo sapi
654	16	9.9	110000	2	AC125156_1	Continuation (2 of	c 711	16	9.9	129992	9	AL354897	AL354897 Human DNA
c 655	16	9.9	110000	2	AC128488_0	AC128488 Rattus no	c 712	16	9.9	130469	9	AC006367	AC006367 Homo sapi
c 656	16	9.9	110000	2	AC139485_1	Continuation (2 of	c 713	16	9.9	130499	8	OSN00142	OSN00142 Oryza sat
657	16	9.9	110000	2	AC146410_0	AC146410 Pan trogl	c 714	16	9.9	131408	9	AC112914	AC112914 Homo sapi
658	16	9.9	110000	2	AC146410_1	Continuation (2 of	c 715	16	9.9	131903	9	HS360E18	HS360E18 Human DNA
c 659	16	9.9	110000	2	BX005127_3	Continuation (4 of	c 716	16	9.9	132438	9	HS0375SNG	HS0375SNG Human DNA

c 717	16	9.9 132508	8	AC141323	AC141323 Medicago	c 774	16	9.9 145564	2	AC134794	AC134794 Mus muscu
c 718	16	9.9 133276	2	AC087147	AC087147 Mus muscu	c 775	16	9.9 145659	2	AC008531	AC008531 Homo sapi
c 719	16	9.9 133508	9	AF241728	AF241728 Homo sapi	c 776	16	9.9 146071	10	AL929061	AL929061 Mouse DNA
c 720	16	9.9 133780	2	AL356293	AL356293 Homo sapi	c 777	16	9.9 146267	2	AC008815	AC008815 Homo sapi
c 721	16	9.9 134082	2	CNS08CAY	AL844875 Oryza sat	c 778	16	9.9 146377	9	AC083963	AC083963 Homo sapi
c 722	16	9.9 134226	14	JH1CG	MT5116 Ictalurid h	c 779	16	9.9 146413	2	AC051652	AC051652 Homo sapi
c 723	16	9.9 135690	2	BX323089	BX323089 Dantio rer	c 780	16	9.9 146454	14	AF410153	AF410153 Swinepox
c 724	16	9.9 135793	8	CNS08CAY	AL177247 Oryza sat	c 781	16	9.9 146690	2	AC102254	AC102254 Mus muscu
c 725	16	9.9 135850	2	AC130193	AC130193 Felis cat	c 782	16	9.9 147205	8	AC146702	AC146702 Genomic s
c 726	16	9.9 136111	9	AC092880	AC092880 Homo sapi	c 783	16	9.9 148248	2	AC147347	AC147347 STLRana
c 727	16	9.9 136249	2	AC143739	AC143739 Macaca mu	c 784	16	9.9 148326	2	AC103619	AC103619 Mus muscu
c 728	16	9.9 136877	9	AL390788	AL390788 Homo sapi	c 785	16	9.9 148454	2	AC070723	AC070723 Homo sapi
c 729	16	9.9 136968	9	AL390788	AL390788 Homo sapi	c 786	16	9.9 148623	2	AC068582	AC068582 Homo sapi
c 730	16	9.9 137481	2	AC027207	AC027207 Homo sapi	c 787	16	9.9 148715	2	BX511217	BX511217 Dantio rer
c 731	16	9.9 137930	2	AC141193	AC141193 Rattus no	c 788	16	9.9 148844	9	AL161738	AL161738 Human DNA
c 732	16	9.9 137941	2	AC128149	AC128149 Rattus no	c 789	16	9.9 149008	2	BX296524	BX296524 Dantio rer
c 733	16	9.9 137995	2	AC008596	AC008596 Homo sapi	c 790	16	9.9 149096	2	AC025083	AC025083 Homo sapi
c 734	16	9.9 138145	9	HS1121J1B	AL031653 Human DNA	c 791	16	9.9 149109	2	AC023181	AC023181 Homo sapi
c 735	16	9.9 138498	2	BX088562	BX088562 Dantio rer	c 792	16	9.9 149198	9	AC070734	AC070734 Homo sapi
c 736	16	9.9 139327	2	AC025017	AC025017 Homo sapi	c 793	16	9.9 149252	9	AC066580	AC066580 Homo sapi
c 737	16	9.9 139327	2	AC025017	AC025017 Homo sapi	c 794	16	9.9 149309	9	AC079895	AC079895 Homo sapi
c 738	16	9.9 139330	8	AC119415	AC119415 Medicago	c 795	16	9.9 149332	2	AC068833	AC068833 Homo sapi
c 739	16	9.9 139388	9	AC007666	AC007666 Homo sapi	c 796	16	9.9 149347	8	AC073392	AC073392 Oryza sat
c 740	16	9.9 139708	2	AC134609	AC134609 Mus muscu	c 797	16	9.9 149527	2	AC147264	AC147264 Mus muscu
c 741	16	9.9 139774	2	AC069339	AC069339 Homo sapi	c 798	16	9.9 149950	9	AC113173	AC113173 Homo sapi
c 742	16	9.9 139823	8	AC104321	AC104321 Oryza sat	c 799	16	9.9 149984	2	AC109789	AC109789 Bos tauru
c 743	16	9.9 139843	2	AL158145	AL158145 Homo sapi	c 800	16	9.9 150332	9	AC004921	AC004921 Lemur cat
c 744	16	9.9 139929	8	AC146525	AC146525 Oryza sat	c 801	16	9.9 150587	2	AC140021	AC140021 Homo sapi
c 745	16	9.9 140098	2	AL390237	AL390237 Human DNA	c 802	16	9.9 150681	9	AC006011	AC006011 Homo sapi
c 746	16	9.9 140120	9	AC092880	AC092880 Homo sapi	c 803	16	9.9 150831	9	AC007719	AC007719 Homo sapi
c 747	16	9.9 140186	2	AC125559	AC125559 Rattus no	c 804	16	9.9 150906	2	AC113550	AC113550 Mus muscu
c 748	16	9.9 140842	2	AC144747	AC144747 Pan trogl	c 805	16	9.9 150936	2	BX255899	BX255899 Dantio rer
c 749	16	9.9 140999	9	AL356415	AL356415 Human DNA	c 806	16	9.9 150994	2	AC024054	AC024054 Homo sapi
c 750	16	9.9 141194	9	AC092611	AC092611 Homo sapi	c 807	16	9.9 151008	2	AC035146	AC035146 Homo sapi
c 751	16	9.9 141350	8	AC135500	AC135500 Oryza sat	c 808	16	9.9 151289	9	AL158164	AL158164 Human DNA
c 752	16	9.9 141420	10	AC133078	AC133078 Mus muscu	c 809	16	9.9 151382	9	AC112221	AC112221 Homo sapi
c 753	16	9.9 141450	2	AC015148	AC015148 Drosophill	c 810	16	9.9 151408	10	AL1732318	AL1732318 Mouse DNA
c 754	16	9.9 141504	2	AC022295	AC022295 Homo sapi	c 811	16	9.9 152118	2	AC013263	AC013263 Homo sapi
c 755	16	9.9 141597	2	AC008455	AC008455 Homo sapi	c 812	16	9.9 152137	2	AP001932	AP001932 Homo sapi
c 756	16	9.9 142037	9	AC025171	AC025171 Homo sapi	c 813	16	9.9 152246	9	AC023473	AC023473 Homo sapi
c 757	16	9.9 142126	2	AC026139	AC026139 Homo sapi	c 814	16	9.9 152281	10	AL672066	AL672066 Mouse DNA
c 758	16	9.9 142420	9	AL138816	AL138816 Human DNA	c 815	16	9.9 152519	2	AC108898	AC108898 Felis cat
c 759	16	9.9 142658	2	AC129074	AC129074 Felis cat	c 816	16	9.9 152572	2	AC067788	AC067788 Homo sapi
c 760	16	9.9 142751	9	AC093714	AC093714 Homo sapi	c 817	16	9.9 152937	2	AC024350	AC024350 Homo sapi
c 761	16	9.9 143093	9	AL442635	AL442635 Human DNA	c 818	16	9.9 153082	2	AC142533	AC142533 Homo sapi
c 762	16	9.9 143192	9	AL954247	AL954247 Pan trogl	c 819	16	9.9 153305	2	AC139606	AC139606 Rattus no
c 763	16	9.9 143823	9	AC019195	AC019195 Homo sapi	c 820	16	9.9 153426	10	AC121949	AC121949 Mus muscu
c 764	16	9.9 144233	2	AC068103	AC068103 Homo sapi	c 821	16	9.9 153485	2	AC090757	AC090757 Homo sapi
c 765	16	9.9 144343	2	AC121027	AC121027 Rattus no	c 822	16	9.9 153950	8	AC104429	AC104429 Oryza sat
c 766	16	9.9 144437	2	AC019273	AC019273 Homo sapi	c 823	16	9.9 154034	2	AC133311	AC133311 Rattus no
c 767	16	9.9 144683	9	AC096534	AC096534 Homo sapi	c 824	16	9.9 154308	10	AC105065	AC105065 Mus muscu
c 768	16	9.9 144962	2	AP005425	AP005425 Oryza sat	c 825	16	9.9 154653	9	AC146050	AC146050 Pan trogl
c 769	16	9.9 145023	2	AC074380	AC074380 Homo sapi	c 826	16	9.9 154671	2	AC021680	AC021680 Homo sapi
c 770	16	9.9 145307	2	AP004745	AP004745 Oryza sat	c 827	16	9.9 154733	2	AC127462	AC127462 Dantio rer
c 771	16	9.9 145366	5	AL929327	AL929327 Zebrafish	c 828	16	9.9 154792	2	AC116605	AC116605 Mus muscu
c 772	16	9.9 145437	2	AC139985	AC139985 Rattus no	c 829	16	9.9 154795	2	AC144678	AC144678 Rattus no
c 773	16	9.9 145504	2	AC141023	AC141023 Rattus no	c 830	16	9.9 154959	9	AC004925	AC004925 Homo sapi

c 831	16	9.9 155015	2	AC144700	AC144700 Oryza sat	888	16	9.9 161635	9	AC083873	AC083873 Homo sapi
c 832	16	9.9 155239	2	AC013818	AC013818 Homo sapi	889	16	9.9 161821	10	AL645968	AL645968 Mouse DNA
833	16	9.9 155364	5	BX088982	BX088982 Zebrafish	c 890	16	9.9 161826	2	AC026157	AC026157 Homo sapi
834	16	9.9 155411	10	AC133602	AC133602 Mus muscu	c 891	16	9.9 162237	2	AC115050	AC115050 Mus muscu
835	16	9.9 155420	8	AC025906	AC025906 Oryza sat	c 892	16	9.9 162249	8	AF061282	AF061282 Sorghum b
c 836	16	9.9 155444	8	AP005799	AP005799 Oryza sat	c 893	16	9.9 162325	9	AC109585	AC109585 Homo sapi
c 837	16	9.9 155856	10	BX572626	BX572626 Mouse DNA	894	16	9.9 162437	10	AL928829	AL928829 Mouse DNA
838	16	9.9 156313	2	AL359702	AL359702 Homo sapi	895	16	9.9 162738	9	AC083812	AC083812 Homo sapi
839	16	9.9 156392	9	AC026341	AC026341 Homo sapi	896	16	9.9 162775	2	AC023006	AC023006 Homo sapi
840	16	9.9 156485	9	AC007422	AC007422 Homo sapi	897	16	9.9 162955	9	AC012527	AC012527 Homo sapi
c 841	16	9.9 156527	9	AL161439	AL161439 Human DNA	c 898	16	9.9 163056	5	AC144826	AC144826 Danio rer
842	16	9.9 156598	2	AC012040	AC012040 Homo sapi	899	16	9.9 163096	9	AC103773	AC103773 Homo sapi
843	16	9.9 156754	9	AC021055	AC021055 Homo sapi	c 900	16	9.9 163100	2	CNS01DU1	CNS01DU1 Human chr
844	16	9.9 156958	9	AC013460	AC013460 Homo sapi	c 901	16	9.9 163104	2	AC145421	AC145421 Human chr
c 845	16	9.9 157193	2	AC122770	AC122770 Mus muscu	902	16	9.9 163132	2	AC121312	AC121312 Mus muscu
c 846	16	9.9 157417	9	AC136261	AC136261 Rattus no	c 903	16	9.9 163355	2	AC117927	AC117927 Mus muscu
c 847	16	9.9 157557	9	AC098808	AC098808 Papio anu	c 904	16	9.9 163473	2	AC144870	AC144870 Pan trogl
c 848	16	9.9 157799	2	AC128320	AC128320 Rattus no	c 905	16	9.9 163539	9	AC096916	AC096916 Homo sapi
849	16	9.9 157836	2	AC060228	AC060228 Homo sapi	906	16	9.9 163713	2	AC069432	AC069432 Homo sapi
c 850	16	9.9 158312	2	AC083922	AC083922 Homo sapi	907	16	9.9 163731	9	AC008949	AC008949 Homo sapi
c 851	16	9.9 158321	2	AC064610	AC064610 Homo sapi	c 908	16	9.9 163979	9	CNS01RM4	CNS01RM4 Human chr
852	16	9.9 158392	9	CNS07EGN	AL591770 Human chr	c 909	16	9.9 164013	9	AL360088	AL360088 Human DNA
c 853	16	9.9 158412	2	AP001134	AP001134 Homo sapi	910	16	9.9 164125	9	AC018693	AC018693 Homo sapi
c 854	16	9.9 158482	14	AY126275	AY126275 Mamestra	c 911	16	9.9 164176	2	AC080147	AC080147 Homo sapi
c 855	16	9.9 158544	2	AC023658	AC023658 Homo sapi	c 912	16	9.9 164280	2	AC025391	AC025391 Homo sapi
856	16	9.9 158579	2	AC012657	AC012657 Homo sapi	913	16	9.9 164288	2	AC016500	AC016500 Homo sapi
857	16	9.9 158759	9	AC144916	AC144916 Homo sapi	914	16	9.9 164290	9	BS000061	BS000061 Pan trogl
858	16	9.9 158913	10	AL645928	AL645928 Mouse DNA	915	16	9.9 164366	2	AC016519	AC016519 Homo sapi
859	16	9.9 159059	2	AC093000	AC093000 Homo sapi	916	16	9.9 164462	2	AC008552	AC008552 Homo sapi
860	16	9.9 159061	2	AP005470	AP005470 Oryza sat	917	16	9.9 164566	2	AC068559	AC068559 Homo sapi
861	16	9.9 159339	10	AC127277	AC127277 Mus muscu	918	16	9.9 164611	2	AC128858	AC128858 Homo sapi
c 862	16	9.9 159371	2	AC011876	AC011876 Homo sapi	919	16	9.9 164805	8	OSJN00174	OSJN00174 Rattus no
c 863	16	9.9 159435	9	AC116564	AC116564 Homo sapi	c 920	16	9.9 164839	8	AP002844	AP002844 Oryza sat
c 864	16	9.9 159521	9	AC098647	AC098647 Homo sapi	c 921	16	9.9 165112	2	AC026920	AC026920 Homo sapi
865	16	9.9 159624	2	AC011021	AC011021 Homo sapi	c 922	16	9.9 165307	10	AC132116	AC132116 Mus muscu
c 866	16	9.9 159653	2	AC115908	AC115908 Mus muscu	923	16	9.9 165365	2	AC011959	AC011959 Homo sapi
c 867	16	9.9 159656	5	AL929243	AL929243 Zebrafish	c 924	16	9.9 165617	5	AL845526	AL845526 Zebrafish
868	16	9.9 159735	2	AC022627	AC022627 Homo sapi	c 925	16	9.9 165749	9	AC007966	AC007966 Homo sapi
c 869	16	9.9 159767	2	AC080178	AC080178 Homo sapi	c 926	16	9.9 165777	10	BX004852	BX004852 Mouse DNA
870	16	9.9 159775	10	AC131787	AC131787 Mus muscu	c 927	16	9.9 165843	2	AC135548	AC135548 Papio anu
c 871	16	9.9 159946	9	AC104840	AC104840 Homo sapi	c 928	16	9.9 165988	2	AC010232	AC010232 Homo sapi
c 872	16	9.9 160073	2	AC025532	AC025532 Homo sapi	c 929	16	9.9 166045	2	AC018543	AC018543 Homo sapi
c 873	16	9.9 160179	2	AC092930	AC092930 Homo sapi	c 930	16	9.9 166118	9	AL355495	AL355495 Human DNA
c 874	16	9.9 160440	10	AC126245	AC126245 Mus muscu	931	16	9.9 166447	9	AC021723	AC021723 Mus muscu
c 875	16	9.9 160603	8	AC084818	AC084818 Oryza sat	932	16	9.9 166451	9	AC018994	AC018994 Homo sapi
876	16	9.9 160636	2	AC024991	AC024991 Homo sapi	933	16	9.9 166540	2	AC142445	AC142445 Homo sapi
877	16	9.9 160746	2	AC044853	AC044853 Homo sapi	c 934	16	9.9 166579	2	AC105366	AC105366 Rattus no
c 878	16	9.9 160920	8	AC137072	AC137072 Genomic s	c 935	16	9.9 167030	2	AC145117	AC145117 Rattus no
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c 880	16	9.9 160961	2	AC145794	AC145794 Silurana	c 937	16	9.9 167159	2	AC073481	AC073481 Homo sapi
c 881	16	9.9 160962	2	AC022862	AC022862 Homo sapi	938	16				
882	16	9.9 161180	2	AC146771	AC146771 Canis fam	939	16				
883	16	9.9 161309	9	AC100839	AC100839 Homo sapi	c 940	16				
c 884	16	9.9 161376	2	BX511150	BX511150 Danio rer	941	16				
885	16	9.9 161416	2	AC026857	AC026857 Homo sapi	c 942	16				
c 886	16	9.9 161461	10	AC124355	AC124355 Mus muscu	c 943	16				
c 887	16	9.9 161602	9	AC022634	AC022634 Homo sapi	c 944	16				

QY 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162
DB 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162

RESULT 2
BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier, D., Gros, P. and Dubow, M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC

COMMENT 05 Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16

PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12M1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02

CC Genome Sequence
FH Key Location/Qualifiers
FT source 1. 41708
FT aureus bacteriophage 77.
FT Location/Qualifiers

source 1. 41708
/organism="unidentified"
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ORIGIN

Query Match 100.0%; Score 162; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2.7e-73;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAGCAACATTATATAAGCTACCTAGTAGCAGATTAATGCTTCACAGTCTTAGCGATT 60
DB 29051 ATAGCAACATTATATAAGCTACCTAGTAGCAGATTAATGCTTCACAGTCTTAGCGATT 29110
QY 61 GTACTATGCGCTTCTATATCTCACTCAAGCATGTCGCGGATTCGCAAGTATC 120
DB 29111 GTACTATGCGCTTCTATATCTCACTCAAGCATGTCGCGGATTCGCAAGTATC 29170

QY 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162
DB 29171 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 29212

RESULT 3
AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier, D., Gros, P. and Dubow, M.
TITLE Compositions and methods involving an essential Staphylococcus aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-APR-2002;
FEATURES Location/Qualifiers
source 1. 41708
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 162; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 2.7e-73;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAGCAACATTATATAAGCTACCTAGTAGCAGATTAATGCTTCACAGTCTTAGCGATT 60
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QY 61 GTACTATGCGCTTCTATATCTCACTCAAGCATGTCGCGGATTCGCAAGTATC 120
DB 29111 GTACTATGCGCTTCTATATCTCACTCAAGCATGTCGCGGATTCGCAAGTATC 29170
QY 121 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 162
DB 29171 GCAACATTCATGTAACAAAGATGCTTTTCAAGATTA 29212

RESULT 4

AX583668 159 bp DNA linear PAT 10-JAN-2003
LOCUS AX583668
DEFINITION Sequences 45 from Patent W002059148.
ACCESSION AX583668
VERSION AX583668.1 GI:27655478

KEYWORDS Staphylococcus aureus
SOURCE Staphylococcus aureus
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 Meinke, A., Nagy, E., von Absen, U., Klade, C., Henics, T., Zauner, W.,
Mih, D. B., Vytvytska, O., Etz, H., Dryla, A., Weichhart, T., Hafner, M.,

Tempelmeier,B., Fraser,C.M. and Gill,S.

TITLE A method for identification, isolation and production of antigens to a specific pathogen

JOURNAL Patent: WO 02059148-A 45 01-AUG-2002;

Clatam Biotechnologies GmbH (AT)

FEATURES

Location/Qualifiers

SOURCE

1..159
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

ORIGIN

Query Match 45.7%; Score 74; DB 6; Length 159;

Best Local Similarity 100.0%; Pred.No.2.9e-27;

Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 ATTGCTATACCGCTTTCTATATCTACATGACAGCATGGTCAATTGCGGATTCGCAAGT 117

DB 58 ATTGCTATACCGCTTTCTATATCTACATGACAGCATGGTCAATTGCGGATTCGCAAGT 117

QY 118 ATCCGACATTCAT 131

DB 118 ATCCGACATTCAT 131

RESULT 5

AX618544

LOCUS AX618544 159 bp DNA linear PAT 20-FEB-2003

DEFINITION Sequence 1507 from Patent WO02094868.

ACCESSION AX618544

VERSION AX618544.1 GI:28448591

KEYWORDS

SOURCE Staphylococcus aureus

ORGANISM Staphylococcus aureus

REFERENCE 1 Bacteria; Firmicutes; Bacillales; Staphylococcus.

AUTHORS

Maignani,V.C., Mora,M.C. and Scarselli,M.C.

TITLE Staphylococcus aureus proteins and nucleic acids

JOURNAL Patent: WO 02094868-A 1507 28-NOV-2002;

Chiron Spa (IT)

FEATURES

Location/Qualifiers

SOURCE

1..159
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

ORIGIN

Query Match 41.4%; Score 67; DB 6; Length 159;

Best Local Similarity 100.0%; Pred.No.1.2e-23;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TATGCTTACAGCTCTAGCGATTGTACTTATGCGCTTTCTATATCTACTACTACAGCATGGT 97

DB 38 TATGCTTACAGCTCTAGCGATTGTACTTATGCGCTTTCTATATCTACTACTACAGCATGGT 97

QY 99 CAATTGC 104

|||||||

DB 98 CAATTGC 104

RESULT 6

AR354422/c

LOCUS AR354422

DEFINITION Sequence 540 from patent US 6593114. 1408 bp DNA linear PAT 17-AUG-2003

ACCESSION AR354422

VERSION AR354422.1 GI:33760506

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 Unpublished.

(bases 1 to 1408)

AUTHORS

Rosen,C.A., Chou,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and

Staphylococcus aureus polynucleotides and sequences

Patent: US 6593114-A 540 15-JUL-2003;

location/Qualifiers

source

1..1408
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 41.4%; Score 67; DB 6; Length 1408;

Best Local Similarity 100.0%; Pred.No.8.1e-24;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TATGCTTACAGCTCTAGCGATTGTACTTATGCGCTTTCTATATCTACTACTACAGCATGGT 97

DB 302 TATGCTTACAGCTCTAGCGATTGTACTTATGCGCTTTCTATATCTACTACTACAGCATGGT 243

QY 98 CAATTGC 104

DB 242 CAATTGC 236

RESULT 7

AF424781

LOCUS AF424781 43604 bp DNA linear PHG 10-JUN-2002

DEFINITION Staphylococcus aureus phage phi 11, complete genome.

ACCESSION AF424781

VERSION AF424781.1 GI:18920487

KEYWORDS

SOURCE

ORGANISM

Staphylococcus aureus phage phi 11

Vituses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.

REFERENCE 1 (bases 1 to 43604)

Iandolo,J.J., Worrell,V., Gretcher,K.H., Qian,Y., Tian,R.,

Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and

Roe,B.A. Comparative analysis of the genomes of the temperate bacteriophages

phi11, phi12 and phi13 of Staphylococcus aureus 8325

JOURNAL

MEDLINE

FUBMED

REFERENCE 2 (bases 1 to 43604)

AUTHORS Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R., Lin,S. and Jia,H.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City, OK 73190, USA

FEATURES Location/Qualifiers
source 1..43604
/organism="Staphylococcus aureus phage phi 11"
/mol_type="genomic DNA"
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/db_xref="GI:18920488"

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CDS
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/db_xref="GI:18920499"

CDS
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/db_xref="GI:18920500"
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/product="phage tail protein"
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/protein_id="AAL82245.1"
/db_xref="GI:18920503"

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/db_xref="GI:18920505"

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/db_xref="GI:18920507"

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/db_xref="GI:18920498"
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/db_xref="GI:18920498"
/translation="MTERTQVDILQGLGVKDISKQNNKREKAIYGRGTGTF
LTKNNALVDINEDGTVEDEAVVOIKVKKFSATIMLPKITEQLBNGKIDV
VIERIQKLADITDDIDNGSKKPTFRNGCATRVISYIKISKQERTQPLATG
HGIKNDDEGSTINPTITTEADQDIKVAISQVSLARTIEHEQDEGTQYVL
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NSQSNFPAFANGRFIEINDDLFP"
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/protein_id="AAL82242.1"
/db_xref="GI:18920501"
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PNNKLSIEQRKIFAMCRDIELHWGEVESTKRLQTELEIKGYEELSLRDSKV
ARELEILIAFNEHQIPMSVETSKLSEDAALVATINNCVIGRPHADLAREVA
VGRGNKNNKNNYDHYVALCRQHNEQHALGVSPDKYHLHDSWIKYDERLIVKLC
GNNGRSIVDKT"
9606..10412
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/db_xref="GI:18920502"
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YNEGYTMSLSENPNEBMLANFNPNISRLAQTEFLAMIEKVNGLKVTMEK
NOSLSVAKHREKRLQROQYREKQKLEKKNVTLRDTSEEESEERKEEYK
NKEEREAFFSSIKYIINLIDKLTVMQKOLGFAIDIGTNAFVAVGYEYTSK
SAHGGYLIKVLNNMAKENVTKEDAKNIAPRNTTDVIAQKEKELSD"
10765..12006
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VMDYGIKHQEIYKATPKDEFLADPTIKLNSDPTGCFEYQGLSSYQJAKA
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CDS
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QAMRSRQOVFIIDYQLMDTDVAVBRVAVKISRLKTIINERGAIIYLSQNR
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KDEGTGIIIEEYKTKRQRTT"
12222..12443
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/db_xref="GI:18920504"
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Query Match 41.4%; Score 67; DB 7; Length 43604;
Best Local Similarity 100.0%; Pred. No. 4.2e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TATGCTCAGCTTACGATTTGACTATGCGGTTCTTACTTACGACGATGCT 97
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DB 6232 TATGCTCAGCTTACGATTTGACTATGCGGTTCTTACTTACGACGATGCT 6291
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QY 98 CAATTC 104
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DB 6292 CAATTC 6298

RESULT 8
AP003135/c
LOCUS
DEFINITION
Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
genome, section 7/10.
AP003135 BA000018
VERSION
AP003135.2 GI:14349227
KEYWORDS
SOURCE
Staphylococcus aureus subsp. aureus N315
Staphylococcus aureus subsp. aureus N315
ORGANISM
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE
AUTHORS
Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Iino,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Uji,Y., Takahashi,N.K., Sekano,T., Inoue,R., Kato,C.,
Sekimizu,K., Hirakawa,H., Kohara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramoto,K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
JOURNAL
MEDLINE
Lancet 357 (9264), 1223-1240 (2001)
PUBMED
21311952
11418146
2 (bases 1 to 291150)
REFERENCE
DIRECTOR-GENERAL, Biotechnology Center, Aoki,K., Oguchi,A.,
Hosoyama,A., Nagai,Y., Kuroda,M., Hiramoto,K. and Kikuchi,H.
TITLE
Direct Submission
Submitted (30-JAN-2001) DIRECTOR-GENERAL, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center, 2chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan

(E-mail:bio@ncte.go.jp, URL: http://www.bio.ncte.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701545.
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DEFINITION Development of novel antibiotics based on bacteriophage genomes.
ACCESSION BD245282
VERSION BD245282.1 GI:33055052
KEYWORDS JP 2002531107-A/17.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 43095)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomes
JOURNAL Patent: JP 2002531107-A 17 24-SEP-2002;
PHARTECH INC

COMMENT OS Staphylococcus aureus bacteriophage 3A
PN JP 2002531107-A/17
PD 24-SEP-2002
PE 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 FI JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
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DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245634
VERSION BD245634.1 GI:33055404
KEYWORDS JP 2002531107-A/369.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 43594)
AUTHORS Pelleterier, V., Gros, P. and Dubow, M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 369 24-SEP-2002;
PHARMATECH INC
OS Staphylococcus aureus bacteriophage 96
PN JP 2002531107-A/369
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
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PELLETIER, PHILIPPE GROS, MICHAEL DUBOW

PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
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sequence.
ACCESSION AB044554
VERSION AB044554.1 GI:8918747
KEYWORDS
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ORGANISM Staphylococcus aureus prophage phiPV83
Staphylococcus aureus prophage phiPV83
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.

REFERENCE 1 (sites)
AUTHORS Kaneko, J., Kimura, T., Kawakami, Y., Tomita, T. and Kamio, Y.
TITLE Panton-valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (sites)
AUTHORS Zou, D., Kaneko, J., Narita, S. and Kamio, Y.
TITLE Complete nucleotide sequence and molecular characterization of prophage PV83pro carrying lukM-lukF-PV(p83) gene cluster in Staphylococcus aureus strain p83 unpublished
3 (bases 1 to 45636)
AUTHORS Kaneko, J., Zou, D. and Kamio, Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Jun Kaneko, Tohoku University, Graduate School of Agricultural Science; 1-1 Tsurumi-dori Aamamiyamachi, Aoba-ku, Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781, Fax: 81-22-717-8780)

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ACCESSION	AP003360.2
VERSION	GI:14246388
KEYWORDS	Staphylococcus aureus subsp. aureus Mu50 Staphylococcus aureus subsp. aureus Mu50
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REFERENCE	1 Kurada M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cul L., Oguchi A., Aoki K., Nagai Y., Iken J., Ito T., Kanamori K., Matsumaru H., Maruyama A., Murekami H., Hosoyama A., Mizutani U. Y., Takahashi N. K., Sawano T., Inoue R., Kaito C., Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H. and Hiratsuka K. Whole genome sequencing of methicillin-resistant Staphylococcus aureus Lancet 357 (9264), 1225-1240 (2001) MEDLINE 21311952 PUBMED 11418146
TITLE	2 (bases 1 to 348527)
JOURNAL	Ohta, T. Direct Submission Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology, 1-1-1 Ten-no-dai, Tsukuba, Ibaraki 305-8577, Japan (E-mail: tohshaka@tsukuba.ac.jp, Tel: 81-298-53-3454, Fax: 81-298-53-3454) On May 29, 2001 this sequence version replaced gi:13874937.
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DB 230191 TACTCTACAGCATGCTCAATTGCGGATTGCGACGAT 230231

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ACCESSION AF424783
VERSION AF424783.1 GI:18920591
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SOURCE Staphylococcus aureus phage phi 13
ORGANISM Staphylococcus aureus phage phi 13
REFERENCE 1 (bases 1 to 42722)
AUTHORS Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and
Ro,B.A.
TITLE Comparative analysis of the genomes of the temperate bacteriophages
JOURNAL Gene 289 (1-2), 109-118 (2002)
MEDLINE 22032962
PUBMED 12036589
REFERENCE 2 (bases 1 to 42722)
AUTHORS Iandolo,J.U., Worrell,V., Ro,B., Qian,Y., Dorman,A., Tian,R.,
Lin,S. and Jia,H.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of
Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City,
OK 73190, USA

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ACCESSION AP004828 BA000033
VERSION AP004828.1 GI:21204850
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ORGANISM Staphylococcus aureus subsp. aureus MW2
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AUTHORS Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
Nagai,Y., Iwama,N., Amano,K., Nishimura,T., Kuroda,H., Oda,L.,
Yamamoto,K. and Hitamatsu,K.
TITLE Genome and virulence determinants of high virulence
community-acquired MRSA
JOURNAL Lancet 359 (9320), 1819-1827 (2002)
MEDLINE 22040717
PUBMED 12044378
REFERENCE 2 (bases 1 to 272850)
AUTHORS Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Director-General, Biotechnology Center, Nagai,Y.,
Director-General, Biotechnology Center, Hitamatsu,K. and
Kikuchi,H.
TITLE Submitted (06-MAR-2002) Director-General, Biotechnology Center,
JOURNAL National Institute of Technology and Evaluation, Biotechnology
Center, 2Chome 49-10 Nishihara, Shibuya-Ku, Tokyo 151-0066, Japan
(E-mail:biotech.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
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DB 257045 ATGAGCAATTATTAAGCTACTAGTAGCAGTA 257010

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VERSION
AP003364.2 GI:14247707
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Staphylococcus aureus subsp. aureus Mu50
ORGANISM
Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
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Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
Cui, L., Oguchi, A., Aoki, K., Nagai, I., Iken, J., Ito, T., Kanamori, M.,
Matsunaga, H., Maruyama, A., Murakami, H., Hosoyama, A.,
Mitsunaga, Y., Takahashi, N. K., Sawano, T., Inoue, R., Kato, C.,
Sekizawa, K., Hiramatsu, H., Kihara, S., Goto, S., Yabuzaki, J.,
Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
TITLE
JOURNAL
Lancet 357 (9264), 1225-1240 (2001)
MEDLINE
21311952
PUBMED
11418146
REFERENCE
2 (bases 1 to 348650)
AUTHORS
Ohta, T.
TITLE
Direct Substitution
Submitted (28-FEB-2001) Tohshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology, 1-1-1 Ten-no-dai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail: tohshiko@tsukuba.ac.jp, Tel: 81-298-53-3454,
Fax: 81-298-53-3454)
COMMENT
On May 29, 2001 this sequence version replaced gi:13873637.
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Query Match 22.2%; Score 36; DB 1; Length 348650;
 Best Local Similarity 100.0%; Pred.No. 3.2e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: October 15, 2004, 03:31:40
 Job time : 897.824 secs

OM nucleotide - nucleotide search, using BW model

Run on: October 14, 2004, 18:55:29 ; Search time 108.072 Seconds

(without alignments)
6368.040 Million cell updates/sec

Title: US-09-407-804A-7

Perfect score: 162

Sequence: 1 atgagcaacattataaag.....aatgcttttcaagaactaa 162

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 2: geneseqn1980s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	162	100.0	41708	3	AAA68247 Bacterioph
3	162	100.0	41708	4	AAc86106 Complete
4	74	45.7	159	7	ABr14900 Pathogen
5	67	41.4	159	7	ACF73074 Staphyloc
6	67	41.4	1408	2	AAV74851 Staphyloc
7	65	40.1	43095	3	AAA68254 Bacterioph

8	55	34.0	43576	3	AAA68609	AAA68609 Bacterioph
9	26	16.0	2049	2	AAV74602	AAV74602 Staphyloc
10	23	14.2	25	3	AAA68911	AAc68911 Bacterioph
11	21	13.0	25	3	AAA68846	AAc68846 Bacterioph
12	19	11.7	4895	4	ADD18757	ADD18757 Human dls
13	19	11.7	4983	4	AAE44629	AAE44629 Novel pro
14	18	11.1	365	6	ABR73359	ABr73359 Bovine em
15	18	11.1	365	6	ABR73269	ABr73269 Bovine em
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44	16	9.9	240	5	ABV25110	ABv25110 Human pro
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47	16	9.9	335	5	ABV37882	ABv37882 Human pro
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49	16	9.9	495	4	AAH12739	AAH12739 Human cDN
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51	16	9.9	592	4	AA117525	AA117525 Probe #74
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53	16	9.9	592	4	AA142434	AA142434 Probe #11
54	16	9.9	592	4	ABR29789	ABr29789 Probe #82
55	16	9.9	592	4	AAK36670	AAK36670 Human bon
56	16	9.9	592	4	AAK10804	AAK10804 Human bra
57	16	9.9	592	6	ABs36328	ABs36328 Human liv
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c 68	16	9.9	2295	4	AA502396	Aa502396 Human sec	c 125	15	9.3	196	4	ABSA45056	ABSA45056 Human liv
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c 75	16	9.9	3307	4	AAK62353	AAK62353 Human imm	c 132	15	9.3	294	6	ABL72956	ABL72956 Corn tass
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c 78	16	9.9	3989	4	ABL26168	AbL26168 Drosophill	c 135	15	9.3	363	4	AAAS3693	AAAS3693 Helicobac
c 79	16	9.9	4317	4	AAH57574	AaH57574 Human bra	c 136	15	9.3	363	7	ACB34892	ACB34892 Prokaryot
c 80	16	9.9	4433	7	ABT19691	AbT19691 Aspergill	c 137	15	9.3	366	8	ACH42642	ACH42642 Human foe
c 81	16	9.9	4504	7	ABT17877	AbT17877 Aspergill	c 138	15	9.3	383	5	ACH07672	ACH07672 Human pro
c 82	16	9.9	4956	4	ABL09357	AbL09357 Drosophill	c 139	15	9.3	391	8	ACH16289	ACH16289 Human adu
c 83	16	9.9	5469	6	ABQ99271	AbQ99271 Human cod	c 140	15	9.3	396	7	ABX52082	ABX52082 Bovine ES
c 84	16	9.9	5561	3	AAA34842	AaA34842 Human ade	c 141	15	9.3	398	4	AAAL01930	AAAL01930 Human rep
c 85	16	9.9	5561	3	AAE20964	AaE20964 Human low	c 142	15	9.3	398	4	ABL97223	ABL97223 Human tes
c 86	16	9.9	5561	3	ABE29658	AbE29658 Human nuc	c 143	15	9.3	401	4	ABA72549	ABA72549 Human foe
c 87	16	9.9	6744	7	ABX14056	AbX14056 cDNA enco	c 144	15	9.3	401	4	AAI52962	AAI52962 Probe #21
c 88	16	9.9	6956	7	ACC72031	Acc72031 BCU0720 g	c 145	15	9.3	401	4	AAK47126	AAK47126 Human bon
c 89	16	9.9	7116	4	ABL26196	AbL26196 Drosophill	c 146	15	9.3	401	4	AAK20973	AAK20973 Human bra
c 90	16	9.9	10470	2	AAV74331	AaV74331 Staphyloc	c 147	15	9.3	401	4	ABS46884	ABS46884 Human liv
c 91	16	9.9	15561	4	AAE25341	AaE25341 Nucleotid	c 148	15	9.3	401	6	ABS21353	ABS21353 Human gen
c 92	16	9.9	19117	4	AAH84829	AaH84829 Human imm	c 149	15	9.3	402	4	AAAS38813	AAAS38813 Novel hum
c 93	16	9.9	22421	3	AAA34844	AaA34844 Human ade	c 150	15	9.3	402	5	AAAS73759	AAAS73759 DNA enco
c 94	16	9.9	22421	3	AAE20966	AaE20966 Human low	c 151	15	9.3	402	5	ADC31885	ADC31885 Human nov
c 95	16	9.9	22421	7	ABZ96660	AbZ96660 Human nuc	c 152	15	9.3	408	7	ABX39009	ABX39009 Bovine ES
c 96	16	9.9	32127	4	AAI99255	AaI99255 Human exc	c 153	15	9.3	421	5	ABV10980	ABV10980 Human pro
c 97	16	9.9	32127	5	AAI63605	AaI63605 Human kid	c 154	15	9.3	423	2	AAK14444	AAK14444 H. pylori
c 98	16	9.9	32767	7	AA056075	Aa056075 Human SNL	c 155	15	9.3	433	3	AAAC26430	AAAC26430 Human sec
c 99	16	9.9	32767	9	AD802437	Ad802437 Human SNL	c 156	15	9.3	443	5	ABV37601	ABV37601 Human pro
c 100	16	9.9	32767	9	ADB82176	AdB82176 Human SNL	c 157	15	9.3	447	2	AAAT83757	AAAT83757 DNA enco
c 101	16	9.9	32767	9	ADB82920	AdB82920 Human SNL	c 158	15	9.3	451	8	ACH14509	ACH14509 Human adu
c 102	16	9.9	35633	4	ABL09356	AbL09356 Drosophill	c 159	15	9.3	457	4	AAK32324	AAK32324 Human bon
c 103	16	9.9	43576	3	AAA68609	AaA68609 Bacteriop	c 160	15	9.3	457	6	ABS32030	ABS32030 Human liv
c 104	16	9.9	72215	4	AAH86832	AaH86832 Human imm	c 161	15	9.3	467	8	ACH24536	ACH24536 Human adu
c 105	16	9.9	110000	2	AAV58840_1	Continuation (2 of	c 162	15	9.3	471	2	AAK32978	AAK32978 S. aureus
c 106	16	9.9	110000	2	AAV21209_10	Continuation (11 of	c 163	15	9.3	488	6	ABN75368	ABN75368 Human ORF
c 107	16	9.9	110000	6	ABK08336_03	Continuation (13 of	c 164	15	9.3	508	2	AAK30869	AAK30869 Streptoco
c 108	16	9.9	110000	6	ABK03041_12	Continuation	c 165	15	9.3	512	6	ABN61185	ABN61185 Human can
c 109	16	9.9	334462	9	ADC24763	AdC24763 Human wil	c 166	15	9.3	528	5	AAAS3766	AAAS3766 Human cDN
c 110	16	9.9	335199	9	ADC24703	AdC24703 Human wil	c 167	15	9.3	540	5	ABV08906	ABV08906 Human pro
c 111	15	9.3	29	2	AAI11651	AaI11651 Heipes st	c 168	15	9.3	549	3	AAAC93947	AAAC93947 Cat flea
c 112	15	9.3	33	6	AAAL43838	AaAL43838 Human cit	c 169	15	9.3	552	4	ABA60008	ABA60008 Human foe
c 113	15	9.3	41	6	AAAL43840	AaAL43840 Human cit	c 170	15	9.3	552	4	AAI39881	AAI39881 Probe #85
c 114	15	9.3	156	7	ACA16693	AcA16693 Prokaryot	c 171	15	9.3	552	4	AAK34158	AAK34158 Human bon
c 115	15	9.3	156	7	ACA16693	AcA16693 Prokaryot	c 172	15	9.3	552	4	AAK08279	AAK08279 Human bra
c 116	15	9.3	186	4	AAI26290	AaI26290 Probe #16	c 173	15	9.3	552	4	ABAS3954	ABAS3954 Human liv
c 117	15	9.3	186	4	ABV74032	AbV74032 Human foe	c 174	15	9.3	552	6	ABSO8919	ABSO8919 Human gen
c 118	15	9.3	186	4	AAI54481	AaI54481 Probe #23	c 175	15	9.3	555	2	AAAT98705	AAAT98705 DNA enco
c 119	15	9.3	186	4	ABA39093	AbA39093 Probe #17	c 176	15	9.3	555	2	AAK58477	AAK58477 Human imm
c 120	15	9.3	186	4	AAK48653	AaK48653 Human bon	c 177	15	9.3	556	5	AAV77296	AAV77296 DNA enco
c 121	15	9.3	186	4	AAK22485	AaK22485 Human bra	c 178	15	9.3	556	5	AAV77296	AAV77296 DNA enco

c 179	15	9.3	564	8	ADA29537	AdA29537 DNA encod	236	15	9.3	1008	6	ABN70591	ABn70591 Streptococ
c 180	15	9.3	580	6	ABK33576	ABk33576 Human eos	237	15	9.3	1008	6	ABN71389	ABn71389 Streptococ
c 181	15	9.3	585	5	AA582260	AA582260 DNA encod	238	15	9.3	1008	7	ACE73799	ACE73799 Streptococ
c 182	15	9.3	590	6	ABN65863	ABn65863 Human can	239	15	9.3	1011	4	AA554805	AA554805 Staphy1loc
c 183	15	9.3	591	4	AA117113	AA117113 Probe #70	240	15	9.3	1011	6	ABA91329	ABa91329 Streptococ
c 184	15	9.3	591	4	ABAB6134	ABa61534 Human foe	241	15	9.3	1011	6	ABA91332	ABa91332 Streptococ
c 185	15	9.3	591	4	AA141443	AA141443 Probe #10	242	15	9.3	1011	6	ABA91328	ABa91328 Streptococ
c 186	15	9.3	591	4	ABAB2943	ABa29243 Probe #77	243	15	9.3	1011	6	ABA91331	ABa91331 Streptococ
c 187	15	9.3	591	4	AAK35728	AAK35728 Human bon	244	15	9.3	1011	6	ABA91248	ABa91248 Streptococ
c 188	15	9.3	591	4	AAK09634	AAK09634 Human bra	245	15	9.3	1011	6	ABA91249	ABa91249 Streptococ
c 189	15	9.3	591	4	AB535446	AB535446 Human liv	246	15	9.3	1011	6	ABA91251	ABa91251 Streptococ
c 190	15	9.3	591	6	AB509996	AB509996 Human gen	247	15	9.3	1011	6	ABA91252	ABa91252 Streptococ
c 191	15	9.3	599	4	AAK72878	AAK72878 Human imm	248	15	9.3	1011	7	ACA18943	ACA18943 Streptococ
c 192	15	9.3	599	4	AAK72880	AAK72880 Human imm	249	15	9.3	1011	7	ACA50325	ACA50325 Streptococ
c 193	15	9.3	599	4	AAK72879	AAK72879 Human imm	250	15	9.3	1011	7	ACA46200	ACA46200 Streptococ
c 194	15	9.3	603	4	AAK57096	AAK57096 Human imm	c 251	15	9.3	1012	6	ABN74774	ABn74774 Bovine em
c 195	15	9.3	605	6	ABK62139	ABK62139 Rat seque	252	15	9.3	1018	3	AA559581	AA559581 Human sec
c 196	15	9.3	605	9	ADB55108	ADB55108 Tox1ctly-	253	15	9.3	1020	7	ACA47671	ACA47671 Streptococ
c 197	15	9.3	605	9	ADB49636	ADB49636 Primary r	254	15	9.3	1035	6	ABN69737	ABn69737 Streptococ
c 198	15	9.3	637	6	ABQ31795	ABQ31795 Oligonuc1	c 255	15	9.3	1030	8	ACD06179	ACD06179 Human c1N
c 199	15	9.3	637	6	ABQ31794	ABQ31794 Oligonuc1	256	15	9.3	1053	6	ABQ70392	ABQ70392 Listeria
c 200	15	9.3	645	5	ABV58266	ABV58266 Human pro	c 257	15	9.3	1068	7	ACE67989	ACE67989 Photocorhab
c 201	15	9.3	654	5	AA573760	AA573760 DNA encod	c 258	15	9.3	1079	2	AAV41891	AAV41891 Streptococ
c 202	15	9.3	662	3	AAA10744	AAA10744 Fragment	259	15	9.3	1080	4	AA555858	AA555858 Streptococ
c 203	15	9.3	663	4	AAH07307	AAH07307 Human c1N	260	15	9.3	1080	4	AA555434	AA555434 Streptococ
c 204	15	9.3	672	7	ABQ82869	ABQ82869 Human 1un	261	15	9.3	1080	7	ACA50132	ACA50132 Streptococ
c 205	15	9.3	678	6	ABN69374	ABn69374 Streptococ	c 262	15	9.3	1083	7	ACA22586	ACA22586 Streptococ
c 206	15	9.3	681	6	AB212468	AB212468 Archae1ops	c 263	15	9.3	1088	2	AAV41890	AAV41890 Nucleotid
c 207	15	9.3	703	4	AAH07260	AAH07260 Human c1N	c 264	15	9.3	1122	7	AACT7673	AACT7673 Staphy1loc
c 208	15	9.3	708	6	ABO69482	ABO69482 Listeria	265	15	9.3	1125	2	AAQ70705	AAQ70705 Plasm1n f
c 209	15	9.3	708	9	ADN34749	ADN34749 Mouse mit	266	15	9.3	1125	4	AAQ66140	AAQ66140 Streptococ
c 210	15	9.3	713	7	ABZ51801	ABZ51801 Asperg111	c 267	15	9.3	1164	7	ADA89862	ADA89862 Staphy1loc
c 211	15	9.3	719	5	ABV23482	ABV23482 Human pro	c 268	15	9.3	1164	7	ADA89858	ADA89858 Staphy1loc
c 212	15	9.3	719	5	ABV29340	ABV29340 Human pro	c 269	15	9.3	1182	6	ABZ14118	ABZ14118 Archae1ops
c 213	15	9.3	720	7	ACA29150	ACA29150 Prokaryot	c 270	15	9.3	1221	2	AAZ96375	AAZ96375 S. pneumo
c 214	15	9.3	729	2	AAK99516	AAK99516 Nucleic a	271	15	9.3	1230	6	ABN67067	ABn67067 Streptococ
c 215	15	9.3	777	3	ACA44445	ACA44445 Archae1ops	272	15	9.3	1272	7	ACA54186	ACA54186 Streptococ
c 216	15	9.3	808	4	AAH04147	AAH04147 Human c1N	273	15	9.3	1275	6	ABQ68879	ABQ68879 Listeria
c 217	15	9.3	822	4	ABU09121	ABU09121 Drosoph11	c 274	15	9.3	1288	5	AAQ88104	AAQ88104 Human FLE
c 218	15	9.3	822	6	ABO68312	ABO68312 Listeria	275	15	9.3	1296	9	ADC93798	ADC93798 E. faec1u
c 219	15	9.3	834	4	ACE74010	ACE74010 Staphy1loc	276	15	9.3	1339	6	ABZ17389	ABZ17389 Archae1ops
c 220	15	9.3	851	6	ABK66888	ABK66888 Helicobac	277	15	9.3	1341	6	ABQ70500	ABQ70500 Listeria
c 221	15	9.3	855	6	ABO67710	ABO67710 Listeria	278	15	9.3	1344	3	AAQ37617	AAQ37617 Streptococ
c 222	15	9.3	873	6	ABO81541	ABO81541 Gene up-r	279	15	9.3	1347	6	ABA91327	ABA91327 Streptococ
c 223	15	9.3	915	7	ABK07572	ABK07572 S. pneumo	c 280	15	9.3	1353	7	ACA31751	ACA31751 Prokaryot
c 224	15	9.3	948	8	ACD06180	ACD06180 Human c1N	c 281	15	9.3	1355	5	AA577302	AA577302 DNA encod
c 225	15	9.3	961	2	AAK14562	AAK14562 H. pylori	c 282	15	9.3	1383	7	ACA22605	ACA22605 Prokaryot
c 226	15	9.3	963	7	ACA21513	ACA21513 Prokaryot	283	15	9.3	1389	6	AA143835	AA143835 Human cit
c 227	15	9.3	992	2	AAV41892	AAV41892 Alternati	284	15	9.3	1394	3	AAK54934	AAK54934 Archae1ops
c 228	15	9.3	1000	2	AAV27350	AAV27350 Streptococ	285	15	9.3	1396	3	AAK33657	AAK33657 Archae1ops
c 229	15	9.3	1000	6	ABO84818	ABO84818 S. pneumo	c 286	15	9.3	1422	4	AA551752	AA551752 Staphy1loc
c 230	15	9.3	1000	6	ADK45134	ADK45134 S. pneumo	c 287	15	9.3	1422	7	ACE74255	ACE74255 Staphy1loc
c 231	15	9.3	1002	5	AA568706	AA568706 DNA encod	c 288	15	9.3	1425	4	AA554921	AA554921 Staphy1loc
c 232	15	9.3	1005	7	ABK07806	ABK07806 S. pneumo	c 289	15	9.3	1425	7	ACA20267	ACA20267 Prokaryot
c 233	15	9.3	1006	4	AA137573	AA137573 Human mus	c 290	15	9.3	1425	7	ACA28992	ACA28992 Prokaryot
c 234	15	9.3	1006	7	ABK60561	ABK60561 cDNA encod	291	15	9.3	1435	1	AAV70101	AAV70101 Sequence
c 235	15	9.3	1008	4	AA551981	AA551981 Stephy1loc	c 292	15	9.3	1497	9	ADC08302	ADC08302 Rice DNA

c 293	15	9.3	1526	6	ABO68969	Abg68969 lIsteria	349	15	9.3	1815	7	ACD04690	AcD04690 Novel hum
c 284	15	9.3	1549	7	ABX70791	Abx70791 Novel hum	350	15	9.3	1815	7	ACD18151	AcD18151 Human sec
c 295	15	9.3	1582	9	ADCO7895	Adc07895 R1ce DNA	351	15	9.3	1815	7	ACD08158	AcD08158 Human sec
c 296	15	9.3	1660	4	AAf32054	Aaf32054 Carnation	352	15	9.3	1815	7	ABX71560	Abx71560 Human cDN
c 297	15	9.3	1660	6	ABK88372	Abk88372 Carnation	353	15	9.3	1815	7	ACB88592	AcB88592 Novel hum
298	15	9.3	1660	5	AA880734	AA880734 DNA encod	354	15	9.3	1815	7	ACB88592	AcB88592 Novel hum
299	15	9.3	1671	4	AAH99737	Aah99737 Human pro	355	15	9.3	1815	7	ACB70034	AcB70034 Human sec
300	15	9.3	1672	6	ABK94904	Abk94904 Human nov	356	15	9.3	1815	7	ACD12256	AcD12256 Novel hum
301	15	9.3	1689	7	ABF113416	Abf113416 Breast sp	357	15	9.3	1815	7	ACD74171	AcD74171 Human sec
302	15	9.3	1737	4	AAc84891	Aac84891 Human SEC	358	15	9.3	1815	7	ACD15799	AcD15799 Human sec
c 303	15	9.3	1743	6	ABK35362	Abk35362 Human cDN	359	15	9.3	1815	7	ACD23567	AcD23567 Novel hum
c 304	15	9.3	1745	7	ADAs2935	Ada52935 Human cod	360	15	9.3	1815	7	ACD17844	AcD17844 Human sec
c 305	15	9.3	1760	4	AAI17483	Aai17483 Mouse sec	361	15	9.3	1815	7	ACB88131	AcB88131 Human sec
306	15	9.3	1762	3	AAI26385	Aai26385 Human sec	362	15	9.3	1815	7	ACD21485	AcD21485 Human sec
307	15	9.3	1763	3	AAI26452	Aai26452 Human sec	363	15	9.3	1815	7	ACD18552	AcD18552 Human sec
c 308	15	9.3	1769	2	AAI21170	Aai21170 Mal2e elo	364	15	9.3	1815	7	ABX98162	Abx98162 Human cDN
309	15	9.3	1795	7	ACD19480	AcD19480 cDNA enco	365	15	9.3	1815	7	ACD13913	AcD13913 Human PRO
310	15	9.3	1812	3	ADc78456	Adc78456 Human PRO	366	15	9.3	1815	7	ACD09693	AcD09693 Human sec
311	15	9.3	1812	6	AB190612	Ab190612 Human pol	367	15	9.3	1815	7	ACB8438	AcB8438 Human sec
312	15	9.3	1815	2	AAK52238	Aak52238 Protein P	368	15	9.3	1815	7	ACD21178	AcD21178 Human cDN
313	15	9.3	1815	4	AAE72296	Aae72296 Human PRO	369	15	9.3	1815	7	ABX97753	Abx97753 Human PRO
314	15	9.3	1815	4	AA545934	Aa545934 Human DNA	370	15	9.3	1815	7	ACB97229	AcB97229 Novel hum
315	15	9.3	1815	7	ABX78537	Abx78537 Human PRO	371	15	9.3	1815	7	ACB57692	AcB57692 Human PRO
316	15	9.3	1815	7	ACA59008	Aca59008 Human PRO	372	15	9.3	1815	7	ACD14220	AcD14220 Human PRO
317	15	9.3	1815	7	ACA75509	Aca75509 Novel hum	373	15	9.3	1815	7	ACB91003	AcB91003 Human sec
318	15	9.3	1815	7	ACA70989	Aca70989 Human sec	374	15	9.3	1815	7	ACB8745	AcB8745 Human sec
319	15	9.3	1815	7	ACB87517	AcB87517 Human sec	375	15	9.3	1815	7	ACD06942	AcD06942 Human PRO
320	15	9.3	1815	7	ACB86903	AcB86903 Human sec	376	15	9.3	1815	7	ACB67393	AcB67393 Human PRO
321	15	9.3	1815	7	ACD04076	AcD04076 Human sec	377	15	9.3	1815	7	ACB81448	AcB81448 Human sec
322	15	9.3	1815	7	ACA69407	Aca69407 cDNA enco	378	15	9.3	1815	7	ACB89052	AcB89052 Human sec
323	15	9.3	1815	7	ACA90252	AcA90252 Novel hum	379	15	9.3	1815	7	ACB89052	AcB89052 Human sec
324	15	9.3	1815	7	ACA98405	Aca98405 cDNA enco	380	15	9.3	1815	7	ACB86408	AcB86408 Human sec
325	15	9.3	1815	7	ACB89359	AcB89359 Human sec	381	15	9.3	1815	7	ACB89666	AcB89666 Human sec
326	15	9.3	1815	7	ACA98150	Aca98150 Novel hum	382	15	9.3	1815	7	ACB92845	AcB92845 Human sec
327	15	9.3	1815	7	ACA93792	Aca93792 Human sec	383	15	9.3	1815	7	ACB72473	AcB72473 Human PRO
328	15	9.3	1815	7	ACD15185	AcD15185 Human sec	384	15	9.3	1815	7	ACB88891	AcB88891 Human sec
329	15	9.3	1815	7	ACD08772	AcD08772 Human sec	385	15	9.3	1815	7	ACB86727	AcB86727 Human sec
330	15	9.3	1815	7	ACB96692	AcB96692 Human sec	386	15	9.3	1815	7	ACB96870	AcB96870 Human sec
331	15	9.3	1815	7	ACF15413	AcF15413 Human sec	387	15	9.3	1815	7	ACB90866	AcB90866 Novel hum
332	15	9.3	1815	7	ACA72780	AcA72780 Human PRO	388	15	9.3	1815	7	ACB70648	AcB70648 Human sec
333	15	9.3	1815	7	ACD02952	AcD02952 Novel hum	389	15	9.3	1815	7	ACB95158	AcB95158 Novel hum
334	15	9.3	1815	7	ACD01767	AcD01767 Novel hum	390	15	9.3	1815	7	ACB86101	AcB86101 Human sec
335	15	9.3	1815	7	ACA91959	AcA91959 Novel hum	391	15	9.3	1815	7	ACB89973	AcB89973 Human sec
336	15	9.3	1815	7	ACA60112	AcA60112 Human cDN	392	15	9.3	1815	7	ACD12581	AcD12581 Human sec
337	15	9.3	1815	7	ACA89384	AcA89384 cDNA enco	393	15	9.3	1815	7	ACF19811	AcF19811 Human sec
338	15	9.3	1815	7	ACA73394	AcA73394 Human sec	394	15	9.3	1815	7	ABX76755	Abx76755 Human PRO
339	15	9.3	1815	7	ACA05709	AcA05709 Human sec	395	15	9.3	1815	7	ABX96129	Abx96129 Human sec
340	15	9.3	1815	7	ACA66543	AcA66543 cDNA enco	396	15	9.3	1815	7	ACB73087	AcB73087 Human sec
341	15	9.3	1815	7	ACD07512	AcD07512 Novel hum	397	15	9.3	1815	7	ACB05450	AcB05450 Novel hum
342	15	9.3	1815	7	ACF20118	AcF20118 Human sec	398	15	9.3	1815	7	ACA66830	AcA66830 Novel hum
343	15	9.3	1815	7	ACF19504	AcF19504 Human sec	399	15	9.3	1815	7	ACB74474	AcB74474 Human sec
344	15	9.3	1815	7	ACD21792	AcD21792 Human sec	400	15	9.3	1815	7	ACB70341	AcB70341 Human sec
345	15	9.3	1815	7	ACF12957	AcF12957 Human sec	401	15	9.3	1815	7	ACD14527	AcD14527 Human PRO
346	15	9.3	1815	7	ACD25060	AcD25060 Human sec	402	15	9.3	1815	7	ACD20117	AcD20117 Human PRO
347	15	9.3	1815	7	ACF00109	AcF00109 Human sec	403	15	9.3	1815	7	ACB68199	AcB68199 Novel hum
348	15	9.3	1815	7	ACA72166	AcA72166 Novel hum	404	15	9.3	1815	7	ABX98664	Abx98664 Novel hum
							405	15	9.3	1815	7	ACB81141	AcB81141 Human sec

406	15	9.3	1815	7	ACA95465	Ac95465	Novel	hum	463	15	9.3	1815	8	ACF41106	AcF41106	Human	sec
407	15	9.3	1815	7	ACD04383	AcD04383	Novel	hum	464	15	9.3	1815	8	ACF15720	AcF15720	Human	sec
408	15	9.3	1815	7	ACB7824	AcB7824	Human	sec	465	15	9.3	1815	8	ACF16027	AcF16027	Human	sec
409	15	9.3	1815	7	ACF12486	AcF12486	Human	sec	466	15	9.3	1815	8	ACD13854	AcD13854	Human	sec
410	15	9.3	1815	7	ACA96201	AcA96201	Human	PRO	467	15	9.3	1815	8	ACF18662	AcF18662	Human	sec
411	15	9.3	1815	7	ACA64975	AcA64975	Human	PRO	468	15	9.3	1815	8	ACF09109	AcF09109	Human	sec
412	15	9.3	1815	7	ACA73701	AcA73701	Human	sec	469	15	9.3	1815	8	ACF78230	AcF78230	Human	sec
413	15	9.3	1815	7	ACA74113	AcA74113	Novel	hum	470	15	9.3	1815	8	ACF51829	AcF51829	Human	sec
414	15	9.3	1815	7	ACA6508	AcA6508	Human	PRO	471	15	9.3	1815	8	ACF26316	AcF26316	Human	sec
415	15	9.3	1815	7	ACD10614	AcD10614	cDNA	encc	472	15	9.3	1815	8	ACF24109	AcF24109	Human	sec
416	15	9.3	1815	7	ACC91310	AcC91310	Human	sec	473	15	9.3	1815	8	ACF63420	AcF63420	Human	sec
417	15	9.3	1815	7	ACD02645	AcD02645	cDNA	encc	474	15	9.3	1815	8	ACF50294	AcF50294	Human	sec
418	15	9.3	1815	7	ACC87210	AcC87210	Human	sec	475	15	9.3	1815	8	ACF07765	AcF07765	Human	sec
419	15	9.3	1815	7	ACC85794	AcC85794	Human	sec	476	15	9.3	1815	8	ACF13571	AcF13571	Human	sec
420	15	9.3	1815	7	ACA65282	AcA65282	Human	PRO	477	15	9.3	1815	8	ACD44497	AcD44497	Human	sec
421	15	9.3	1815	7	ACA94099	AcA94099	Human	sec	478	15	9.3	1815	8	ACF31910	AcF31910	Human	sec
422	15	9.3	1815	7	ACA97843	AcA97843	Human	PRO	479	15	9.3	1815	8	ACF23188	AcF23188	Human	sec
423	15	9.3	1815	7	ACA91345	AcA91345	Novel	hum	480	15	9.3	1815	8	ACF39878	AcF39878	Human	sec
424	15	9.3	1815	7	ACA90559	AcA90559	Novel	hum	481	15	9.3	1815	8	ACD45400	AcD45400	Human	sec
425	15	9.3	1815	7	ACD16106	AcD16106	Human	sec	482	15	9.3	1815	8	ACF35057	AcF35057	Human	sec
426	15	9.3	1815	7	ACD17267	AcD17267	Human	sec	483	15	9.3	1815	8	ACF27237	AcF27237	Human	sec
427	15	9.3	1815	7	ACC91924	AcC91924	Human	sec	484	15	9.3	1815	8	ACF45075	AcF45075	Human	sec
428	15	9.3	1815	7	ACA74781	AcA74781	cDNA	encc	485	15	9.3	1815	8	ACF29693	AcF29693	Human	sec
429	15	9.3	1815	7	ACA91652	AcA91652	Human	PRO	486	15	9.3	1815	8	ACD98769	AcD98769	Human	sec
430	15	9.3	1815	7	ACA71296	AcA71296	Human	sec	487	15	9.3	1815	8	ACD84550	AcD84550	Human	PRO
431	15	9.3	1815	7	ACC90696	AcC90696	Human	sec	488	15	9.3	1815	8	ACD98710	AcD98710	Human	PRO
432	15	9.3	1815	7	ACA65706	AcA65706	cDNA	encc	489	15	9.3	1815	8	ACF77002	AcF77002	Human	sec
433	15	9.3	1815	7	ACA54920	AcA54920	Novel	hum	490	15	9.3	1815	8	ACF76695	AcF76695	Human	sec
434	15	9.3	1815	7	ACA94851	AcA94851	cDNA	encc	491	15	9.3	1815	8	ACF49680	AcF49680	Human	sec
435	15	9.3	1815	7	ACD16413	AcD16413	Human	sec	492	15	9.3	1815	8	ACF49987	AcF49987	Human	sec
436	15	9.3	1815	7	ACD15492	AcD15492	Human	sec	493	15	9.3	1815	8	ACD03386	AcD03386	Human	sec
437	15	9.3	1815	7	ABX16595	AbX16595	Human	CDN	494	15	9.3	1815	8	ACD08465	AcD08465	Human	sec
438	15	9.3	1815	8	ACA97936	AcA97936	Human	PRO	495	15	9.3	1815	8	ACF12179	AcF12179	Human	sec
439	15	9.3	1815	8	ACA98985	AcA98985	Novel	hum	496	15	9.3	1815	8	ACC94687	AcC94687	Human	sec
440	15	9.3	1815	8	ACC91617	AcC91617	Human	sec	497	15	9.3	1815	8	ACD22406	AcD22406	Human	sec
441	15	9.3	1815	8	ACD11028	AcD11028	Novel	hum	498	15	9.3	1815	8	ACF15106	AcF15106	Human	sec
442	15	9.3	1815	8	ACD14878	AcD14878	Human	sec	499	15	9.3	1815	8	ACC97201	AcC97201	Human	sec
443	15	9.3	1815	8	ACD19755	AcD19755	Human	sec	500	15	9.3	1815	8	ADL18197	AdL18197	Human	sec
444	15	9.3	1815	8	ACD11642	AcD11642	Human	sec	501	15	9.3	1815	8	ACD66902	AcD66902	Human	CDN
445	15	9.3	1815	8	ACC95771	AcC95771	Human	sec	502	15	9.3	1815	8	ACC92231	AcC92231	Human	sec
446	15	9.3	1815	8	ACF16334	AcF16334	Human	sec	503	15	9.3	1815	8	ACF13878	AcF13878	Human	sec
447	15	9.3	1815	8	ACF02452	AcF02452	Human	sec	504	15	9.3	1815	8	ACF14185	AcF14185	Human	sec
448	15	9.3	1815	8	ACF02759	AcF02759	Human	sec	505	15	9.3	1815	8	ACF09416	AcF09416	Human	sec
449	15	9.3	1815	8	ACF21346	AcF21346	Human	sec	506	15	9.3	1815	8	ACD45707	AcD45707	Human	sec
450	15	9.3	1815	8	ACF10030	AcF10030	Human	sec	507	15	9.3	1815	8	ACD47856	AcD47856	Human	sec
451	15	9.3	1815	8	ACF77923	AcF77923	Human	sec	508	15	9.3	1815	8	ACF67587	AcF67587	Human	sec
452	15	9.3	1815	8	ACD46628	AcD46628	Human	sec	509	15	9.3	1815	8	ACF25395	AcF25395	Human	sec
453	15	9.3	1815	8	ACD49391	AcD49391	Human	sec	510	15	9.3	1815	8	ACF29079	AcF29079	Human	sec
454	15	9.3	1815	8	ACF28158	AcF28158	Human	sec	511	15	9.3	1815	8	ACD84857	AcD84857	Human	sec
455	15	9.3	1815	8	ACD88848	AcD88848	Human	sec	512	15	9.3	1815	8	ACD89336	AcD89336	Human	PRO
456	15	9.3	1815	8	ACD84243	AcD84243	Human	PRO	513	15	9.3	1815	8	ACD87927	AcD87927	Human	sec
457	15	9.3	1815	8	ACD99017	AcD99017	cDNA	encc	514	15	9.3	1815	8	ACF30614	AcF30614	Human	sec
458	15	9.3	1815	8	ADA77771	AdA77771	Human	sec	515	15	9.3	1815	8	ACF32217	AcF32217	Human	sec
459	15	9.3	1815	8	ACF48759	AcF48759	Human	sec	516	15	9.3	1815	8	ACH11877	AcH11877	CDN	encc
460	15	9.3	1815	8	ADB29341	AcD29341	Human	sec	517	15	9.3	1815	8	ACH12184	AcH12184	CDN	encc
461	15	9.3	1815	8	ACD09079	AcD09079	Human	sec	518	15	9.3	1815	8	ACD40576	AcD40576	Human	sec
462	15	9.3	1815	8	ACF11872	AcF11872	Human	sec	519	15	9.3	1815	8	ACF18048	AcF18048	Human	sec

520	15	9.3	1815	8	ACF08495	Acf08495	Human	sec	577	15	9.3	1815	8	ACF21039	Acf21039	Human	sec
521	15	9.3	1815	8	ACF31296	Acf31296	Human	sec	578	15	9.3	1815	8	ACF20732	Acf20732	Human	sec
522	15	9.3	1815	8	ACF92136	Acf92136	Human	sec	579	15	9.3	1815	8	ACD47549	Acf47549	Human	sec
523	15	9.3	1815	8	ACD50005	Acf50005	Human	sec	580	15	9.3	1815	8	ACF47531	Acf47531	Human	sec
524	15	9.3	1815	8	ACF38708	Acf38708	Human	sec	581	15	9.3	1815	8	ACF53364	Acf53364	Human	sec
525	15	9.3	1815	8	ACF26623	Acf26623	Human	sec	582	15	9.3	1815	8	ACF86399	Acf86399	Human	sec
526	15	9.3	1815	8	ACF24723	Acf24723	Human	sec	583	15	9.3	1815	8	ACH04947	Acf04947	cdNA	encc
527	15	9.3	1815	8	ACF46303	Acf46303	Human	sec	584	15	9.3	1815	8	ACF44444	Acf44444	Human	sec
528	15	9.3	1815	8	ACF27851	Acf27851	Human	sec	585	15	9.3	1815	8	AD442317	Ad442317	Human	sec
529	15	9.3	1815	8	ACD89155	Acf89155	Human	sec	586	15	9.3	1815	8	AD481290	Ad481290	Human	sec
530	15	9.3	1815	8	ACF63727	Acf63727	Human	sec	587	15	9.3	1815	8	ACD22099	Acf22099	Human	sec
531	15	9.3	1815	8	ACF60367	Acf60367	Human	sec	588	15	9.3	1815	8	ACD24446	Acf24446	Human	sec
532	15	9.3	1815	8	ACH12491	ACH12491	cdNA	encc	589	15	9.3	1815	8	ACD39649	Acf39649	cdNA	encc
533	15	9.3	1815	8	ACH09914	ACH09914	Human	sec	590	15	9.3	1815	8	ACD39956	Acf39956	cdNA	encc
534	15	9.3	1815	8	ACH003769	ACH003769	Human	sec	591	15	9.3	1815	8	ACF13264	Acf13264	Human	sec
535	15	9.3	1815	8	ACH010307	ACH010307	Human	sec	592	15	9.3	1815	8	ACF03066	Acf03066	Human	sec
536	15	9.3	1815	8	ACH011949	ACH011949	Human	sec	593	15	9.3	1815	8	ACD23241	Acf23241	Human	sec
537	15	9.3	1815	8	ACD83063	Acf83063	Human	PRO	594	15	9.3	1815	8	ACF27544	Acf27544	Human	PRO
538	15	9.3	1815	8	ACF42334	Acf42334	Human	sec	595	15	9.3	1815	8	ACF11238	Acf11238	Human	sec
539	15	9.3	1815	8	ADA16172	Ad16172	Human	sec	596	15	9.3	1815	8	ACF50601	Acf50601	Human	sec
540	15	9.3	1815	8	ACH18355	ACH18355	Human	sec	597	15	9.3	1815	8	ACF34096	Acf34096	Human	sec
541	15	9.3	1815	8	ACH02145	ACH02145	Human	sec	598	15	9.3	1815	8	ACD46321	Acf46321	Human	sec
542	15	9.3	1815	8	ACH021653	ACH021653	Human	sec	599	15	9.3	1815	8	ACD48163	Acf48163	Human	sec
543	15	9.3	1815	8	ACH10337	ACH10337	Human	sec	600	15	9.3	1815	8	ACF27544	Acf27544	Human	sec
544	15	9.3	1815	8	ACH33789	ACH33789	Human	sec	601	15	9.3	1815	8	ACD24416	Acf24416	Human	sec
545	15	9.3	1815	8	ACH44751	ACH44751	Human	sec	602	15	9.3	1815	8	ACH085471	ACH085471	Human	sec
546	15	9.3	1815	8	ACH090383	ACH090383	Human	sec	603	15	9.3	1815	8	ACH090076	ACH090076	Human	sec
547	15	9.3	1815	8	ACH09096	ACH09096	Human	sec	604	15	9.3	1815	8	ACH083629	ACH083629	Human	PRO
548	15	9.3	1815	8	ACH30307	ACH30307	Human	sec	605	15	9.3	1815	8	ACH07151	ACH07151	Human	sec
549	15	9.3	1815	8	ACH087006	ACH087006	Human	sec	606	15	9.3	1815	8	ACH07438	ACH07438	Human	sec
550	15	9.3	1815	8	ACH60060	ACH60060	Human	sec	607	15	9.3	1815	8	ACH08072	ACH08072	Human	sec
551	15	9.3	1815	8	ACH46610	ACH46610	Human	sec	608	15	9.3	1815	8	ACH11263	ACH11263	cdNA	encc
552	15	9.3	1815	8	ACH73467	ACH73467	Human	sec	609	15	9.3	1815	8	ACH11570	ACH11570	cdNA	encc
553	15	9.3	1815	8	ADA79563	Ad79563	Human	sec	610	15	9.3	1815	8	ACH10221	ACH10221	Human	sec
554	15	9.3	1815	8	ACH17127	ACH17127	Human	sec	611	15	9.3	1815	8	ACH01224	ACH01224	Human	sec
555	15	9.3	1815	8	ACH22881	ACH22881	Human	sec	612	15	9.3	1815	8	ACH0799	ACH0799	Human	sec
556	15	9.3	1815	8	ACH07881	ACH07881	Human	sec	613	15	9.3	1815	8	ACH24139	ACH24139	Human	sec
557	15	9.3	1815	8	ACH08188	ACH08188	Human	sec	614	15	9.3	1815	8	ACH31240	ACH31240	Human	sec
558	15	9.3	1815	8	ACH40492	ACH40492	Human	sec	615	15	9.3	1815	8	ACH32524	ACH32524	Human	sec
559	15	9.3	1815	8	ACH53671	ACH53671	Human	sec	616	15	9.3	1815	8	ACH17741	ACH17741	Human	sec
560	15	9.3	1815	8	ACH46935	ACH46935	Human	sec	617	15	9.3	1815	8	ACH32524	ACH32524	Human	sec
561	15	9.3	1815	8	ACH47838	ACH47838	Human	sec	618	15	9.3	1815	8	ACH40185	ACH40185	Human	sec
562	15	9.3	1815	8	ACH47224	ACH47224	Human	sec	619	15	9.3	1815	8	ACH48145	ACH48145	Human	sec
563	15	9.3	1815	8	ACH45996	ACH45996	Human	sec	620	15	9.3	1815	8	ACH38094	ACH38094	Human	sec
564	15	9.3	1815	8	ACH08085	ACH08085	Human	sec	621	15	9.3	1815	8	ACH25030	ACH25030	Human	sec
565	15	9.3	1815	8	ACH52443	ACH52443	Human	sec	622	15	9.3	1815	8	ACH26930	ACH26930	Human	sec
566	15	9.3	1815	8	ACH52750	ACH52750	Human	sec	623	15	9.3	1815	8	ACH29386	ACH29386	Human	sec
567	15	9.3	1815	8	ACH64743	ACH64743	Human	sec	624	15	9.3	1815	8	ACH087620	ACH087620	Human	sec
568	15	9.3	1815	8	ACH76388	ACH76388	Human	sec	625	15	9.3	1815	8	ACH76081	ACH76081	Human	sec
569	15	9.3	1815	8	ACH61288	ACH61288	Human	sec	626	15	9.3	1815	8	ACH49373	ACH49373	Human	sec
570	15	9.3	1815	8	ACH61595	ACH61595	Human	sec	627	15	9.3	1815	8	ACH43830	ACH43830	Human	sec
571	15	9.3	1815	8	ACH30626	ACH30626	Human	sec	628	15	9.3	1815	8	ACH06175	ACH06175	cdNA	encc
572	15	9.3	1815	8	ACH31547	ACH31547	Human	sec	629	15	9.3	1815	8	ACH06482	ACH06482	cdNA	encc
573	15	9.3	1815	8	ACH32468	ACH32468	Human	sec	630	15	9.3	1815	8	ACH083088	ACH083088	Human	sec
574	15	9.3	1815	8	ACH17434	ACH17434	Human	sec	631	15	9.3	1815	8	ACH292538	ACH292538	Human	sec
575	15	9.3	1815	8	ACH07267	ACH07267	Human	sec	632	15	9.3	1815	8	ACH3152	ACH3152	Human	sec
576	15	9.3	1815	8	ACH20425	ACH20425	Human	sec	633	15	9.3	1815	8	ACH19197	ACH19197	Human	sec

634	15	9.3	1815	8	ACD12888	Accl2888	Human	sec	691	15	9.3	1815	8	ADA1893	Ada1893	Human	sec
635	15	9.3	1815	8	ACF06346	AcF06346	Human	sec	692	15	9.3	1815	8	ACC90280	Acc90280	Human	sec
636	15	9.3	1815	8	ACC94380	Acc94380	Human	sec	693	15	9.3	1815	8	ACF10644	AcF10644	Human	sec
637	15	9.3	1815	8	ACC97808	Acc97808	Human	sec	694	15	9.3	1815	8	ACC93459	Acc93459	Human	sec
638	15	9.3	1815	8	ACC94073	Acc94073	Human	sec	695	15	9.3	1815	8	ACC96078	Acc96078	Human	sec
639	15	9.3	1815	8	ACF42027	AcF42027	Human	sec	696	15	9.3	1815	8	ACD24753	AcD24753	Human	sec
640	15	9.3	1815	8	ACD30933	AcD30933	Human	sec	697	15	9.3	1815	8	ADA17240	Ada17240	Human	sec
641	15	9.3	1815	8	ACD42962	AcD42962	cdNA	encco	698	15	9.3	1815	8	ACF01838	AcF01838	Human	sec
642	15	9.3	1815	8	ACD43269	AcD43269	cdNA	encco	699	15	9.3	1815	8	ACF21960	AcF21960	Human	sec
643	15	9.3	1815	8	ACF14799	AcF14799	Human	sec	700	15	9.3	1815	8	ACF08802	AcF08802	Human	sec
644	15	9.3	1815	8	ACF01531	AcF01531	Human	sec	701	15	9.3	1815	8	ACF33138	AcF33138	Human	sec
645	15	9.3	1815	8	ACF31603	AcF31603	Human	sec	702	15	9.3	1815	8	ACF34592	AcF34592	Human	sec
646	15	9.3	1815	8	ACD67280	AcD67280	cdNA	encco	703	15	9.3	1815	8	ACF48452	AcF48452	Human	sec
647	15	9.3	1815	8	ACD48470	AcD48470	Human	sec	704	15	9.3	1815	8	ACD47242	AcD47242	Human	sec
648	15	9.3	1815	8	ACD48777	AcD48777	Human	sec	705	15	9.3	1815	8	ACD49084	AcD49084	Human	sec
649	15	9.3	1815	8	ACF51215	AcF51215	Human	sec	706	15	9.3	1815	8	ACF37787	AcF37787	Human	sec
650	15	9.3	1815	8	ACF53978	AcF53978	Human	sec	707	15	9.3	1815	8	ACF33000	AcF33000	Human	sec
651	15	9.3	1815	8	ACF25702	AcF25702	Human	sec	708	15	9.3	1815	8	ACD87313	AcD87313	Human	sec
652	15	9.3	1815	8	ACF39015	AcF39015	Human	sec	709	15	9.3	1815	8	ACF61902	AcF61902	Human	sec
653	15	9.3	1815	8	ACF28772	AcF28772	Human	sec	710	15	9.3	1815	8	ACH10835	ACH10835	Human	sec
654	15	9.3	1815	8	ACD90689	AcD90689	Human	sec	711	15	9.3	1815	8	ADA42743	Ada42743	Human	sec
655	15	9.3	1815	8	ACD86392	AcD86392	Human	sec	712	15	9.3	1815	8	ACD10000	AcD10000	Human	sec
656	15	9.3	1815	8	ACH05254	ACH05254	cdNA	encco	713	15	9.3	1815	8	ACD16725	AcD16725	cdNA	encco
657	15	9.3	1815	8	ACF65050	AcF65050	Human	sec	714	15	9.3	1815	8	ACC99022	Acc99022	Human	sec
658	15	9.3	1815	8	ADB20131	AdB20131	Human	sec	715	15	9.3	1815	8	ACF00416	AcF00416	Human	sec
659	15	9.3	1815	8	ACF43523	AcF43523	Human	sec	716	15	9.3	1815	8	ACD40883	AcD40883	Human	sec
660	15	9.3	1815	8	ACH08993	ACH08993	Human	sec	717	15	9.3	1815	8	ACF14492	AcF14492	Human	sec
661	15	9.3	1815	8	ACH09300	ACH09300	Human	sec	718	15	9.3	1815	8	ACF22267	AcF22267	Human	sec
662	15	9.3	1815	8	ADA78383	Ada78383	Human	sec	719	15	9.3	1815	8	ACF78844	AcF78844	Human	sec
663	15	9.3	1815	8	ACF09723	AcF09723	Human	sec	720	15	9.3	1815	8	ACF11565	AcF11565	Human	sec
664	15	9.3	1815	8	ACF50908	AcF50908	Human	sec	721	15	9.3	1815	8	ACF31522	AcF31522	Human	sec
665	15	9.3	1815	8	ACF23802	AcF23802	Human	sec	722	15	9.3	1815	8	ACF33445	AcF33445	Human	sec
666	15	9.3	1815	8	ACH88234	ACH88234	Human	sec	723	15	9.3	1815	8	ACD37480	AcD37480	Human	sec
667	15	9.3	1815	8	ACH09607	ACH09607	Human	sec	724	15	9.3	1815	8	ACF28465	AcF28465	Human	sec
668	15	9.3	1815	8	ACH10528	ACH10528	Human	sec	725	15	9.3	1815	8	ACD88541	AcD88541	Human	sec
669	15	9.3	1815	8	ACD11335	AcD11335	Human	sec	726	15	9.3	1815	8	ACF75160	AcF75160	Human	sec
670	15	9.3	1815	8	ACC96385	Acc96385	Human	sec	727	15	9.3	1815	8	ACF60981	AcF60981	Human	sec
671	15	9.3	1815	8	ACC98415	Acc98415	Human	sec	728	15	9.3	1815	8	ACF44137	AcF44137	Human	sec
672	15	9.3	1815	8	ADA16596	Ada16596	Human	sec	729	15	9.3	1815	8	ACH08379	ACH08379	Human	sec
673	15	9.3	1815	8	ACF41720	AcF41720	Human	sec	730	15	9.3	1815	8	ACH93766	ACH93766	Human	sec
674	15	9.3	1815	8	ACF16641	AcF16641	Human	sec	731	15	9.3	1815	8	ACD20871	AcD20871	Human	sec
675	15	9.3	1815	8	ADA13025	Ada13025	Human	sec	732	15	9.3	1815	8	ACF06653	AcF06653	Human	sec
676	15	9.3	1815	8	ACD32161	AcD32161	Human	sec	733	15	9.3	1815	8	ACD20564	AcD20564	Human	sec
677	15	9.3	1815	8	ACD30319	AcD30319	Human	sec	734	15	9.3	1815	8	ACD22713	AcD22713	Human	sec
678	15	9.3	1815	8	ACD41190	AcD41190	Human	sec	735	15	9.3	1815	8	ACF41413	AcF41413	Human	sec
679	15	9.3	1815	8	ACF07574	AcF07574	Human	sec	736	15	9.3	1815	8	ACF06960	AcF06960	Human	sec
680	15	9.3	1815	8	ACF30989	AcF30989	Human	sec	737	15	9.3	1815	8	ACD23603	AcD23603	Human	PRO
681	15	9.3	1815	8	ACF77309	AcF77309	Human	sec	738	15	9.3	1815	8	ACF77616	AcF77616	Human	sec
682	15	9.3	1815	8	ACF10951	AcF10951	Human	sec	739	15	9.3	1815	8	ACD46014	AcD46014	Human	sec
683	15	9.3	1815	8	ACF32831	AcF32831	Human	sec	740	15	9.3	1815	8	ACF46917	AcF46917	Human	sec
684	15	9.3	1815	8	ACF26009	AcF26009	Human	sec	741	15	9.3	1815	8	ACF54285	AcF54285	Human	sec
685	15	9.3	1815	8	ACD83322	AcD83322	Human	PRO	742	15	9.3	1815	8	ACF45689	AcF45689	Human	sec
686	15	9.3	1815	8	ACF23495	AcF23495	Human	sec	743	15	9.3	1815	8	ACF43382	AcF43382	Human	sec
687	15	9.3	1815	8	ACF42909	AcF42909	Human	sec	744	15	9.3	1815	8	ACF38401	AcF38401	Human	sec
688	15	9.3	1815	8	ACF43216	AcF43216	Human	sec	745	15	9.3	1815	8	ACD89462	AcD89462	Human	sec
689	15	9.3	1815	8	ACH05868	ACH05868	cdNA	encco	746	15	9.3	1815	8				
690	15	9.3	1815	8	ACH08686	ACH08686	Human	sec	747	15	9.3	1815	8				

748	15	9.3	1815	8	ACD85164	AcD85164 Human sec	805	15	9.3	2082	2	AAT05901	Aat05901 Human IL-
749	15	9.3	1815	8	ACD85778	AcD85778 Human sec	806	15	9.3	2088	2	AAQ14479	Aaq14479 Truncated
750	15	9.3	1815	8	ACF75774	AcF75774 Human sec	807	15	9.3	2151	6	ABE12355	AbE12355 Arctidops
751	15	9.3	1815	8	ACF60674	AcF60674 Human sec	808	15	9.3	2179	5	AA576333	AA576333 DNA encod
752	15	9.3	1815	8	ACH05561	AcH05561 cDNA emco	809	15	9.3	2292	6	AB189940	Ab189940 Human pol
753	15	9.3	1815	8	ADA82454	AdA82454 Human sec	810	15	9.3	2297	3	AAE21718	AAE21718 Human bre
754	15	9.3	1815	8	ACF55820	AcF55820 Human sec	811	15	9.3	2394	4	AAH16440	AAH16440 Human cDN
755	15	9.3	1815	8	ACF55206	AcF55206 Human sec	812	15	9.3	2478	7	ADA53202	AdA53202 Human cod
756	15	9.3	1815	9	ADB74662	AdB74662 Human sec	813	15	9.3	2490	9	ADC30181	AdC30181 Human nov
757	15	9.3	1815	9	ADB874798	AdB874798 Human sec	814	15	9.3	2499	3	AAZ95233	AAZ95233 Human pho
758	15	9.3	1815	9	ACF56127	AcF56127 Human sec	815	15	9.3	2499	3	AAZ95234	AAZ95234 Human pho
759	15	9.3	1815	9	ACF56434	AcF56434 Human sec	816	15	9.3	2499	3	AAZ95234	AAZ95234 Human pho
760	15	9.3	1815	9	ACF56434	AcF56434 Human sec	817	15	9.3	2499	3	AAZ95234	AAZ95234 Human pho
761	15	9.3	1815	9	ACF56434	AcF56434 Human sec	818	15	9.3	2503	4	AAE99963	AAE99963 Human cGM
762	15	9.3	1815	9	ACF56434	AcF56434 Human sec	819	15	9.3	2533	4	AAE99963	AAE99963 Human cGM
763	15	9.3	1815	9	ACF56434	AcF56434 Human sec	820	15	9.3	2604	6	ABA96980	ABa96980 Human rib
764	15	9.3	1815	9	ACF56434	AcF56434 Human sec	821	15	9.3	2637	2	AAQ23614	AAQ23614 Human pro
765	15	9.3	1815	9	ACF56434	AcF56434 Human sec	822	15	9.3	2645	2	AAQ79715	AAQ79715 Human pro
766	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	823	15	9.3	2645	2	AAV62158	AAV62158 Human pro
767	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	824	15	9.3	2645	2	AAV62158	AAV62158 Human pro
768	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	825	15	9.3	2645	2	AAV62158	AAV62158 Human pro
769	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	826	15	9.3	2666	7	ACA21437	ACa21437 cDNA emco
770	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	827	15	9.3	2666	7	ACA21437	ACa21437 cDNA emco
771	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	828	15	9.3	2704	2	AAV22792	AAV22792 cDNA em
772	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	829	15	9.3	2706	7	ACC46813	ACc46813 cDNA for
773	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	830	15	9.3	2706	7	ACC46813	ACc46813 cDNA for
774	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	831	15	9.3	2707	8	ADA20928	ADa20928 Mouse BAX
775	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	832	15	9.3	2709	7	AAE71303	AAE71303 Heptep SI
776	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	833	15	9.3	2712	1	AAE71303	AAE71303 Heptep SI
777	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	834	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
778	15	9.3	1815	9	ADCI8986	AdCI8986 Human sec	835	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
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781	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	838	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
782	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	839	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
783	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	840	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
784	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	841	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
785	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	842	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
786	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	843	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
787	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	844	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
788	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	845	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
789	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	846	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
790	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	847	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
791	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	848	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
792	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	849	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
793	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	850	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
794	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	851	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
795	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	852	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
796	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	853	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
797	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	854	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
798	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	855	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
799	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	856	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
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803	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	860	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI
804	15	9.3	1815	10	ADCI8986	AdCI8986 Human sec	861	15	9.3	2724	1	AAE71303	AAE71303 Heptep SI

862	15	9.3	3057	4	AAc84395	919	15	9.3	5737	7	ABZ96657	ABZ96657 Human nuc
863	15	9.3	3057	4	AAc84393	920	15	9.3	5839	2	AAV46335	AAV46335 Hydra hea
864	15	9.3	3072	6	ABK66731	921	15	9.3	5848	6	AA594835	AA594835 Human DNA
865	15	9.3	3098	1	AAAB60195	922	15	9.3	5869	7	ABX08745	ABX08745 Angiogene
866	15	9.3	3157	2	AAQ13316	923	15	9.3	5894	4	AAH57511	AAH57511 Human Kid
867	15	9.3	3313	6	ABK72883	924	15	9.3	6048	2	AAV74439	AAV74439 Stephyloc
868	15	9.3	3372	4	AAQ14494	925	15	9.3	6105	4	ABL09402	ABL09402 Streptophill
869	15	9.3	3381	2	AAAI4957	926	15	9.3	6127	6	ABL13614	ABL13614 Human Imm
870	15	9.3	3382	2	AAQ62300	927	15	9.3	6529	2	AAV41889	AAV41889 Nucleotid
871	15	9.3	3390	5	AAE75054	928	15	9.3	6749	4	ABL28594	ABL28594 Drosophill
872	15	9.3	3461	1	AAAT70681	929	15	9.3	6854	2	AAV52333	AAV52333 Streptoco
873	15	9.3	3465	2	AAQ14478	930	15	9.3	7267	4	AAK69457	AAK69457 Human Imm
874	15	9.3	3471	1	AAAT93650	931	15	9.3	7468	9	ADE53840	ADE53840 Human pro
875	15	9.3	3472	1	AAAT80907	932	15	9.3	7571	2	AAV52135	AAV52135 Streptoco
876	15	9.3	3472	2	AAQ48496	933	15	9.3	7808	8	ACD19234	ACD19234 E. coli 0
877	15	9.3	3472	2	AAQ48497	934	15	9.3	7818	8	ACD01335	ACD01335 Enteroha
878	15	9.3	3473	2	AAAT93651	935	15	9.3	11050	2	AAV74407	AAV74407 Stephyloc
879	15	9.3	3474	1	AAAT80908	936	15	9.3	12701	9	ADD46676	ADD46676 Human gen
880	15	9.3	3489	4	AAI07139	937	15	9.3	16768	4	ABL15650	ABL15650 Drosophill
881	15	9.3	3556	9	AAE75055	938	15	9.3	16825	4	ABK42608	ABK42608 Connectiv
882	15	9.3	3590	9	ADAI8507	939	15	9.3	16825	8	ABE60764	ABE60764 Human cat
883	15	9.3	3642	1	AAAT50364	940	15	9.3	17841	4	ABL04868	ABL04868 Drosophill
884	15	9.3	3771	3	AAAI0741	941	15	9.3	21129	4	AA536234	AA536234 Human cat
885	15	9.3	3774	9	ADE57960	942	15	9.3	21129	9	ADE46928	ADE46928 Human cat
886	15	9.3	3774	9	ADE83401	943	15	9.3	23636	7	ACC48894	ACC48894 Rhodococ
887	15	9.3	3774	9	ADE57956	944	15	9.3	26464	4	AAK81246	AAK81246 Human Imm
888	15	9.3	3780	6	ABE31833	945	15	9.3	26639	9	ADE35685	ADE35685 Mouse mCG
889	15	9.3	3932	4	ABE109146	946	15	9.3	26642	8	ADA03059	ADA03059 Mouse Ken
890	15	9.3	3996	1	AAAT50516	947	15	9.3	26642	8	ADA66343	ADA66343 Mouse Ken
891	15	9.3	4066	6	ABV76591	948	15	9.3	26642	8	ABM72797	ABM72797 Mouse Ken
892	15	9.3	4249	6	ABE161770	949	15	9.3	28690	2	AAK13075	AAK13075 Enterococ
893	15	9.3	4249	6	ABE161770	950	15	9.3	28690	6	AB598870	AB598870 Enterococ
894	15	9.3	4273	9	ADB89105	951	15	9.3	31814	7	AAAD47150	AAAD47150 Human Ras
895	15	9.3	4360	4	ABE24698	952	15	9.3	32195	5	AA532232	AA532232 Human DNA
896	15	9.3	4605	4	ABE14308	953	15	9.3	32195	6	AB567535	AB567535 Novel hum
897	15	9.3	4738	9	ADD18755	954	15	9.3	33206	6	ABN95882	ABN95882 Gene #238
898	15	9.3	4741	4	AAI07140	955	15	9.3	35776	4	AAK68321	AAK68321 Human Imm
899	15	9.3	4779	6	ABE78809	956	15	9.3	37322	6	ABL61996	ABL61996 Colton ade
900	15	9.3	4790	7	ABK49963	957	15	9.3	62782	8	AAAD58281	AAAD58281 Human tum
901	15	9.3	4862	7	ABE442317	958	15	9.3	62782	8	AAAD58281	AAAD58281 Human tum
902	15	9.3	4862	9	ADB58780	959	15	9.3	63020	6	ABQ67197	ABQ67197 Continuation (12 o
903	15	9.3	4862	9	ADB53480	960	15	9.3	66479	6	ABQ80567	ABQ80567 Mutant hu
904	15	9.3	4895	7	ABK63018	961	15	9.3	66479	6	ABQ80566	ABQ80566 Mutant hu
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906	15	9.3	4911	9	ADBS3715	963	15	9.3	66479	6	ABQ80566	ABQ80566 Mutant hu
907	15	9.3	4928	7	ABE117988	964	15	9.3	87977	8	ADA02639	ADA02639 Mouse Znf
908	15	9.3	4929	7	ABE119802	965	15	9.3	87977	9	ADB72377	ADB72377 Mouse Znf
909	15	9.3	4992	9	ADD69642	966	15	9.3	90541	6	AB552847	AB552847 Human SR
910	15	9.3	5211	7	ACC47334	967	15	9.3	90583	7	ACD13447	ACD13447 Mouse DNA
911	15	9.3	5290	6	ABE76452	968	15	9.3	96593	9	ADCB5367	ADCB5367 Mouse BIm
912	15	9.3	5448	2	AAV65229	969	15	9.3	96594	8	ADA02888	ADA02888 Human BIm
913	15	9.3	5535	4	AAV90649	970	15	9.3	96594	8	ADB72626	ADB72626 Human BIm
914	15	9.3	5576	7	ACC48897	971	15	9.3	96595	8	ADA03068	ADA03068 Human PPP
915	15	9.3	5737	2	AAQ58034	972	15	9.3	96595	8	ADB72806	ADB72806 Human PPP
916	15	9.3	5737	2	AAQ58034	973	15	9.3	96596	8	ADA66332	ADA66332 Human PPP
917	15	9.3	5737	2	AAQ58034	974	15	9.3	99500	6	AAAD1740	AAAD1740 Human REC
918	15	9.3	5737	3	AAE20963	975	15	9.3	105184	6	ABK24122	ABK24122 Bacterial

c 976	15	9.3 106286	6	AB553320_4	Continuation (5 of
c 977	15	9.3 110000	2	AAV21209_08	Continuation (9 of
c 978	15	9.3 110000	2	AAV21209_09	Continuation (10 o
c 979	15	9.3 110000	2	AAV21209_14	Continuation (15 o
c 980	15	9.3 110000	2	AAK20248_05	Continuation (6 of
c 981	15	9.3 110000	4	AAK95240_00	Continuation (10 o
c 982	15	9.3 110000	4	AAK95240_09	Continuation (10 o
c 983	15	9.3 110000	4	AAK96733_00	Continuation (10 o
c 984	15	9.3 110000	4	AAK96733_09	Continuation (10 o
c 985	15	9.3 110000	6	ABN71527_07	Continuation (8 of
c 986	15	9.3 110000	6	ABN71527_09	Continuation (11 o
c 987	15	9.3 110000	6	ABN71527_10	Continuation (11 o
c 988	15	9.3 110000	6	ABN71527_10	Continuation (11 o
c 989	15	9.3 110000	6	ABN71527_17	Continuation (18 o
c 990	15	9.3 110000	6	AB553320_1	Continuation (2 of
c 991	15	9.3 110000	6	ABT00010_00	Continuation (10 o
c 992	15	9.3 110000	6	ABT00010_09	Continuation (8 of
c 993	15	9.3 110000	6	ABX08336_07	Continuation (12 o
c 994	15	9.3 110000	6	ABG69245_11	Continuation (11 o
c 995	15	9.3 110000	6	ABG69245_12	Continuation (11 o
c 996	15	9.3 110000	6	ABG67197_10	Continuation (11 o
c 997	15	9.3 110000	6	ABT01503_00	Continuation (10 o
c 998	15	9.3 110000	6	ABT01503_09	Continuation (25 o
c 999	15	9.3 110000	6	ABA03041_24	Continuation (16 o
c 1000	15	9.3 110000	7	AB556454_15	Continuation (16 o

ALIGNMENTS

RESULT 1					
AAA68231					
ID	AAA68231	standard; DNA; 162 BP.			
XX					
AC	AAA68231				
XX					
DT	15-SEP-2003	(revised)			
DT	06-AUG-2003	(revised)			
DT	27-OCT-2000	(first entry)			
XX					
DE	Bacteriophage 77	77ORF102 nucleotide sequence.			
XX					
KW	Bacteriophage; antimicrobial; genome; identification; antibacterial;				
KW	bacterial growth inhibition; bacterial infection; ds.				
XX					
OS	Staphylococcus aureus; bacteriophage 77.				
XX					
PN	WO200032825-A2.				
XX					
PD	08-JUN-2000.				
XX					
PF	03-DEC-1999;	99WC-1B002040.			
XX					
PR	03-DEC-1998;	98US-0110992P.			
PR	03-JUN-1999;	99US-00326144.			
PR	28-SEP-1999;	99US-00407804.			
PR	30-SEP-1999;	99US-0157218P.			

PR	01-DEC-1999;	99US-0168777P.			
PR	02-DEC-1999;	99US-00454252.			
XX					
PA	(PHAG-) PHAGE TECH INC.				
XX					
PI	Pelletier J, Gros P, Dubow M;				
XX					
DR	WPI; 2000-412361/35.				
XX					
PT	P-PSDB; AAB16526.				
PT	Identifying a bacteriophage coding region for treating bacterial				
PT	infections comprises identifying a nucleic acid encoding a product that				
XX	inhibits bacteria when a bacteriophage infects a bacterium.				
XX					
PS	Disclosure; Page 159; 456pp; English.				
XX					
CC	The present invention describes a method for identifying a bacteriophage				
CC	coding region encoding a product active on an essential bacterial target.				
CC	The method comprises identifying a nucleic acid sequence encoding a gene				
CC	product that provides a bacteria-inhibiting function when an				
CC	uncharacterised bacteriophage infects a pathogenic bacterium. The				
CC	compound active on a target of a bacteriophage inhibitor protein in a				
CC	bacteria is used to treat or prevent a bacterial infection in an animal.				
CC	AAA68243 to AAB169442 and AAB16523 to AAB16954 represent bacteriophage				
CC	nucleotide and protein sequences which are used in the exemplification of				
CC	the present invention. (Updated on 06-AUG-2003 to correct 05 field.)				
XX	(Updated on 15-SEP-2003 to standardise 05 field)				
SQ	Sequence 162 BP; 52 A; 32 C; 27 G; 51 T; 0 U; 0 Other;				

Query Match					
Best Local Similarity 100.0%; Score 162; DB 3; Length 162;					
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

QY	1	ATGAGCACTTTATAAAAGCTAGTACGATGATTTATGCTGACAGCTTAGCGATT	60
DB	1	ATGAGCACTTTATAAAAGCTAGTACGATGATTTATGCTGACAGCTTAGCGATT	60
QY	61	GTACTTATGCCGTTTCTATCTTACCTGACATGAGCATGTCGCGGATTCGCAAGTATC	120
DB	61	GTACTTATGCCGTTTCTATCTTACCTGACATGAGCATGTCGCGGATTCGCAAGTATC	120
QY	121	GCAACATTCATGCTACTACAAAGATGCTTTTCAAGATTA	162
DB	121	GCAACATTCATGCTACTACAAAGATGCTTTTCAAGATTA	162

RESULT 2					
AAA68247					
ID	AAA68247	standard; DNA; 41708 BP.			
XX					
AC	AAA68247;				
XX					
DT	15-SEP-2003	(revised)			
DT	06-AUG-2003	(revised)			
DT	27-OCT-2000	(first entry)			
XX					

DE Bacteriophage 77 complete genome sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
XX bacterial growth inhibition; bacterial infection; ds.
OS Staphylococcus aureus; bacteriophage 77.
XX
XX W0200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-1B002040.
XX
XX 03-DEC-1998; 98US-0110992P.
XX 03-JUN-1999; 99US-00326144.
XX 28-SEP-1999; 99US-00407804.
XX 30-SEP-1999; 99US-0157218P.
XX 01-DEC-1999; 99US-0168777P.
XX 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
XX
XX WPI; 2000-412361/35.
XX
XX Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
XX inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Example 3; Page 141-151; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
XX coding region encoding a product active on an essential bacterial target.
XX The method comprises identifying a nucleic acid sequence encoding a gene
XX product that provides a bacteria-inhibiting function when an
XX uncharacterized bacteriophage infects a pathogenic bacterium. The
XX compound active on a target of a bacteriophage inhibitor protein in a
XX bacteria is used to treat or prevent a bacterial infection in an animal.
XX AA68243 to AA69442 and AB16523 to AB16954 represent bacteriophage
XX nucleotide and protein sequences which are used in the exemplification of
XX the present invention. (Updated on 06-AUG-2003 to correct OS field.)
XX (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
XX
XX
XX Query Match 100.0%; Score 162; DB 3; Length 41708;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-74;
XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGAGCAACATTATAAAGCTAGTACGAGTATTGCTTCAAGCTTAGCGATT 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 29051 ATGAGCAACATTATAAAGCTAGTACGAGTATTGCTTCAAGCTTAGCGATT 29110
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 GTACTTATGCGTTTCTATCTATCACTACAGCATGTCGATTCGGGAAATGCAAGTATC 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 29111 GTACTTATGCGTTTCTATCTATCACTACAGCATGTCGATTCGGGAAATGCAAGTATC 29170

QY 121 GCAACATTCATGACTACAAAGATGCTTTTCMAAGATTA 162
DB 29171 GCAACATTCATGACTACAAAGATGCTTTTCMAAGATTA 29212
||||||||||||||||||||||||||||||||||||||||||||||||||
RESULT 3
AAC86106
ID AAC86106 standard; cDNA; 41708 BP.
XX
XX AAC86106;
XX
XX 06-AUG-2003 (revised)
XX 29-AUG-2001 (first entry)
XX
XX Complete genome of bacteriophage 77.
XX
XX Dnal; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
XX screening assay; ss.
XX
XX Bacteriophage.
XX
XX W0200146383-A2.
XX
XX 28-JUN-2001.
XX
XX 21-DEC-2000; 2000WO-US035180.
XX 22-DEC-1999; 99US-00470512.
XX 12-OCT-2000; 2000US-00689952.
XX
XX (PHAG-) PHAGETECH INC.
XX (WILL/) WILLIAMS K M.
XX
XX Pelletier J, Gros P, Dubow M;
XX
XX WPI; 2001-418052/44.
XX
XX Novel Dnal polypeptides useful for treating and diagnosing microbial,
XX preferably bacterial, diseases such as those caused by Staphylococcus
XX aureus.
XX
XX Disclosure; Fig 2; 107pp; English.
XX
XX This sequence represents the genome of Bacteriophage 77. The growth
XX inhibitory gene product of ORF 104 interacts with Dnal polypeptides and
XX aureus, to form the basis of a screening assay. Dnal polypeptides and
XX polynucleotides are useful for treating microbial, preferably bacterial,
XX especially Staphylococcal, infections. Dnal polypeptides and
XX polynucleotides are useful for biological, diagnostic, prophylactic,
XX clinical and therapeutic use, and as components in databases useful for
XX search analyses as well as in sequence analysis algorithms. (Updated on
XX 06-AUG-2003 to correct OS field.)
XX
XX Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 162; DB 4; Length 41708;

XX (CHIR-) CHIRON SPA.
 XX
 XX Malignant V, Mora M, Scarselli M;
 XX WPI; 2003-120786/11.
 DR P-PSDB; ABM71514.
 XX
 XX New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 XX
 XX Claim 6; SEQ ID NO 1507; 49pp; English.
 XX
 XX The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus genes of the invention
 XX
 SQ Sequence 159 BP; 51 A; 30 C; 26 G; 52 T; 0 U; 0 Other;
 Query Match 41.4%; Score 67; DB 7; Length 159;
 Best Local Similarity 100.0%; Pred. No. 8-26-25;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTACAGCATGCT 97
 DB 38 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTACAGCATGCT 97
 QY 98 CAATGC 104
 DB 98 CAATGC 104
 RESULT 6
 ID AAV74851/c
 ID AAV74851 standard; DNA; 1408 BP.
 XX
 AC AAV74851;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus contig SEQ ID #540.
 XX
 XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX

EH Key Location/Qualifiers
 FT misc_feature 1081..1140
 FT /'tag' a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 XX
 XX EP786519-A2.
 PN
 XX
 XX 30-JUL-1997.
 PD
 XX
 XX 07-JAN-1997; 97EP-00100117.
 PP
 XX
 XX 05-JAN-1996; 96US-0009861P.
 PR
 XX
 XX (HUMAN) HUMAN GENOME SCI INC.
 PA
 XX
 XX Kunesh CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 PI WPI; 1997-374922/35.
 DR
 XX
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S. aureus vaccines.
 XX
 XX Claim 1; Page 1475-1476; 3271pp; English.
 PS
 XX
 XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S. aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S. aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S. aureus DNA sequences contained on the computer
 CC readable medium
 XX
 SQ Sequence 1408 BP; 332 A; 250 C; 218 G; 543 T; 0 U; 65 Other;
 Query Match 41.4%; Score 67; DB 2; Length 1408;
 Best Local Similarity 100.0%; Pred. No. 8e-25;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTACAGCATGCT 97
 DB 302 TATGCTTACAGCTTAGCGATTGACTTATGCCGTTCTATCTTACAGCATGCT 243

QY 98 CAATTGC 104
|||||
Db 242 CAATTGC 236

RESULT 7

AAA68254
ID AAA68254 standard; DNA; 43095 BP.

AAA68254;

DT 06-AUG-2003 (rev1eas)
DT 27-OCT-2000 (first entry)

DE Bacteriophage 3a complete genome sequence.

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
bacterial growth inhibition; bacterial infection; ds.

OS Staphylococcus phage 3a.

PN W0200032825-A2.

PD 08-JUN-2000.

PF 03-DEC-1999; 99W0-1B002040.

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00434252.

PA (PHAG-) PHAGETECH INC.

PI Polletier J, Gros P, Dubow M;

DR WPI; 2000-412361/35.

PT Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

PS Disclosure; Page 175-183; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterized bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a

CC bacteriophage is used to treat or prevent a bacterial infection in an animal.

CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

CC nucleotide and protein sequences which are used in the exemplification of

CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)

XX

SQ Sequence 43095 BP; 16332 A; 5908 C; 8513 G; 12342 T; 0 U; 0 Other;

Query Match 40.1%; Score 65; DB 3; Length 43095;

Best Local Similarity 100.0%; Pred. No. 8.2e-24;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGCGTTTCTACTTACACGATGGTCATTCGGGATTCGCAAGTATCGCAACA 126

Db 29508 ATGCGTTTCTACTTACACGATGGTCATTCGGGATTCGCAAGTATCGCAACA 29567

QY 127 TTCAT 131
|||||

Db 29568 TTCAT 29572

RESULT 8
AAA68609
ID AAA68609 standard; DNA; 43576 BP.

AAA68609;

DT 15-SEP-2003 (rev1eas)

DT 06-AUG-2003 (rev1eas)

DT 27-OCT-2000 (first entry)

DE Bacteriophage 96 complete genome sequence.

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

bacterial growth inhibition; bacterial infection; ds.

OS Staphylococcus aureus; bacteriophage 96.

PN W0200032825-A2.

PD 08-JUN-2000.

PF 03-DEC-1999; 99W0-1B002040.

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00434252.

PA (PHAG-) PHAGETECH INC.

PI Polletier J, Gros P, Dubow M;

DR WPI; 2000-412361/35.

PT Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

PS Disclosure; Page 190-198; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterized bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a

CC The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteriophage is used to treat or prevent a bacterial infection in an animal.
CC AAA689243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 43576 BP; 16057 A; 6485 C; 8769 G; 12265 T; 0 U; 0 Other;
Query Match 34.0%; Score 55; DB 3; Length 43576;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 TATGCTTACAGCTGCTAGCATTTGACTTATGCCCTTCTATCTTACTTACACG 92
DB 4475 TATGCTTACAGCTGCTAGCATTTGACTTATGCCCTTCTATCTTACTTACACG 4529
RESULT 9
AAV74602
ID AAV74602 standard; DNA; 2049 BP.
AC AAV74602;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus contig SEQ ID #291.
XX
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT misc_feature 1681..1740
FT /tag= a
FT /note= "these bases represent a line of missing text in
FT the sequence listing in the specification. They are
FT included to maintain the nucleotide numbering given in
FT the specification for this DNA sequence"
XX
XX EP786519-A2.
XX
PD 30-JUL-1997.
XX
XX 07-JAN-1997; 97EP-00100117.
XX
XX 05-JAN-1996; 96US-0009861P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA

XX
F1 Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX WPI; 1997-374922/35.
XX
DR
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S.aureus vaccines.
PS
XX Claim 1; Page 1117-1118; 3271pp; English.
XX
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the computer
CC readable medium
XX
SQ Sequence 2049 BP; 768 A; 272 C; 382 G; 562 T; 0 U; 65 Other;
Query Match 16.0%; Score 26; DB 2; Length 2049;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 TACTTCACTACAGCATGTCATTCG 104
DB 713 TACTTCACTACAGCATGTCATTCG 738
RESULT 10
AAA68911
ID AAA68911 standard; DNA; 25 BP.
XX
AC AAA68911;
XX
XX 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 96 ORF RBS sequence 96ORF303.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; PCR primer; RBS; ribosome binding site;
KW bacterial infection; ss.
XX

05 Staphylococcus aureus; bacteriophage 96.
XX W0200032825-A2.
PN 08-JUN-2000.
PD 03-DEC-1999; 99WO-1B002040.
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX (PHAG-) PHAGETECH INC.
PA Pelletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 203; 456pp; English.
PS
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AA66243 to AA69442 and AB16523 to AB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 25 BP; 10 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 14.2%; Score 23; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 ATAAAGCTACTAGTACGCA 36
DB 1 ATAAAGCTACTAGTACGCA 23
RESULT 11
AA66846
ID AA66846 standard; DNA; 23 BP.
XX
AC AA66846;
XX
DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 96 ORF RBS sequence 96ORF237.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; PCR primer; RBS; ribosome binding site;
KW bacterial infection; ss.
XX
OS Staphylococcus aureus; bacteriophage 96.
XX W0200032825-A2.
XX 08-JUN-2000.
PD 03-DEC-1999; 99WO-1B002040.
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX (PHAG-) PHAGETECH INC.
PA Pelletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 202; 456pp; English.
PS
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AA66243 to AA69442 and AB16523 to AB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 13.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 TATGCTCAGCGCTTACGCA 58
DB 5 TATGCTCAGCGCTTACGCA 25

RESULT 12
 ID ADD18757/c
 AC ADD18757 standard; DNA; 4895 BP.
 XX
 AC ADD18757;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human disease related protein DNA sequence SeqID188.
 XX
 KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiatherosclerotic; vulnerary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transport; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018621-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-GB003892.
 XX
 PR 23-AUG-2001; 2001GB-00020558.
 XX
 PR 05-OCT-2001; 2001GB-00024037.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX
 DR WPI; 2003-290046/28.
 XX
 DR P-PSDB; ADD18736.
 XX
 PT New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX
 PS Claim 27; SEQ ID NO 188; 424bp; English.
 XX
 CC This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory,
 CC ophthalmological, antiatherosclerotic or vulnerary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions,
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transport, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion

CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein encoding DNA sequence of the invention.
 XX
 SQ Sequence 4895 BP; 1597 A; 754 C; 916 G; 1628 T; 0 U; 0 Other;
 Query Match 11.7%; Score 19; DB 9; Length 4895;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AGCAACATTATAAAGCT 22
 DB 3016 AGCAACATTATAAAGCT 2998
 RESULT 13
 ID AAF44629/c
 AC AAF44629 standard; cDNA; 4983 BP.
 XX
 AC AAF44629;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase cDN, SEQ ID NO: 8.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014842.
 XX
 PR 28-MAY-1999; 99US-0136503P.
 XX
 PA (SUGEN-) SUGEN INC.
 XX
 PI Ploewman GD, Martinez R, Whyte D, Sudersanam S;
 XX
 DR WPI; 2001-032161/04.
 XX
 DR P-PSDB; AAB65603.
 XX
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 XX
 PS Example 1; Fig 2; 310pp; English.
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and

CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 CC stress related disorders, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhabdits, autoimmunity, diabetes, cancers and reproductive
 CC disorders

SQ Sequence 4983 BP; 1607 A; 782 C; 954 G; 1640 T; 0 U; 0 Other;

Query Match 11.7%; Score 19; DB 4; Length 4983;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AGCAACATTATATAAGCT 22
 DB 3103 AGCAACATTATATAAGCT 3085
 |||||

RESULT 14
 ID AEN73359 standard; cDNA; 365 BP.
 AC AEN73359;
 XX 03-JUL-2002 (first entry)
 DT
 XX
 DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 45.
 XX
 KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
 XX development; gene; ss.
 OS Bos taurus.
 XX
 PN WO200194550-A2.
 PD 13-DEC-2001.
 XX
 PF 07-JUN-2001; 2001WO-US018576.
 XX
 PR 07-JUN-2000; 2000US-0209874P.
 XX 06-JUN-2001; 2001US-00876143.
 PA (INF1-) INFIGEN INC.
 XX
 PI Ellertsen KJ, Pfister-Genskow M, Childs L;
 XX WPI; 2002-351289/38.
 XX

PT An expressed sequence tag (EST), the expression of which, or its
 PT complementary sequence, in a cell identifies the cell as a
 PT developmentally competent or incompetent cell.
 XX
 PS Example 16; Page 157; 584bp; English.

CC The present invention describes an expressed sequence tag (EST), where
 CC the EST is an isolated, enriched, or purified nucleic acid sequence
 CC representing all or part of a gene, the expression of which, or its
 CC complementary sequence, in a cell identifies the cell as a
 CC developmentally competent or incompetent cell. Molecules which induce
 CC developmental competence in a cell line are useful for inducing
 CC totipotence in one or more cells. Molecules which induce developmental
 CC incompetence in a cell line are useful for preventing a full term
 CC pregnancy in an animal and inhibiting totipotence. The molecules are also
 CC useful for treating a disease in an animal by inducing development of one
 CC or more cells of the animal into a specific cell type. The present
 CC sequence represents a bovine EST which is given in the exemplification of
 CC the present invention

SQ Sequence 365 BP; 101 A; 52 C; 68 G; 143 T; 0 U; 1 Other;

Query Match 11.1%; Score 18; DB 6; Length 365;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGAGCAACATTATATAAA 19
 DB 170 TGAGCAACATTATATAAA 187
 |||||

RESULT 15
 ID AEN73269 standard; cDNA; 365 BP.
 AC AEN73269;
 XX 03-JUL-2002 (first entry)
 DT
 XX
 DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 45.
 XX
 KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
 XX development; gene; ss.
 OS Bos taurus.
 XX
 PN WO200194550-A2.
 PD 13-DEC-2001.
 XX
 PF 07-JUN-2001; 2001WO-US018576.
 XX
 PR 07-JUN-2000; 2000US-0209874P.
 XX 06-JUN-2001; 2001US-00876143.
 PA (INF1-) INFIGEN INC.
 XX

PI Ellertsen KJ, Pfister-Genskow M, Childs L;
XX
XX WPI; 2002-351289/38.
DR

XX An expressed sequence tag (EST), the expression of which, or its
XX
XX complementary sequence, in a cell identifies the cell as a
XX
XX developmentally competent or incompetent cell.
XX

XX Example 16, Page 139, 584pp; English.
XX

XX The present invention describes an expressed sequence tag (EST), where
XX the EST is an isolated, enriched, or purified nucleic acid sequence
XX representing all or part of a gene, the expression of which, or its
XX complementary sequence, in a cell identifies the cell as a
XX developmentally competent or incompetent cell. Molecules which induce
XX developmental competence in a cell line are useful for inducing
XX totipotency in one or more cells. Molecules which induce developmental
XX incompetence in a cell line are useful for preventing a full term
XX pregnancy in an animal and inhibiting totipotency. The molecules are also
XX useful for treating a disease in an animal by inducing development of one
XX or more cells of the animal into a specific cell type. The present
XX sequence represents a bovine EST which is given in the exemplification of
XX the present invention

XX Sequence 365 BP; 101 A; 52 C; 68 G; 143 T; 0 U; 1 Other;

Query Match 11.1%; Score 18; DB 6; Length 365;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAGCAACATTATATAA 19
DB 170 TGAGCAACATTATATAA 187

Search completed: October 15, 2004, 00:17:05
Job time : 144.072 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 22:42:59 ; Search time 757.155 Seconds
(without alignments)

6389,277 Million cell updates/sec

Title: US-09-407-804X-7

Perfect score: 162

Sequence: 1 atgagcacattataaaag.....aatgctttccaagaataa 162

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:
1: em_estda:*
2: em_estnum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gsa_hum:*
18: em_gsa_inv:*
19: em_gsa_pin:*
20: em_gsa_vrt:*
21: em_gsa_fun:*
22: em_gsa_mem:*
23: em_gsa_nus:*
24: em_gsa_pro:*
25: em_gsa_rtd:*
26: em_gsa_png:*
27: em_gsa_vrl:*

28: gp_ges1:*
29: gp_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	12.3	673 28 A0083798	A0083798 CpG0636A
2	19	11.7	151 29 C5578291	C5578291 OST21462
3	19	11.7	203 14 NS4725	NS4725 yz10H07.r1
4	19	11.7	276 9 AA370794	AA370794 EST82486
5	19	11.7	304 9 AA626426	AA626426 ab49e07.r
6	19	11.7	307 9 A1193401	A1193401 qe5Bb04.x
7	19	11.7	411 10 AW993583	AW993583 RC3-BN003
8	19	11.7	522 13 BX869118	BX869118 BX869118
9	19	11.7	563 10 BE813366	BE813366 RC3-BN003
10	19	11.7	568 9 AV713963	AV713963 AV713963
11	19	11.7	576 10 AW993702	AW993702 RC3-BN003
12	19	11.7	591 9 AL600769	AL600769 DFE26313C
13	19	11.7	623 10 AW957241	AW957241 EST368311
14	19	11.7	628 10 AW957243	AW957243 EST368313
15	19	11.7	664 12 BG528724	BG528724 602858184
16	19	11.7	673 13 BX073823	BX073823 BX073823
17	19	11.7	684 13 CA044602	CA044602 ssa1p1mb5
18	19	11.7	695 10 AW963975	AW963975 EST376048
19	19	11.7	741 13 BX073824	BX073824 BX073824
20	19	11.7	749 14 CD101799	CD101799 AGENCOURT
21	19	11.7	762 13 BX104583	BX104583 BX104583
22	19	11.7	764 13 BX083417	BX083417 BX083417
23	19	11.7	785 13 BX083416	BX083416 BX083416
24	19	11.7	786 13 BX873875	BX873875 BX873875
25	19	11.7	788 10 BF254557	BF254557 HVSMEF000
26	19	11.7	788 13 BU744406	BU744406 CH1#001_H
27	19	11.7	832 14 CB310205	CB310205 AGENCOURT
28	19	11.7	843 13 BQ432932	BQ432932 AGENCOURT
29	19	11.7	888 13 BX745780	BX745780 BX745780
30	19	11.7	920 13 BQ892400	BQ892400 AGENCOURT
31	19	11.7	976 12 BG429709	BG429709 602493714
32	19	11.7	3062 11 BC014782	BC014782 Homo sapi
33	18	11.1	229 9 A1235862	A1235862 EST232424
34	18	11.1	280 10 BB342911	BB342911 BB342911
35	18	11.1	307 10 BB343033	BB343033 BB343033
36	18	11.1	344 9 AJ539901	AJ539901 AJ539901
37	18	11.1	438 9 AL805128	AL805128 AL805128
38	18	11.1	450 10 AW636634	AW636634 B149803.w
39	18	11.1	454 9 AJ97350	AJ97350 AJ497350
40	18	11.1	496 10 BF604820	BF604820 270997 MA
41	18	11.1	517 28 AA510134	AA510134 nbmb0094J
42	18	11.1	524 13 BQ458119	BQ458119 kos6c05.y
43	18	11.1	530 9 AL776006	AL776006 AL776006
44	18	11.1	552 28 A0799690	A0799690 HS_5270_A
45	18	11.1	588 10 AM177700	AM177700 RC1-CT019
46	18	11.1	588 14 CK242373	CK242373 rx09b11.y
47	18	11.1	590 14 CD312883	CD312883 StrPUB21.
48	18	11.1	617 13 BW308302	BW308302 BW308302
49	18	11.1	687 13 BX316709	BX316709 BX316709
50	18	11.1	752 28 B2806865	B2806865 PUBR662TD
51	18	11.1	759 28 B2014438	B2014438 oeg83612.
52	18	11.1	760 13 BU758826	BU758826 BU758826
53	18	11.1	780 12 BG108352	BG108352 BG108352
54	18	11.1	845 28 B2137144	B2137144 CH230-288
55	18	11.1	847 13 BU900161	BU900161 AGENCOURT
56	18	11.1	893 28 B2806863	B2806863 PUBR662TD
57	18	11.1	922 14 CA793590	CA793590 AGENCOURT
58	18	11.1	927 13 BQ735465	BQ735465 AGENCOURT
59	18	11.1	962 28 B2672269	B2672269 PUBC777TD
60	18	11.1	1195 13 BX363006	BX363006 BX363006
61	18	11.1	131 9 AA279401	AA279401 z88Bb05.r
62	17	10.5	164 12 BG132884	BG132884 EST465776
63	17	10.5	206 12 BU088191	BU088191 BU088191
64	17	10.5	220 12 BU051025	BU051025 BU051025
65	17	10.5	293 10 BE344400	BE344400 EST313491
66	17	10.5	311 28 AZ116417	AZ116417 RPCT-23-1
67	17	10.5	313 9 AA251965	AA251965 zs1a07.r
68	17	10.5	356 9 A1111363	A1111363 UT-R-YO-m
69	17	10.5	356 28 CC337070	CC337070 OG1AM07TH
70	17	10.5	360 10 BF332870	BF332870 CH1-BT077
71	17	10.5	364 9 A1111366	A1111366 UT-R-YO-m
72	17	10.5	365 12 B1478270	B1478270 dal12a08.
73	17	10.5	374 28 BH823870	BH823870 BACP2-NO
74	17	10.5	378 13 BX108983	BX108983 BX108983
75	17	10.5	379 9 AU090766	AU090766 AU090766
76	17	10.5	381 10 BE319415	BE319415 NF016604R
77	17	10.5	386 12 A0167982	A0167982 HS_3142_B
78	17	10.5	386 12 BG810948	BG810948 da639c01.
79	17	10.5	391 12 BM106404	BM106404 510126 MA
80	17	10.5	393 29 CE577727	CE577727 t1gr-gsa-
81	17	10.5	409 12 B1575867	B1575867 RH32209.5
82	17	10.5	413 28 A0679885	A0679885 HS_5457_A
83	17	10.5	414 9 A1205993	A1205993 q91h11.x
84	17	10.5	420 14 CD002158	CD002158 EST0156 N
85	17	10.5	421 14 CB150226	CB150226 K-EST0206
86	17	10.5	423 10 AM746461	AM746461 da6b0b3.x
87	17	10.5	426 12 BG345336	BG345336 da640c06.
88	17	10.5	430 28 AZ462181	AZ462181 IMN268B19
89	17	10.5	434 29 CG488119	CG488119 OF523518
90	17	10.5	435 10 BE950430	BE950430 UT-M-CEO-
91	17	10.5	437 12 B1509581	B1509581 B3170018A
92	17	10.5	439 14 CA515844	CA515844 KS09048C0
93	17	10.5	454 28 B2184275	B2184275 CH230-340
94	17	10.5	461 10 BF615601	BF615601 da63f02.x
95	17	10.5	464 13 BQ823512	BQ823512 BQ823512
96	17	10.5	465 10 BG020189	BG020189 dc48e01.x
97	17	10.5	467 13 BU876861	BU876861 v026c04 P
98	17	10.5	470 29 CE521115	CE521115 t1gr-gsa-
99	17	10.5	486 13 BQ384797	BQ384797 t1gr-gsa-
100	17	10.5	496 29 CG736918	CG736918 ZPM8B032
101	17	10.5	497 13 BQ384798	BQ384798 N1C_mn08
102	17	10.5	503 13 BQ815812	BQ815812 1030053A1

103	17	10.5	506	28	B2184427	B2184427	CH230-.465	c	160	17	10.5	671	28	BH016955	BH016955	TDCR70TH	
104	17	10.5	515	10	BF232047	BF232047	dd98b03.x	c	161	17	10.5	675	10	BF025209	BF025209	dF98d08.x	
c	105	17	10.5	517	28	AQ260984	CITBI-EI-	c	162	17	10.5	678	13	BQ511092	BQ511092	EST618507	
106	17	10.5	521	29	CE519620	CE519620	t1gr-gss-	c	163	17	10.5	679	14	CB044177	CB044177	NISC_gcc02	
c	107	17	10.5	526	12	B1563669	B1563669	RH3436.5	c	164	17	10.5	685	14	CD815699	CD815699	BN15_-027D
108	17	10.5	529	12	BM262108	BM262108	dag40h01.	c	165	17	10.5	686	12	BD443510	BD443510	Bj443510	
c	109	17	10.5	532	29	AC224664	AC224664	Lotus cor	c	166	17	10.5	711	12	BG888775	BG888775	EST514626
110	17	10.5	538	10	AW917383	AW917383	EST346867	c	167	17	10.5	717	28	BF611888	BF611888	d69e05.Y	
c	111	17	10.5	543	13	BK282869	BK282869	RH65193.5	c	168	17	10.5	717	28	CC153009	CC153009	CSU-K34.1
112	17	10.5	544	14	CF358004	CF358004	rm98c08.Y	c	169	17	10.5	717	29	CG096235	CG096235	PUI7171B	
113	17	10.5	545	12	BC553581	BC553581	dF03e11.x	c	170	17	10.5	724	29	CE123318	CE123318	t1gr-gss-	
114	17	10.5	555	12	BD446646	BD446646	dae78n07.	c	171	17	10.5	728	14	CD819044	CD819044	BN20_.047L	
c	116	17	10.5	559	29	CE193474	CE193474	t1gr-gss-	c	172	17	10.5	729	14	CA509002	CA509002	UI-R-F50-
117	17	10.5	565	10	BE441742	BE441742	925009B01	c	173	17	10.5	730	14	CD833681	CD833681	BN15_.001D	
c	118	17	10.5	566	12	BM002957	BM002957	1031107F0	c	174	17	10.5	732	10	BF211587	BF211587	daeB6c02.x
c	119	17	10.5	567	10	AW931215	AW931215	EST357058	c	175	17	10.5	743	29	CG047336	CG047336	PUI71947B
c	120	17	10.5	570	12	BG600823	BG600823	EST505718	c	176	17	10.5	754	29	CG415356	CG415356	ZMBB6c002
c	121	17	10.5	574	13	BU649461	BU649461	1112080D0	c	177	17	10.5	759	12	BQ047754	BQ047754	ZMBB6c002
122	17	10.5	576	12	BI350279	BI350279	dae65h07.	c	178	17	10.5	767	12	BM408310	BM408310	EST596872	
123	17	10.5	581	12	BM383994	BM383994	UI-R-DM1-	c	179	17	10.5	768	14	CD833966	CD833966	EST592637	
124	17	10.5	583	14	CD819895	CD819895	BN20_.050H	c	180	17	10.5	769	12	BG437931	BG437931	602489685	
125	17	10.5	588	14	CA945909	CA945909	UI-R-F50-	c	181	17	10.5	772	29	CG234107	CG234107	OGC5167V	
126	17	10.5	588	28	AE197761	AE197761	SP_1036_A	c	182	17	10.5	774	29	CG039307	CG039307	PUIB0157B	
c	127	17	10.5	589	28	BH112159	BH112159	RPCI-24-3	c	183	17	10.5	775	28	CC198298	CC198298	ZMBB6c031
c	128	17	10.5	590	12	BH106854	BH106854	EST556390	c	184	17	10.5	775	29	CC854357	CC854357	NDL_119J2
129	17	10.5	596	10	AW981577	AW981577	PC14C06 P	c	185	17	10.5	780	29	CC838538	CC838538	ZMBB6c049	
c	130	17	10.5	600	13	BU904521	BU904521	AGENCOURT	c	186	17	10.5	791	14	CD815682	CD815682	BN15_.027C
131	17	10.5	607	10	AW215836	AW215836	uo99h09.x	c	187	17	10.5	791	29	CC525221	CC525221	CH240_.399	
132	17	10.5	609	12	BI446959	BI446959	dae91c08.	c	188	17	10.5	796	28	BZ608215	BZ608215	WHACAL3TF	
c	133	17	10.5	610	14	CD299343	CD299343	ScFpu336.	c	189	17	10.5	801	12	BG128412	BG128412	EST474058
134	17	10.5	616	14	CF358053	CF358053	rm98g12.Y	c	190	17	10.5	806	12	BP122340	BP122340	BP122340	
135	17	10.5	619	12	BI878237	BI878237	963122H10	c	191	17	10.5	809	28	BZ272365	BZ272365	CH230-.263	
c	136	17	10.5	627	14	CA731358	CA731358	w1plc.pk0	c	192	17	10.5	830	9	AV400830	AV400830	AV400830
137	17	10.5	627	14	CF358064	CF358064	rm99a01.Y	c	193	17	10.5	835	14	CB199253	CB199253	AGENCOURT	
138	17	10.5	630	29	EX137310	EX137310	Danlo rer	c	194	17	10.5	840	14	CD327729	CD327729	AGENCOURT	
c	139	17	10.5	631	10	AM187417	AM187417	BNLGH140	c	195	17	10.5	841	29	CC530277	CC530277	CH240_.406
c	140	17	10.5	633	12	BU416595	BU416595	BM416595	c	196	17	10.5	853	28	BH163374	BH163374	ENTTM64TF
141	17	10.5	636	29	CE628613	CE628613	t1gr-gss-	c	197	17	10.5	855	29	CC594584	CC594584	OGHVI97H	
142	17	10.5	637	13	CA039998	CA039998	ssalshc50	c	198	17	10.5	855	29	CG444577	CG444577	OGHVI97H	
143	17	10.5	641	14	CD834236	CD834236	BN45_.041A	c	199	17	10.5	864	28	B2148143	B2148143	CH230-.406	
c	144	17	10.5	643	29	CE761914	CE761914	t1gr-gss-	c	200	17	10.5	879	29	CG101857	CG101857	PUI71047B
145	17	10.5	646	10	AM806167	AM806167	MRI-UM010	c	201	17	10.5	880	29	CG444585	CG444585	OGHVI97V	
146	17	10.5	646	14	CD829126	CD829126	BN40_.041C	c	202	17	10.5	882	14	CB197889	CB197889	AGENCOURT	
c	147	17	10.5	648	12	BG592490	BG592490	EST491168	c	203	17	10.5	885	14	CD256565	CD256565	AGENCOURT
c	148	17	10.5	649	10	AW907036	AW907036	EST343068	c	204	17	10.5	886	29	CC484890	CC484890	CH240_.314
c	149	17	10.5	650	9	AV336688	AV336688	AV336688	c	205	17	10.5	887	28	CC095939	CC095939	CSU-K34.1
150	17	10.5	650	13	BX869160	BX869160	BN40_.040E	c	206	17	10.5	892	14	CK268012	CK268012	EST714090	
151	17	10.5	653	14	CD828880	CD828880	BN40_.040E	c	207	17	10.5	901	14	CB561106	CB561106	AGENCOURT	
c	152	17	10.5	653	28	BH074563	BH074563	RPCI-24-2	c	208	17	10.5	907	29	CG765366	CG765366	TcB43_.2_C
153	17	10.5	660	14	CF358027	CF358027	rm98e09.Y	c	209	17	10.5	908	13	BU214454	BU214454	603108563	
154	17	10.5	662	12	BI447009	BI447009	dae92c07.	c	210	17	10.5	910	14	CB984261	CB984261	AGENCOURT	
155	17	10.5	663	29	BK221062	BK221062	Danlo rer	c	211	17	10.5	929	14	CB560981	CB560981	AGENCOURT	
c	156	17	10.5	668	29	CE745740	CE745740	t1gr-gss-	c	212	17	10.5	930	29	CD517912	CD517912	AGENCOURT
c	157	17	10.5	668	29	AC057950	AC057950	Pan tcoyl	c	213	17	10.5	936	29	CC838802	CC838802	ZMBB6c049
158	17	10.5	669	9	AT768217	AT768217	w982e11.x	c	214	17	10.5	968	29	CG063792	CG063792	PUMCY197D	
159	17	10.5	671	10	BF863192	BF863192	963041H04	c	215	17	10.5	984	28	CC265194	CC265194	CH261-.37A	
									c	216	17	10.5	997	29	CG457228	CG457228	PURXJ077D

c 217	17	10.5	1034	28	BH157253	BH157253	ENTRHO3TF	c 274	16	9.9	378	28	B96541	B96541	T30GI9TR TA
c 218	17	10.5	1070	28	B2607705	B2607705	WHADCC2TR	c 275	16	9.9	379	9	A1019049	A1019049	uB18C06.r
c 219	17	10.5	1110	28	CC291185	CC291185	CH261-341	c 276	16	9.9	383	29	AG230477	AG230477	Lotus cor
c 220	17	10.5	1144	28	CC294442	CC294442	CH261-631	c 277	16	9.9	384	14	R33779	R33779	yH82607.r1
c 221	17	10.5	1153	29	CG753656	CG753656	P048-4-Cl	c 278	16	9.9	385	13	BY046240	BY046240	AM478171
c 222	17	10.5	1191	29	AG039728	AG039728	Pan treg1	c 279	16	9.9	388	10	AM478171	AM478171	18864 MNR
c 223	17	10.5	1303	10	AW914571	AW914571	ESR345875	c 280	16	9.9	388	12	BG439838	BG439838	da627g09.
c 224	17	10.5	1518	28	CC185828	CC185828	CH261-17E	c 281	16	9.9	395	28	CC102196	CC102196	BY701432
c 225	16	9.9	1115	28	B2378781	B2378781	SALK_1119	c 282	16	9.9	396	13	BY701432	BY701432	CSU-K34.1
c 226	16	9.9	126	10	AM176573	AM176573	RCS-CT007	c 283	16	9.9	401	28	BH399296	BH399296	BM939296
c 227	16	9.9	126	28	A2819734	A2819734	2M0091G03	c 284	16	9.9	402	10	AM978069	AM978069	ESR390178
c 228	16	9.9	168	29	AG205814	AG205814	Oryza sat	c 285	16	9.9	403	14	R16121	R16121	y651f11.r2
c 229	16	9.9	176	9	AA750246	AA750246	ISCA0139	c 286	16	9.9	404	10	BG075015	BG075015	H3142C05-
c 230	16	9.9	195	9	AA750239	AA750239	ISCA0131	c 287	16	9.9	405	10	AM626986	AM626986	Pa22f03.y
c 231	16	9.9	197	28	A2848927	A2848927	2M0150G10	c 288	16	9.9	406	10	BF566104	BF566104	UI-R-BTL-
c 232	16	9.9	198	14	CD961678	CD961678	SDX_224 G	c 289	16	9.9	407	9	AA585635	AA585635	SM309CA36
c 233	16	9.9	198	14	CD966727	CD966727	SEQ_13 G6	c 290	16	9.9	407	29	CE695663	CE695663	t1gT-gss-
c 234	16	9.9	208	9	AA257261	AA257261	MB45LMB4	c 291	16	9.9	408	14	CB188998	CB188998	k427f06.y
c 235	16	9.9	222	9	A1516182	A1516182	LD41962.5	c 292	16	9.9	408	28	A2924920	A2924920	4906.1d95
c 236	16	9.9	249	14	CB000202	CB000202	S345T_B03	c 293	16	9.9	409	29	CG686758	CG686758	mp92a09.r
c 237	16	9.9	250	10	AM409395	AM409395	sa19B5_5a	c 294	16	9.9	411	14	AA119853	AA119853	2M02Bc016
c 238	16	9.9	250	28	B2898399	B2898399	CH240_14G	c 295	16	9.9	413	14	CE528923	CE528923	UI-1-BC1P
c 239	16	9.9	251	9	AV150344	AV150344	AV150344	c 296	16	9.9	414	14	N71833	N71833	y230c10.r1
c 240	16	9.9	258	13	BU791214	BU791214	PN158_P0P	c 297	16	9.9	418	10	BB704473	BB704473	BB704473
c 241	16	9.9	260	10	AM409231	AM409231	Fb4_b4_Fb	c 298	16	9.9	422	10	BB679407	BB679407	BB679407
c 242	16	9.9	261	28	A0028260	A0028260	1(3)TL4032	c 299	16	9.9	424	12	B1501385	B1501385	kx31612.y
c 243	16	9.9	263	9	AA507360	AA507360	oJ70901.s	c 300	16	9.9	424	13	BQ913853	BQ913853	Q4H8K07.y
c 244	16	9.9	266	10	BB226218	BB226218	BB226218	c 301	16	9.9	427	29	CC866059	CC866059	NDL13081
c 245	16	9.9	291	28	A2880482	A2880482	RPCT-23-1	c 302	16	9.9	427	29	AG023387	AG023387	Oryza sat
c 246	16	9.9	291	28	CG387008	CG387008	ZMMBc056	c 303	16	9.9	427	29	DR15H2YT	DR15H2YT	Dn10.r
c 247	16	9.9	300	14	CD373157	CD373157	UI-R-G00-	c 304	16	9.9	428	28	BH618928	BH618928	SALK_0399
c 248	16	9.9	307	10	AM435734	AM435734	74786 MAR	c 305	16	9.9	430	10	BF524438	BF524438	zW55f10.s
c 249	16	9.9	309	12	BH825967	BH825967	K-EST0097	c 306	16	9.9	432	12	BG468046	BG468046	daB10901.
c 250	16	9.9	313	9	AA917738	AA917738	on38601.s	c 307	16	9.9	432	12	Bj380703	Bj380703	UI-R-C3-t
c 251	16	9.9	314	9	AUI65032	AUI65032	AUI65032	c 308	16	9.9	433	12	Bj380703	Bj380703	UI-R-C3-t
c 252	16	9.9	314	14	CB410910	CB410910	C3G10_smb	c 309	16	9.9	437	29	CC874631	CC874631	NDL10081
c 253	16	9.9	320	9	AA421440	AA421440	zu27h03.r	c 310	16	9.9	438	14	H04510	H04510	y116601.r1
c 254	16	9.9	323	14	R69376	R69376	y144H09.r1	c 311	16	9.9	439	28	AQ625342	AQ625342	CITB1-EL-
c 255	16	9.9	326	10	BE145725	BE145725	TL5-HT020	c 312	16	9.9	442	28	AZ095146	AZ095146	RPCT-23-4
c 256	16	9.9	330	14	CF625595	CF625595	zmcwz05.0	c 313	16	9.9	452	9	AU090135	AU090135	AU090135
c 257	16	9.9	332	10	BE081191	BE081191	QV1-BF063	c 314	16	9.9	460	29	BX150359	BX150359	Dn10.r
c 258	16	9.9	339	9	AA175449	AA175449	msB7g01.r	c 315	16	9.9	462	28	AQ755111	AQ755111	HS_3035_B
c 259	16	9.9	344	28	A0106640	A0106640	HS_3080_B	c 316	16	9.9	464	28	AQ38780	AQ38780	HS_2210_B
c 260	16	9.9	345	9	AA842817	AA842817	M-EST134	c 317	16	9.9	465	10	BF730525	BF730525	maB64e08.
c 261	16	9.9	345	9	AA842817	AA842817	M-EST134	c 318	16	9.9	466	28	Bj342698	Bj342698	Bj342698
c 262	16	9.9	346	14	CF128759	CF128759	UI-HF-ES0	c 319	16	9.9	467	9	A1518449	A1518449	LD37964.5
c 263	16	9.9	347	28	AQ107687	AQ107687	HS_3109_A	c 320	16	9.9	469	28	BH384490	BH384490	AG-ND-132
c 264	16	9.9	353	10	AM695637	AM695637	NF097C045	c 321	16	9.9	470	10	AM588438	AM588438	pa14b03.y
c 265	16	9.9	353	14	CF039219	CF039219	QC433f04.	c 322	16	9.9	473	12	B1884233	B1884233	fo20d03.x
c 266	16	9.9	357	14	CF385803	CF385803	RTDR1_6_G	c 323	16	9.9	473	28	B2102865	B2102865	CH230-226
c 267	16	9.9	359	28	AQ333339	AQ333339	HS_5001_A	c 324	16	9.9	476	9	AA905277	AA905277	oJ96362.5
c 268	16	9.9	360	14	D53191	D53191	CELK018C7F	c 325	16	9.9	477	9	AA905277	AA905277	oJ96362.5
c 269	16	9.9	361	29	CE712804	CE712804	t1gT-gss-	c 326	16	9.9	477	13	BY435205	BY435205	BY435205
c 270	16	9.9	363	28	BU0789	BU0789	csRL-11c8-u	c 327	16	9.9	479	14	CA874008	CA874008	K0329D12-
c 271	16	9.9	366	13	BU317513	BU317513	603854841	c 328	16	9.9	479	29	CE097366	CE097366	t1gT-gss-
c 272	16	9.9	378	14	CM378116	CM378116	PTM403285	c 329	16	9.9	479	29	CE097366	CE097366	t1gT-gss-
c 273	16	9.9	378	14	CM378116	CM378116	PTM403285	c 330	16	9.9	479	29	CE097366	CE097366	t1gT-gss-

c 331	16	9.9	480	14	CA873992	CA873992 K0929A05-	388	16	9.9	561	13	BX48885	BX48885 BX48885
c 332	16	9.9	481	29	CE178598	CE178598 t1gr-gsa-	c 389	16	9.9	561	29	CG990071	CG990071 CH240.148
c 333	16	9.9	483	12	BG553261	BG553261 dec23h09.	c 390	16	9.9	562	10	AM44906	AM44906 UI-M-BH3-
c 334	16	9.9	484	28	A2632981	A2632981 1M0487K22	c 391	16	9.9	564	28	A2061798	A2061798 RPT-23-4
c 335	16	9.9	487	14	CB929887	CB929887 t169d03.y	c 392	16	9.9	566	12	BM893671	BM893671 1138b10.x
c 336	16	9.9	488	9	AA170152	AA170152 ms81h11.r	c 393	16	9.9	567	28	AA0176792	AA0176792 HS_3213.A
c 337	16	9.9	490	10	BE212504	BE212504 IPBHn0012	c 394	16	9.9	569	9	AU043928	AU043928 AU043928
c 338	16	9.9	493	29	CE063030	CE063030 t1gr-gsa-	c 395	16	9.9	571	14	CF038515	CF038515 QCH24a10.
c 339	16	9.9	495	9	AU157133	AU157133 u06b08.y	c 396	16	9.9	573	12	B1234171	B1234171 RE29827.5
c 340	16	9.9	496	10	BE629288	BE629288 u06b08.y	c 397	16	9.9	576	28	A2792847	A2792847 2M0045B07
c 341	16	9.9	504	10	BU45873	BU45873 603764244	c 398	16	9.9	580	12	BM485622	BM485622 pmlc-p0
c 342	16	9.9	505	13	BU45873	BU45873 603764244	c 399	16	9.9	581	29	CE513203	CE513203 R5732098
c 343	16	9.9	506	14	CA547648	CA547648 K01496044	c 400	16	9.9	583	10	AM187106	AM187106 BNLGH952
c 344	16	9.9	508	28	AO598820	AO598820 HS_5348.A	c 401	16	9.9	584	29	CE181601	CE181601 t1gr-gsa-
c 345	16	9.9	509	28	AO557391	AO557391 HS_2081.A	c 402	16	9.9	586	28	A2071742	A2071742 RPT-23-4
c 346	16	9.9	510	28	A2447929	A2447929 1M0245N15	c 403	16	9.9	587	28	B23361	B23361 F882ZTR 1GF
c 347	16	9.9	511	28	BH383582	BH383582 AG-ND-175	c 404	16	9.9	587	29	CE634172	CE634172 t1gr-gsa-
c 348	16	9.9	513	12	BM902423	BM902423 rc35p04.y	c 405	16	9.9	588	10	BE775871	BE775871 M3-0001U
c 349	16	9.9	515	28	AA0401929	AA0401929 HS_5005.A	c 406	16	9.9	588	14	CD075410	CD075410 MA3-0001U
c 350	16	9.9	516	12	BS521314	BS521314 ps47e03.y	c 407	16	9.9	590	9	A1532453	A1532453 SD03976.5
c 351	16	9.9	520	9	AV712276	AV712276 AV712276	c 408	16	9.9	592	29	CG846339	CG846339 CG846339
c 352	16	9.9	520	14	CD483518	CD483518 atc01-14m	c 409	16	9.9	593	9	AA060977	AA060977 mj86g07.r
c 353	16	9.9	521	13	BQ542151	BQ542151 ps93h11.y	c 410	16	9.9	593	12	BM330788	BM330788 P1C1_56.F
c 354	16	9.9	521	14	CF038214	CF038214 QCH18d01.	c 411	16	9.9	593	29	CE425669	CE425669 t1gr-gsa-
c 355	16	9.9	522	14	CF048856	CF048856 QCL4c02.y	c 412	16	9.9	594	28	DR12E135	DR12E135 BX103371
c 356	16	9.9	522	14	CF048857	CF048857 QCL4c03.y	c 413	16	9.9	596	13	AX103371	AX103371 BX103371
c 357	16	9.9	529	29	CC384950	CC384950 t1gr-gsa-	c 414	16	9.9	597	28	A2030184	A2030184 RPT-23-3
c 358	16	9.9	530	28	CC384950	CC384950 OGJAE19TV	c 415	16	9.9	597	28	AG071624	AG071624 H3101C08-
c 359	16	9.9	533	28	AO822194	AO822194 HS_5494.A	c 416	16	9.9	597	12	BM876941	BM876941 h73d08.x
c 360	16	9.9	534	29	CNS00USF	AO091389 ArbdIdops	c 417	16	9.9	599	28	BM403628	BM403628 AG-ND-138
c 361	16	9.9	537	14	CB533975	CB533975 767275.MA	c 418	16	9.9	600	29	BM403628	BM403628 AG-ND-138
c 362	16	9.9	539	9	AL823328	AL823328 AL923328	c 419	16	9.9	602	14	CF545349	CF545349 lae78a03.
c 363	16	9.9	540	10	BF499749	BF499749 AT14388.5	c 420	16	9.9	603	12	B1636086	B1636086 SD17554.5
c 364	16	9.9	540	28	AQ788523	AQ788523 HS_2088.B	c 421	16	9.9	604	9	AA540077	AA540077 LD19430.5
c 365	16	9.9	540	29	CE852968	CE852968 t1gr-gsa-	c 422	16	9.9	606	13	BU320640	BU320640 603486696
c 366	16	9.9	541	14	CB395924	CB395924 OSTR16368	c 423	16	9.9	607	13	CE068986	CE068986 t1gr-gsa-
c 367	16	9.9	541	14	CF038680	CF038680 QCH27B12.	c 424	16	9.9	607	29	AG121466	AG121466 BX555119
c 368	16	9.9	542	9	AI520380	AI520380 LD40523.5	c 425	16	9.9	608	9	AA540077	AA540077 LD19430.5
c 369	16	9.9	543	14	CF794572	CF794572 B90100.MA	c 426	16	9.9	608	10	BM067378	BM067378 H3060D05-
c 370	16	9.9	545	10	AM812203	AM812203 RC4-ST01.7	c 427	16	9.9	609	9	AI692185	AI692185 wd37f12.x
c 371	16	9.9	545	14	CD562175	CD562175 B0443F08-	c 428	16	9.9	610	29	CE000811	CE000811 t1gr-gsa-
c 372	16	9.9	547	10	BE667228	BE667228 151477.MA	c 429	16	9.9	611	13	BU986819	BU986819 HFI2824r
c 373	16	9.9	549	13	BM085247	BM085247 1h73d08.y	c 430	16	9.9	611	14	CD563461	CD563461 B046A04-
c 374	16	9.9	550	28	AZ054344	AZ054344 RPT-23-4	c 431	16	9.9	612	28	BM877417	BM877417 h737d02.g
c 375	16	9.9	550	29	CE023655	CE023655 t1gr-gsa-	c 432	16	9.9	613	9	AL602935	AL602935 DKEFP686E
c 376	16	9.9	551	9	AI518700	AI518700 LD38384.5	c 433	16	9.9	613	12	B1630176	B1630176 R5912.5
c 377	16	9.9	551	12	BM257782	BM257782 521636.MA	c 434	16	9.9	614	10	BE775477	BE775477 M3-01-D-0
c 378	16	9.9	551	14	CB373904	CB373904 rg60f06.y	c 435	16	9.9	615	28	A2397894	A2397894 1M0163N05
c 379	16	9.9	551	29	CE206231	CE206231 t1gr-gsa-	c 436	16	9.9	616	12	BM616700	BM616700 B02614913
c 380	16	9.9	551	29	CE718017	CE718017 t1gr-gsa-	c 437	16	9.9	617	10	BB161636	BB161636 B02614913
c 381	16	9.9	553	12	B1813367	B1813367 PFSSTceal	c 438	16	9.9	618	14	CB429326	CB429326 605134.MA
c 382	16	9.9	553	28	AQ766761	AQ766761 HS_2181.A	c 439	16	9.9	618	29	CE531186	CE531186 t1gr-gsa-
c 383	16	9.9	554	14	CF788428	CF788428 860377.MA	c 440	16	9.9	618	29	CE531186	CE531186 t1gr-gsa-
c 384	16	9.9	555	10	BF693832	BF693832 602082382	c 441	16	9.9	618	29	CE531186	CE531186 t1gr-gsa-
c 385	16	9.9	556	10	BB756027	BB756027 BB756027	c 442	16	9.9	618	29	CE531186	CE531186 t1gr-gsa-
c 386	16	9.9	556	14	CB532876	CB532876 737360.MA	c 443	16	9.9	618	29	CE531186	CE531186 t1gr-gsa-
c 387	16	9.9	558	12	BM358080	BM358080 RH122_66	c 444	16	9.9	618	29	CE531186	CE531186 t1gr-gsa-

445	16	9.9	619	29	CEB25113	t1gr-gsa-	502	16	664	14	CF789214
c 446	16	9.9	620	29	CE559277	CE559277 t1gr-gsa-	c 503	16	664	14	CF810779
447	16	9.9	622	10	AMS35071	AMS35071 L0249503-	c 504	16	664	28	AQ157286
448	16	9.9	622	10	BU439174	BU439174 604142919	c 505	16	664	28	CC086559
449	16	9.9	622	14	CA211066	CA211066 SCEPSB113	c 506	16	665	14	CF623971
450	16	9.9	622	14	CK098124	CK098124 A005P08.5	c 507	16	667	14	CF623971
c 451	16	9.9	623	9	AA949183	AA949183 LD27982.5	c 508	16	667	14	CF623971
c 452	16	9.9	623	9	AI438630	AI438630 486012610	c 509	16	668	28	AZ568861
c 453	16	9.9	624	28	A2994473	A2994473 2M0279X09	c 510	16	668	28	AZ568861
454	16	9.9	624	29	AG226080	AG226080 Lotus cor	c 511	16	668	28	AQ250794
455	16	9.9	626	12	BAG23623	BAG23623 170006875	c 512	16	671	28	BZ601681
c 456	16	9.9	626	28	BH515668	BH515668 BOHNM62TF	c 513	16	671	28	BZ601681
c 457	16	9.9	627	14	CB455966	CB455966 713182 MA	c 514	16	672	28	BH702051
458	16	9.9	627	28	BH319373	BH319373 CH230-196	c 515	16	673	29	CG153373
459	16	9.9	628	28	A0897310	A0897310 HS_314_A	c 516	16	674	9	AVB821927
460	16	9.9	628	29	CCB857793	CCB857793 ND.L.118L1	c 517	16	675	14	CB455280
c 461	16	9.9	629	14	CA365723	CA365723 640919 NC	c 518	16	676	28	AZ659169
c 462	16	9.9	630	9	AI405818	AI405818 GH25953.5	c 519	16	676	29	CE719078
c 463	16	9.9	631	10	BB629376	BB629376 BB629376	520	16	677	29	CNS05AJ7
464	16	9.9	634	29	CE277247	CE277247 t1gr-gsa-	521	16	678	28	AZ575158
c 465	16	9.9	636	13	BK099019	BK099019 BX099019	522	16	679	28	BH178932
c 466	16	9.9	636	14	CB538309	CB538309 776276 MA	523	16	679	29	CNS07LAU
c 467	16	9.9	637	10	AW791396	AW791396 D00514-F	c 524	16	679	29	LBAP029G09
c 468	16	9.9	638	28	A2987216	A2987216 2M0269P07	c 525	16	680	10	BM691686
c 469	16	9.9	639	10	BG067505	BG067505 H3055808-	c 526	16	680	10	BE325920
c 470	16	9.9	639	13	BO517268	BO517268 EST624683	c 527	16	681	14	CK003897
471	16	9.9	640	12	B6268946	B6268946 Lr_CA12.0	c 528	16	684	14	BB653687
c 472	16	9.9	640	29	CCB60672	CCB60672 ND.L.18J3	c 529	16	684	14	CF200052
473	16	9.9	641	28	A2401200	A2401200 1M0167L14	c 530	16	687	28	AZ668036
c 474	16	9.9	642	12	BI231463	BI231463 RE21934.5	c 531	16	688	29	CE223207
c 475	16	9.9	642	29	CE359090	CE359090 t1gr-gsa-	c 532	16	689	9	AU129220
c 476	16	9.9	643	10	BB185310	BB185310 BB185310	c 533	16	692	12	BH341247
477	16	9.9	643	13	BK717850	BK717850 BX717850	534	16	692	28	BH999290
c 478	16	9.9	643	13	BK717850	BK717850 BX717850	c 535	16	693	13	EX845303
479	16	9.9	646	14	CA359249	CA359249 632152 NC	c 536	16	693	28	AZ952120
c 480	16	9.9	646	14	CA359242	CA359242 MMSF0003	537	16	694	9	AA141003
481	16	9.9	647	28	AQ200875	AQ200875 RPCI11-6T	c 538	16	695	28	AZ987589
c 482	16	9.9	648	28	AG955759	AG955759 LEAP81TR	c 539	16	695	28	AZ987589
c 483	16	9.9	651	28	BZ334376	BZ334376 hx79a07.9	c 540	16	695	28	BH421862
485	16	9.9	651	29	CC065596	CC065596 PUKAC57TB	c 541	16	695	28	BZ010906
486	16	9.9	652	29	AG243390	AG243390 Lotus cor	c 542	16	699	14	CA384766
487	16	9.9	653	28	BZ373337	BZ373337 1a86903.b	c 543	16	699	14	CA384766
488	16	9.9	655	28	A2401025	A2401025 1M0167L06	544	16	700	13	BQ190789
c 489	16	9.9	655	28	BZ892684	BZ892684 Hm7_0109.	c 545	16	700	13	BQ190789
c 490	16	9.9	656	29	CE273976	CE273976 t1gr-gsa-	546	16	703	29	CE464734
c 491	16	9.9	657	14	CF788067	CF788067 856783 MA	c 547	16	703	13	BUT68129
c 492	16	9.9	657	28	BZ343375	BZ343375 hx79a07.b	c 548	16	706	13	BUT58918
c 493	16	9.9	658	28	A2420339	A2420339 1M0198F10	c 549	16	706	28	BZ951448
494	16	9.9	660	10	BH168452	BH168452 BH169452	551	16	710	9	A1200883
495	16	9.9	660	12	BH993569	BH993569 UI-H-DT0-	c 552	16	711	14	CB428754
c 496	16	9.9	660	13	BH138813	BH138813 NF007803P	553	16	715	28	BH403106
c 497	16	9.9	660	13	BY741957	BY741957 BY741957	c 554	16	716	12	EM606494
c 498	16	9.9	660	14	CF628999	CF628999 zmcw48.0	c 555	16	717	28	BZ786072
499	16	9.9	660	29	CC590740	CC590740 CH240.390	c 556	16	720	28	BZ891966
500	16	9.9	662	9	AI405617	AI405617 GH25702.5	c 557	16	721	14	CB427237
c 501	16	9.9	664	12	BZ293160	BZ293160 602390106	558	16	722	14	CA447176

c 559	16	9.9	722	29	CG949817	MBEHB61TR	c 616	16	9.9	795	28	BH389992	BH389992 AG-ND-138
c 560	16	9.9	722	29	BK233518	Datlo ref	c 617	16	9.9	796	9	AUI37771	AUI37771 AUI37771
c 561	16	9.9	726	13	BU249040	603784017	c 618	16	9.9	797	28	BH335464	BH335464 CH230-110
c 562	16	9.9	727	13	BK683341	BK683341	c 619	16	9.9	798	13	BU333177	BU333177 603406448
c 563	16	9.9	727	28	BH485224	BH485224 BOHCH19TF	c 620	16	9.9	798	29	CE425788	CE425788 t1qf-gss-
c 564	16	9.9	727	29	CC641738	OGFY36TV	c 621	16	9.9	799	28	BH021670	BH021670 GH_MEB000
c 565	16	9.9	728	28	BH583083	BH583083 BOGLA80TF	c 622	16	9.9	801	29	BK185384	BK185384 Datlo ref
c 566	16	9.9	730	12	BH359737	BH359737 GA_E6002	c 623	16	9.9	802	14	CAJ318126	CAJ318126 UI-M-FW0-
c 567	16	9.9	731	28	BH402292	BH402292 AG-ND-173	c 624	16	9.9	803	29	BK243830	BK243830 Datlo ref
c 568	16	9.9	731	29	CC707343	CC707343 OGJLA66TH	c 625	16	9.9	804	29	BK167787	BK167787 Datlo ref
c 569	16	9.9	736	14	CK024960	CK024960 AGENCOURT	c 626	16	9.9	807	13	CAJ51038	CAJ51038 SCFMR2200
c 570	16	9.9	736	28	BZ247285	BZ247285 CH230-314	c 627	16	9.9	809	13	BU247028	BU247028 603779718
c 571	16	9.9	738	28	BZ267545	BZ267545 CH230-509	c 628	16	9.9	809	28	BH581997	BH581997 BOCCG65TR
c 572	16	9.9	740	13	BK308145	BK308145	c 629	16	9.9	811	14	CB987011	CB987011 AGENCOURT
c 573	16	9.9	740	14	CF440504	CF440504 EST676849	c 630	16	9.9	812	14	CB643080	CB643080 OSJNBE03J
c 574	16	9.9	740	28	AQ579380	AQ579380 rdbd0084E	c 631	16	9.9	813	14	CB652581	CB652581 OSJNBE02L
c 575	16	9.9	741	28	CC122947	CC122947 ND.L.24H7.	c 632	16	9.9	815	29	CC702332	CC702332 OGJAH15TV
c 576	16	9.9	742	28	BZ442381	BZ442381 BONQ028TF	c 633	16	9.9	816	13	BK054352	BK054352 BX054352
c 577	16	9.9	742	29	CG961933	CG961933 MBEGB52TF	c 634	16	9.9	818	28	BZ427573	BZ427573 BONKJ97TR
c 578	16	9.9	743	29	CC304722	CC304722 t1qf-gss-	c 635	16	9.9	819	9	AA439751	AA439751 IDJ4392.5
c 579	16	9.9	745	13	BU631677	BU631677 UI-H-FL0-	c 636	16	9.9	824	14	CB628438	CB628438 OST1EB04A
c 580	16	9.9	745	13	BW017012	BW017012 BWP017012	c 637	16	9.9	825	28	BZ444844	BZ444844 BONKJ79TR
c 581	16	9.9	748	29	AG095742	AG095742 Pan treq1	c 638	16	9.9	828	28	CC753721	CC753721 ZMWMB013
c 582	16	9.9	754	14	CK111978	CK111978 V060F12.P	c 639	16	9.9	829	13	BQ930760	BQ930760 AGENCOURT
c 583	16	9.9	754	14	CK111978	CK111978	c 640	16	9.9	830	28	BZ612705	BZ612705 WHBHW3TR
c 584	16	9.9	756	29	BK215180	BK215180	c 641	16	9.9	833	28	CC075430	CC075430 CSU-K31F.
c 585	16	9.9	758	12	B1333881	B1333881	c 642	16	9.9	835	14	CF436537	CF436537 EST672882
c 586	16	9.9	758	28	BZ481949	BZ481949 BONBF64TR	c 643	16	9.9	836	29	CG173131	CG173131 PUFTH35TR
c 587	16	9.9	758	29	CG944722	CG944722 MBEFW65TR	c 644	16	9.9	842	14	CB625678	CB625678 BOTHE47TF
c 588	16	9.9	759	29	CC870064	CC870064 ND.L.52114	c 645	16	9.9	844	29	AG035722	AG035722 Pan treq1
c 589	16	9.9	762	28	AG057071	AG057071 rdbd0004J	c 646	16	9.9	847	14	CF253967	CF253967 mdm110.b
c 590	16	9.9	764	29	CC542550	CC542550	c 647	16	9.9	847	28	AZ128522	AZ128522 OSJNBE009
c 591	16	9.9	765	29	CC738960	CC738960	c 648	16	9.9	848	29	CG108421	CG108421 PUGN35TR
c 592	16	9.9	766	13	BU631648	BU631648 UI-H-FL0-	c 649	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 593	16	9.9	768	13	BU928780	BU928780	c 650	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 594	16	9.9	770	10	BE738201	BE738201 601572625	c 651	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 595	16	9.9	770	28	BE297517	BE297517 PUGG545TD	c 652	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 596	16	9.9	772	28	BZ16431	BZ16431 1f67d07.g	c 653	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 597	16	9.9	776	28	BZ150589	BZ150589 CH230-395	c 654	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 598	16	9.9	776	29	CG151708	CG151708 PUFQ662TR	c 655	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 599	16	9.9	778	28	AZ828358	AZ828358 2M0107B05	c 656	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 600	16	9.9	780	13	BU630464	BU630464 UI-H-FL0-	c 657	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 601	16	9.9	780	14	CF483412	CF483412 POLI.22.D	c 658	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 602	16	9.9	781	29	BK222679	BK222679	c 659	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 603	16	9.9	783	29	CC859732	CC859732 ND.L.111M2	c 660	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 604	16	9.9	783	29	CC669492	CC669492 t1qf-gss-	c 661	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 605	16	9.9	784	28	BH199999	BH199999 Sml-35B18	c 662	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 606	16	9.9	785	29	CC923947	CC923947 t072e24ba	c 663	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 607	16	9.9	786	12	BG185998	BG185998 RST4954.A	c 664	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 608	16	9.9	786	12	BG208101	BG208101 RST27591	c 665	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 609	16	9.9	788	28	BH694188	BH694188 BOMAT35TF	c 666	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 610	16	9.9	789	28	BZ422320	BZ422320 1d52c09.b	c 667	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 611	16	9.9	790	13	BQ438031	BQ438031 AGENCOURT	c 668	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 612	16	9.9	792	29	CC923973	CC923973 t072h02ba	c 669	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 613	16	9.9	793	28	CC128692	CC128692 ND.L.35F18	c 670	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 614	16	9.9	794	13	BU751446	BU751446 CH4#002.B	c 671	16	9.9	848	29	AG035722	AG035722 Pan treq1
c 615	16	9.9	795	14	CG301791	CG301791 AGENCOURT	c 672	16	9.9	848	29	AG035722	AG035722 Pan treq1

673	16	9.9	882	28	B2563263	B2563263	pacx2-164	c 730	16	9.9	991	12	BM470743	BM470743	AGENCOURT
674	16	9.9	882	28	B2674444	B2674444	PUGC96TB	731	16	9.9	995	28	CC188842	CC188842	CC188842
675	16	9.9	882	29	CG31617	CG31617	OGIAR28TH	732	16	9.9	997	10	BF105334	BF105334	BF105334
676	16	9.9	883	14	CF619324	CF619324	AGENCOURT	733	16	9.9	999	28	B2799407	B2799407	B2799407
677	16	9.9	885	29	CG153374	CG153374	PUIFEL4TD	c 734	16	9.9	1002	12	BM465904	BM465904	BM465904
678	16	9.9	889	28	B2152441	B2152441	CH230-300	735	16	9.9	1004	9	AA142280	AA142280	AGENCOURT
679	16	9.9	891	13	BU218483	BU218483	603105678	c 736	16	9.9	1004	14	CD081586	CD081586	CD081586
680	16	9.9	891	29	CG362146	CG362146	OGIDE90TH	c 737	16	9.9	1004	29	CG462023	CG462023	CG462023
681	16	9.9	893	28	AQ745410	HS_2276_A		c 738	16	9.9	1011	28	CC191499	CC191499	CC191499
682	16	9.9	894	29	CG31626	OGIAR28TV		739	16	9.9	1011	28	CC257436	CC257436	CC257436
683	16	9.9	894	29	CG946014	MBECG81TR		740	16	9.9	1014	28	CC253070	CC253070	CC253070
684	16	9.9	895	14	CF375319	AGENCOURT		741	16	9.9	1017	28	CC271663	CC271663	CC271663
685	16	9.9	896	13	BK371377	BK371377		c 742	16	9.9	1034	28	BM692631	BM692631	BM692631
686	16	9.9	898	29	CG976966	MBED25TR		743	16	9.9	1038	28	CC245241	CC245241	CC245241
687	16	9.9	903	29	CG362154	OGIDE90TV		744	16	9.9	1042	29	CNS05EVH	CNS05EVH	CNS05EVH
688	16	9.9	904	13	BK716763	BK716763	AL222888	c 745	16	9.9	1047	12	BG873533	BG873533	BG873533
689	16	9.9	904	29	CNS03021	Tetradon		c 746	16	9.9	1050	28	CC240612	CC240612	CC240612
690	16	9.9	909	12	BM523195	603175292		747	16	9.9	1063	10	BE548664	BE548664	BE548664
691	16	9.9	910	12	BG420928	602451139		c 748	16	9.9	1072	14	CF594645	CF594645	CF594645
692	16	9.9	910	28	BH139789	ENTND15TR		749	16	9.9	1082	28	CC238259	CC238259	CC238259
693	16	9.9	914	12	B1690101	603310579		750	16	9.9	1101	29	CNS00221	CNS00221	CNS00221
694	16	9.9	914	13	BU517782	AGENCOURT		c 751	16	9.9	1106	28	AQ446181	AQ446181	AQ446181
695	16	9.9	915	29	CG151709	PURFG62TD		752	16	9.9	1108	28	CC262998	CC262998	CC262998
696	16	9.9	916	29	CG436376	OGVGF48TV		753	16	9.9	1125	28	CC185298	CC185298	CC185298
697	16	9.9	919	28	CC130183	NDL_18816		754	16	9.9	1129	10	BE905413	BE905413	BE905413
698	16	9.9	921	13	BK773762	BK773762		c 755	16	9.9	1136	28	A2916351	A2916351	A2916351
699	16	9.9	923	29	CG131415	PUDJ384TD		c 756	16	9.9	1139	12	BM467431	BM467431	BM467431
700	16	9.9	924	12	BM423230	PLATE3_HO		c 757	16	9.9	1168	28	CC298383	CC298383	CC298383
701	16	9.9	925	28	CC125527	NDL_34P9		c 758	16	9.9	1173	12	BM51289	BM51289	BM51289
702	16	9.9	931	13	BK410931	BK410931		759	16	9.9	1175	28	CC256247	CC256247	CC256247
703	16	9.9	933	28	BH137941	ENTOKO9TF		c 760	16	9.9	1201	13	BK335869	BK335869	BK335869
704	16	9.9	934	13	BU148598	AGENCOURT		c 761	16	9.9	1216	28	CC235126	CC235126	CC235126
705	16	9.9	935	29	CNS042CH	Tetradon		c 762	16	9.9	1224	12	BM802570	BM802570	BM802570
706	16	9.9	936	28	B237678	CH230-382		763	16	9.9	1272	13	BU598573	BU598573	BU598573
707	16	9.9	937	29	CG392166	FHCRC-GT-		764	16	9.9	1294	14	BM463932	BM463932	BM463932
708	16	9.9	939	13	BQ959509	AGENCOURT		765	16	9.9	1324	12	BM913824	BM913824	BM913824
709	16	9.9	940	29	CG108498	NDL_32K16		c 766	16	9.9	1333	13	BM065958	BM065958	BM065958
710	16	9.9	940	29	CG057912	PUDGN4TD		c 767	16	9.9	1486	28	CC287785	CC287785	CC287785
711	16	9.9	942	13	BU914651	AGENCOURT		c 768	16	9.9	1510	28	CC194715	CC194715	CC194715
712	16	9.9	944	13	BU511146	AGENCOURT		c 769	16	9.9	1533	28	CC286541	CC286541	CC286541
713	16	9.9	945	28	CC126815	NDL_76B2		770	16	9.9	1545	29	AV413932	AV413932	AV413932
714	16	9.9	945	29	CG957595	MBEGP67TR		771	16	9.9	1562	29	AV413931	AV413931	AV413931
715	16	9.9	951	29	CNS020MD	Tetradon		772	16	9.9	1652	12	BG847977	BG847977	BG847977
716	16	9.9	954	12	BT453051	603170023		c 773	16	9.9	2416	11	AK037904	AK037904	AK037904
717	16	9.9	957	28	CC389388	PURH139TD		774	16	9.9	3378	11	AK045737	AK045737	AK045737
718	16	9.9	958	29	CG354429	OGW6114TV		775	16	9.9	4488	11	BC057291	BC057291	BC057291
719	16	9.9	962	28	CC004068	PUDG250TD		c 776	16	9.9	123	10	AW384173	AW384173	AW384173
720	16	9.9	965	12	BG180043	602329604		c 777	15	9.3	125	12	BM029376	BM029376	BM029376
721	16	9.9	965	13	BQ963710	AGENCOURT		778	15	9.3	130	13	BC097827	BC097827	BC097827
722	16	9.9	967	13	BU520154	CSU-K33F-		779	15	9.3	132	14	CF384710	CF384710	CF384710
723	16	9.9	967	28	CC066430	BZ799408		780	15	9.3	132	14	CF384720	CF384720	CF384720
724	16	9.9	970	28	BZ799408	PURFR79TD		781	15	9.3	133	13	BQ557397	BQ557397	BQ557397
725	16	9.9	974	29	CG143065	PUNKR21TB		c 782	15	9.3	138	29	BM094377	BM094377	BM094377
726	16	9.9	980	28	BZ477598	BONK49TF		c 783	15	9.3	140	13	BQ094377	BQ094377	BQ094377
727	16	9.9	981	12	BG105901	602290078		c 784	15	9.3	143	28	BH893664	BH893664	BH893664
728	16	9.9	983	29	CNS010MW	BONME6TF		785	15	9.3	153	9	AV446540	AV446540	AV446540
729	16	9.9	986	28	BH721819	BONME6TF		c 786	15	9.3	155	14	CN851790	CN851790	CN851790

787	15	9.3	157	9	A1897395	A1897395	EST26638	844	15	9.3	259	29	CC492856	CC492856	OST30869
788	15	9.3	157	14	R36155	R36155	yh2n01.s1	845	15	9.3	260	28	A2728924	A2728924	A2728924
789	15	9.3	160	9	AA585483	AA585483	JTH124 HT	846	15	9.3	261	9	AV2744245	AV2744245	AV2744245
790	15	9.3	160	28	CC101623	CC101623	CSU-K34.1	847	15	9.3	263	10	BE944498	BE944498	CML-NN021
791	15	9.3	162	9	AL697631	AL697631	DKFZP686L	848	15	9.3	263	10	AW999244	AW999244	MRO-BN007
792	15	9.3	164	14	CA366132	CA366132	ZF001-P00	849	15	9.3	263	12	B3048993	B3048993	B3048993
793	15	9.3	165	28	A2078777	A2078777	RPCT-23-4	850	15	9.3	264	28	B2383089	B2383089	B3048993
794	15	9.3	171	12	BA306592	BA306592	fmi1b06.y	851	15	9.3	268	28	A2922543	A2922543	SL0C1C11
795	15	9.3	172	14	CA852306	CA852306	E06A05.B0	852	15	9.3	270	10	AW837391	AW837391	QV2-LT003
796	15	9.3	173	28	AQ586709	AQ586709	RPCT-11-4	853	15	9.3	272	9	AV041419	AV041419	QV2-LT003
797	15	9.3	175	12	BG458592	BG458592	947047C03	854	15	9.3	273	9	AL691760	AL691760	DKFZD313M
798	15	9.3	177	9	AA783108	AA783108	clai2a1.f	855	15	9.3	273	9	AA598875	AA598875	ae38a02.s
799	15	9.3	180	14	CF607110	CF607110	GERMA01.0	856	15	9.3	274	9	AA377023	AA377023	EST89522
800	15	9.3	182	29	CE816250	CE816250	cligt-gas-	857	15	9.3	274	13	BY307529	BY307529	BY307529
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Search completed: October 15, 2004, 06:27:11
Job time : 820.155 sec

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Run on: October 14, 2004, 09:12:14 ; Search time 831.586 Seconds

(without alignments)
8443.595 Million cell updates/sec

Title: US-09-407-804A-7

Perfect score: 162
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	142.8	88.1	1408	AR354422	AR354422 Sequence
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10	138	85.2	42722	AF424783	AF424783 Staphyloc
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37 33.6 20.7 259289 2 AC096268
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ALIGNMENTS

RESULT 1
BD245278 162 bp DNA linear PAT 17-JUL-2003
LOCUS BD245278
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245278.1 GI:33055048
VERSION JP 2002531107-A/13.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 162)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 13 24-SEP-2002;
PUBTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/13
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FH Key Location/Qualifiers
FT source 1..162
FT aureus bacteriophage 77',
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DB 121 GCAACATTCATGTAACAAAGAAATGCTTTTCAAGATAA 162
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RESULT 2
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LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PUBTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
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FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage 77',
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 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 29111 GTACTATGCGGTTTCTATACCTCACTACAGATGTCATTCGCGGATTGCGAAGTATC 29170
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 DB 29171 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 29212

RESULT 3
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 LOCUS AR368770 41708 bp DNA linear PAT 12-SEP-2003
 DEFINITION Sequence 3 from patent US 6376652.
 ACCESSION AR368770
 VERSION AR368770.1 GI:34603077
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 41708)
 AUTHORS Palletier,J., Gros,P. and Dubow,M.
 TITLE Compositions and methods involving an essential *Staphylococcus aureus* gene and its encoded protein
 JOURNAL Patent: US 6376652-A 3 23-APR-2002;
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ORIGIN

Query Match 100.0%; Score 162; DB 6; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 2.8e-36;
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 DB 29111 GTACTATGCGGTTTCTATACCTCACTACAGATGTCATTCGCGGATTGCGAAGTATC 29170
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 QY 121 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 162
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 DB 29171 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 29212

RESULT 4
 BD245634
 LOCUS BD245634 43594 bp DNA linear PAT 17-JUL-2003
 DEFINITION Development of novel antibiotics based on bacteriophage genomes.
 ACCESSION BD245634
 VERSION BD245634.1 GI:33053404
 KEYWORDS JP 2002531107-A/369.
 SOURCE JP 2002531107-A/369.
 ORGANISM unidentified
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 43594)
 AUTHORS Palletier,J., Gros,P. and Dubow,M.
 TITLE Development of novel antibiotics based on bacteriophage genomes
 JOURNAL Patent: JP 2002531107-A 369 24-SEP-2002;
 COMMENT PHAGEGEN INC
 OS *Staphylococcus aureus* bacteriophage 96
 PN JP 2002531107-A/369

PD 24-SEP-2002
 PF 03-DEC-1999 JP 2000585456
 PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
 28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
 01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
 PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
 PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
 PC C12N1/00,
 PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
 C12N15/00,
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 FT aureus bacteriophage
 FT Location/Qualifiers
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ORIGIN

Query Match 89.1%; Score 144.4; DB 6; Length 43594;
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 QY 61 GTACTATGCGGTTTCTATACCTCACTACAGATGTCATTCGCGGATTGCGAAGTATC 120
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 DB 4576 GCAACATTCATGTACTACAAAGATGCTTTTCAAGATTA 4617

RESULT 5
AR354422/c AR354422 1408 bp DNA linear PAT 17-AUG-2003
LOCUS AR354422 540 from patent US 6593114.
DEFINITION AR354422
ACCESSION AR354422
VERSION AR354422.1 GI:33760506
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1408)
AUTHORS Kuech,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 540 15-JUL-2003;
FEATURES
source location/Qualifiers
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Query Match 88.1%; Score 142.8; DB 6; Length 1408;
Best Local Similarity 92.6%; Pred. No. 1.4e-30;
Matches 150; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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DB 339 ATGACGACATTATATAAGCTAGTACGATATTAGCTTCAAGCTTAGCGATT 280
61 GTACTTATGCGCTTCTATCTACTGACGATGATGATGCGGATTCGAGATGAC 120
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DB 279 GTACTTATGCGCTTCTATCTACTGACGATGATGATGCGGATTCGAGATGAC 220
QY 121 GCMCAATGCTACTACAAAGATGCTTTTCAAGATTA 162
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DB 219 GCMCAATGCTACTATCTATTAAGATGATTTTATGAAGATGA 178
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RESULT 6
AF424781 43604 bp DNA linear PHG 10-JUN-2002
LOCUS AF424781
DEFINITION Staphylococcus aureus phage phi 11, complete genome.
ACCESSION AF424781
VERSION AF424781.1 GI:18920487
KEYWORDS
SOURCE Staphylococcus aureus phage phi 11
ORGANISM Staphylococcus aureus phage phi 11
REFERENCE Viruses; deDNA viruses; no RNA stages; Caudovirales; Siphoviridae.
1 (bases 1 to 43604)
AUTHORS Iandolo,J.J., Worrell,V., Groelcher,K.H., Qian,Y., Tian,R., Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and Roe,B.A.
TITLE Comparative analysis of the genomes of the temperate bacteriophages phi11, phi12 and phi13 of Staphylococcus aureus 8325
JOURNAL Gene 289 (1-2), 109-118 (2002)
MEDLINE 22032962
PUBMED 12036589
REFERENCE 2 (bases 1 to 43604)
AUTHORS Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R., Lin,S. and Jia,H.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.E. Young Blvd, Oklahoma City, OK 73190, USA
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source location/Qualifiers
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NANDLPASLRKTOILETVNDKDFETHVEAVDFNSKRLATISLLGRALEIMCRLI
LAKFDKDIKQTPDKYNITFTFNMENNDLIEELKHSYKAAIEHRNSIWHGKITEE
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Query Match

Best Local Similarity 92.6%; Score 142.8; DB 7; Length 43604;
Matches 150; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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61 GTACTATGCCGTTCTATGACTGACGATGCGGATGCGGATGCGAGTATC 120
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DB 6255 GTACTATGCCGTTCTATGACTGACGATGCGGATGCGGATGCGAGTATC 6314
QY 121 GCAACATTCATGCTACGACGATGCTTTTCAAGAA 162
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DB 6315 GCAACATTCATGCTACGACGATGCTTTTCAAGAA 6316

RESULT 7

AX618544
LOCUS AX618544 159 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 1507 from Patent WO02094868.
ACCESSION AX618544
VERSION AX618544.1 GI:28448591

KEYWORDS

ORGANISM

Staphylococcus aureus

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ORIGIN

1 Masignani, V.C., Mora, M.C. and Scareselli, M.C.
Staphylococcus aureus proteins and nucleic acids
JOURNAL Patent: WO 02094868-A 1507 28-NOV-2002;
Chiron Spa (IT)
Location/Qualifiers
1..159
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Query Match

Best Local Similarity 93.1%; Score 141.4; DB 6; Length 159;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 121 GCAACATTCATGCTACGACGATGCTTTTCAAGAA 159
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DB 121 GCAACATTCATGCTACGACGATGCTTTTCAAGAA 159

RESULT 8

AP003135/c
LOCUS AP003135 291150 bp DNA linear BCT 11-JAN-2003
DEFINITION Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
genome, section 7/10.
ACCESSION AP003135 BA000018
VERSION AP003135.2 GI:14349227
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Imai, Y., Ito, T., Kanemori, M.,
Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A.,
Mizumori, U.Y., Takahashi, N.K., Sawano, T., Inoue, R., Katso, C.,
Sekizawa, K., Haraoka, H., Kohara, S., Goto, S., Yabuzaki, J.,
Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
Lancet 357 (9264), 1225-1240 (2001)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

ORIGIN

gene

1..291150
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 /codon_start=1
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 /db_xref="GI:13701548"
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 /gene="SA1574"
 /note="ORFID:SA1574"
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 /transl_table=11
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 /db_xref="GI:13701549"
 /translation="WMDKELANKNGETRNWQQLKGLANNAVEQYISKRTIIEP
 NKRTIVRGELEIETENVYITMLNRKGTISATDEESKSTVLEIDPEQHLNIFVGRD
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 PALITYIINDQTSHTVYEGKTHQVKRWFHSIQNEVHLHRLKIADLELSDLSGEYR
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 /gene="SA1575"
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 /codon_start=1
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 TGGTSVQPGSGTGQGYKEAQDLGHTITTELPVLTYSAEFTIKSNLKGSLKDEL
 SYLKNKGRKRSIQHQMPLFTHFGISGPAALCSQFYKQKQNKQTHISMIIDAFPL
 NHHQLKQHTLSISDTPDKITIKNSLGLLEERYVILNMLQAGIDENSTSHLSNQQLN
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 CDS
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 /note="ORFID:SA1577"
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 /codon_start=1
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 /db_xref="GI:13701552"
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 PTISQVSTPSAKQNNNHTQDQNTATETVSNANNKQVSNNTLVNPKNTNGSGSHLT
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Db	Accession	Definition	Location/Qualifiers
240667	240726	GCACATTACGCGTTTCCTATCTCACTACACAGCATGTCATTGCAGGATTCGCAATGATC	
QY	121	GCACATTACGCGTTTCCTATCTCACTACACAGCATGTCATTGCAGGATTCGCAATGATC	
Db	240666	GCACATTACATCTCTATAGAGATACCTTTTGTAGAGATAA 240625	
RESULT 9			
LOCUS	AX583668	159 bp DNA Linear PAT 10-JAN-2003	
DEFINITION	Sequence 45 from Patent WO02059148.		
ACCESSION	AX583668		
VERSION	AX583668.1 GI:27655478		
KEYWORDS			
SOURCE	Staphylococcus aureus		
ORGANISM	Staphylococcus aureus		
REFERENCE	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
AUTHORS	Meinke, A., Nagy, E., von Ahnen, U., Klade, C., Henics, T., Zauner, W., Mihm, D.B., Vytvytska, O., Etz, H., Dryja, A., Weichenh, T., Haefner, K., Tempelmeier, B., Frieser, C.M., and Gail, S.		
TITLE	A method for identification, isolation and production of antigens to a specific pathogen		
JOURNAL	Patent: WO 02059148-A 45 01-AUG-2002;		
FEATURES	Cistem Biotechnologies GmbH (AT)		
source	Location/Qualifiers		
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	/organism="Staphylococcus aureus"		
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	/db_xref="taxon:1280"		
ORIGIN			
Query Match	85.38; Score 138.2; DB 6; Length 159;		
Best Local Similarity	91.88; Fred. No. 3.8e-29;		
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;			
QY	1	ATGAGCAACATTTATAAGACTAGTACAGATATTTGCTTCACAGCTTACGATT 60	
Db	1	ATGAGCAACATTTATAAGACTAGTACAGATATTTGCTTCACAGCTTACGATT 60	
QY	61	GACTTATGCGCTTTCTATCTCACTACACAGCATGTCATTGCGGGATTGCAATGATC 120	
Db	61	GACTTATGCGCTTTCTATCTCACTACACAGCATGTCATTGCGGGATTGCAATGATC 120	
QY	121	GCACATTACGCGTTTCCTATCTCACTACACAGCATGTCATTGCAGGATTCGCAATGATC 159	
Db	121	GCACATTACGCGTTTCCTATCTCACTACACAGCATGTCATTGCAGGATTCGCAATGATC 159	
RESULT 10			
LOCUS	AF424783	42722 bp DNA Linear PHG 10-JUN-2002	
DEFINITION	Staphylococcus aureus phage phi 13, complete genome.		
ACCESSION	AF424783		
VERSION	AF424783.1 GI:18920591		
KEYWORDS			

ORGANISM	Staphylococcus aureus phage phi 13
REFERENCE AUTHORS	Virtuous, David virtuous, no RNA stage; Caudovirales; Siphoviridae. 1 (baaes 1 to 42722) Iandolo,J.J., Worrell,V., Groicher,K.H., Qian,Y., Tian,R., Kanton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and Roe,B.A.
TITLE	Comparative analysis of the genomes of the temperate bacteriophages phi11, phi12 and phi13 of Staphylococcus aureus 8325
JOURNAL MEDLINE	Gene 269 (1-2), 109-116 (2002)
PUBLISHED	22032962
REFERENCE	2 (baaes 1 to 42722)
AUTHORS	Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tian,R., Lin,S. and Jia,H.
TITLE	Direct Submision
JOURNAL	Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.L. Young Blvd, Oklahoma City, OK 73190, USA
FEATURES	Location/Qualifiers 1..42722 /organism="Staphylococcus aureus phage phi 13" /proviral /mol_type="genomic DNA" /specific_host="Staphylococcus aureus strain 8325" /db_xref=taxon:186153" complement(59..1096) /codon_start=1 /transl_table=1 /product="integrase" /protein_id="AAL82331.1" /db_xref=Gt:18920592" /translation="MKTRCYDGRKMYEFHKGKRYRKGFRTKEANSAGLDKINELRSQFNIDNYITLAEYENWIKTYKQPVKENTYRHYRNALOHIGKHIGQELESKIRNGVOAKINDYSKEHAKETIRKTNAGISALDALYGLRNPAYKNVYKSGPTKSEGEKTSVEYTEILKDHYRKRRTRSSIALPLMTCTGCSCGANIKRIHNQVNIPIDEBRTSTSPRYSIKSDMKRMHDVISTPAISYDGIPEASGIIINDOAINNALMSACRVNNIPITISHALNTHICSTILANGVSITRIKRLGHANIATITSVSHLEEKNEEDKRTKILELSM"
CDS	1204..1818 /note="OfcC" /codon_start=1 /transl_table=1 /product="unknown" /protein_id="AAL82332.1" /db_xref=Gt:18920593" /translation="MTOFGALLLTGVLYPYKYLTMIGLVSEKKKIINTPVLILFSLIECLWFYTFTLIENNVDLRNLISLLQLTGLKANIFLILFVLYVFNPLAVKFILWLNTKRFNFLLDCISILDNRDLGNNGKRPVIYIKDFENRIIEEGELTKYNASQSDFDLAEVRDPFYKSDLPSENDELVTGHIVTLDKQIKMLDYLMANEY"
CDS	complement(2378..3148) /codon_start=1 /transl_table=1 /product="ci-like repressor" /protein_id="AAL82333.1" /db_xref=Gt:18920594" /translation="MRKNSNLKIHKIRLNIAKQVDINKSKPYOKKLGISLKSTLS
CDS	OYNVOSPOQRDIYVLSKTLNIGEMAMNGVD/SIRVPDERODETINSKINIISQ LTFPQQEADVINARLEBOQRKTSIDG/KESKSIVYIINCAETAAGIGELYDDILAE EVFEKEDTPSNADFCLINAGDSMEPMHKQGTAAFKREDSIKDGTIALVYLDLSIL KRVIDCEBYINLVSINPRYDIDIVASFSDIMWGKVV/L"
CDS	3307..3531 /note="similar to phiPVL of 31a" /codon_start=1 /transl_table=1 /product="repressor-like protein" /protein_id="AAL82334.1" /db_xref=Gt:18920595" /translation="MCQYSRISLGIVKEVGYQYNFAIMKLSRSLSLKNGVMGWK DSEIWKOLDIDIPEKTIHLYPEKKAHVY"
CDS	3528..3809 /codon_start=1 /transl_table=1 /product="phi PVL of 32-like protein" /protein_id="AAL82335.1" /db_xref=Gt:18920596" /translation="MWLRRGMEOLITRKECYEOCCINKDKLLDRNQOILEGVSE STRYGARNKLTETIKIASHSFTEHASVITYIKALKKDEKINAFTPK"
CDS	complement(3833..4372) /codon_start=1 /transl_table=1 /product="phi PVL of 33-like protein" /protein_id="AAL82336.1" /db_xref=Gt:18920597" /translation="MDIYACIAISFILTAARYIDMYKQSINIDVITPSNRYLWD DKSNDITFINETFPISVTDVEFDINKNKQKTFKRIYKQKNSIPTLCPYS VCTETLEEYPVIMEDVITIKYTNKGIVIKPVYIESRTERESEQVTELTSANKVS ALSXPKDFLKEFLVHLKP"
CDS	4429..5178 /codon_start=1 /transl_table=1 /product="anti-repressor" /protein_id="AAL82337.1" /db_xref=Gt:18920598" /translation="MQALTKRSNIGBMENIOERENGELAIISARELYKALEVKKFSAM AEINLKHKENRDFTSVLTSTVNVNAGVROLEDVALTDVAHHVAMSGETGEDFEE VFIOVERKAMSPEMIKRAKLIANNINOLETETIKERDKPIVPADVAVATTSTSYSE LAKTIKONGINIGORALEFWLRONGELLKRWGDYNMPQVSMERLEFIEKTSITHS DGHTSISRTPKYTGAGQOYEVNKEFGKQTS"
CDS	5194..5391 /codon_start=1 /transl_table=1 /product="phi PVL of 35-like protein" /protein_id="AAL82338.1" /db_xref=Gt:18920599" /translation="MQAQNKVYYTYDEAGRPPVNIQYNDGYDLMDPFLEMTLE RHPLKNNFYGLDKREEKIDL"
CDS	6585..6746 /codon_start=1 /transl_table=1 /product="phi PVL of 38-like protein" /protein_id="AAL82339.1" /db_xref=Gt:18920600" /translation="WSNIYSYLAVALCFVIALVIMPLEVFTTAWSIAGASIAIFI

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CDS
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KQTAIEYVQGFSTKEPSLILQSGYGTGKSHLAVIAKAVAKGHTVAFMAHPMLDR
IKATVNNAAVETTEDLVRLSDIDLVLIDMGVANT EHTLTKLFSTVNRVGRNNLEF
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11578..11799
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/db_xref="GI:18920608"
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Query Match 85.2%; Score 138; DB 7; Length 42722;
Best Local Similarity 90.7%; Pred. No. 2.2e-29;
Matches 147; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATAGGCACTTATTAAGCTACCTAGTACGATGATTTGTTCAAGCTTACGCAATT 60
DB 6585 ATAGGCACTTATTAAGCTACCTAGTACGATGCTGCTTACAGCTTACGCAATT 6644
QY 61 GTACTTATGCCGTTCTATTACTCACTACAGCATGTCATTGCCGATTCGCAAGTATC 120
DB 6645 GTACTTATGCCGTTCTATTACTCACTACGATGTCATTGCCGATTCGCAAGTATC 6704
QY 121 GCAACATTCATGTACTACAAAGAAATGCTTTTCAAGAGATAA 162
DB 6705 GCAACATTCATGTACTACAAAGAAATGCTTTTCAAGAGATAA 6746
RESULT 11
AP004828/c 272850 bp DNA linear BCT 20-DEC-2002
LOCUS
DEFINITION
Staphylococcus aureus subsp. aureus MW2 DNA, complete genome,
strain:MW2, section 7/10.
ACCESSION
AP004828 BAO00033
VERSION
AP004828.1 GI:21204850
KEYWORDS
Staphylococcus aureus subsp. aureus MW2
SOURCE
Staphylococcus aureus subsp. aureus MW2
ORGANISM
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
Yamamoto,K. and Hiramatsu,K.

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TTDEKGNITFTINSDDTASHILNTAFNLAEIQAQGEMLVAPHQDVLIDIRN
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RGAKASAKMIDPVAFFVDCSPANDYKSGPSLGEIGKTLIRIKDGTNLIKPFVNDY
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/product="conserved hypothetical protein"
Query Match 85.2%; Score 138; DB 1; Length 272850;
Best Local Similarity 90.7%; Pred. No. 1.8e-29;
Matches 147; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGAGCAATTATATAAAGCTACCTAGTACGAGCATATGCTTACAGCTTACGATT 60
DB 237045 ATGAGCAATTATATAAAGCTACCTAGTACGAGCATATGCTTACAGCTTACGATT 60
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QY 61 GTACTTATGCCGTTTCTATACCTACACGAGCATGTCATTGCCGAGTTGCCAGTATC 120
DB 236985 GTACTTATGCCGTTTCTATACCTACACGAGCATGTCATTGCCGAGTTGCCAGTATC 120
236926
QY 121 GCAACATTCATGACTACAAAGAAAGCTTTTCAAGATTA 162
DB 236925 GCAACATTCATGACTACAAAGAAAGCTTTTCAAGATTA 162
236984
RESULT 12
BD245282
LOCUS BD245282 43095 bp DNA linear PAT 17-JUL-2003
DEFINITION Development of novel antibiotics based on bacteriophage genomes.
ACCESSION BD245282
VERSION BD245282.1 GI:33055052
KEYWORDS JP 2002531107-A/17.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 43095)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomes
JOURNAL Patent: JP 2002531107-A 17 24-SEP-2002;
PHAGE TECH INC
OS Staphylococcus aureus bacteriophage 3A
PN JP 2002531107-A/17
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1999 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR

01-DEC-1999 US 60/168777.02-DEC-1999 US 09/454252 P1 JERRY
PELLETIER, PHILLIP GR05, MICHAEL DUBOW
PC C12N15/00, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12M1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT Source 1. .43095
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aureus bacteriophage 3A1"
FT Location/Qualifiers
1. .43095
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ORIGIN

Query Match 83.2%; Score 134.8; DB 6; Length 43095;
Best Local Similarity 89.5%; Pred. No. 1.9e-28;
Matches 145; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGAGCAATTATTAAGCTAGTACGATATTAAGCTTACGATTCAGCATC 60
DB 29442 ATGAGCAACATTAAGCTAGTACGATATTAAGCTTACGATTCAGCATC 29501
QY 61 GTACTTATGCGTTTCTATTAATTCATACGATGTCATTCGCGGATTCGCAATATC 120
DB 29502 GTACTTATGCGTTTCTATTAATTCATACGATGTCATTCGCGGATTCGCAATATC 29561
QY 121 GCAACATTCATGACTACAAAGATGCTTTTCAAGATTA 162
DB 29562 GCAACATTCATGACTACAAAGATGCTTTTCAAGATTA 29603

RESULT 13

AB009866 41401 bp DNA linear PHG 23-MAY-2000
LOCUS Bacteriophage phi PVL proviral DNA, complete sequence.
DEFINITION
ACCESSION AB009866
VERSION AB009866.2 GI:8051688
KEYWORDS
dUTPase; ssDNA binding protein; anti repressor; repressor;
integrase; LukE-PV; LukS-PV; holin; amidase (peptidoglycan
hydrolase); capsid protein; portal protein.
SOURCE
ORGANISM
Staphylococcus aureus bacteriophage PVL
Staphylococcus aureus bacteriophage PVL
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
REFERENCE
1 (et al.)
AUTHORS Kaneko, J., Kimura, T., Naito, S., Tomita, T. and Kamio, Y.
TITLE Pantom-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Bacteriol. Biotechnol. Blochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (et al.)

AUTHORS Kaneko, J., Kimura, T., Naito, S., Tomita, T. and Kamio, Y.
TITLE Complete nucleotide sequence and molecular characterization of the
temperate staphylococcal bacteriophage phiPVL carrying
Panton-Valentine leukocidin genes
JOURNAL
MEDLINE 98332719
PUBMED 966077
REFERENCE 3 (bases 1 to 41401)
AUTHORS Kaneko, J., Kimura, T., Naito, S., Tomita, T. and Kamio, Y.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1997) Jun Kaneko, Tohoku University, Dept. Appl.
Biol. Chem., Faculty of Agriculture, 1-1 Tsutsumi-dori
Aramiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-717-8780)
On May 24, 2000 this sequence version replaced gi:3341907.
COMMENT
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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Query Match 81.2%; Score 131.6; DB 1; Length 333750;
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RESULT 15
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LOCUS Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
DEFINITION Sequence, section 3/9.
ACCESSION AP003360 BA000017
VERSION AP003360.2 GI:14246398
KEYWORDS
SOURCE Staphylococcus aureus subsp. aureus Mu50
ORGANISM Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE
1 Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Imai, J., Ito, T., Kanamori, M.,
Matsunari, H., Maruyama, A., Murakami, H., Hosoyama, A.,
Mizutani-Uli, Y., Takahashi, N. K., Sawano, T., Inoue, R., Kaito, C.,
Sekimizu, K., Hiraoka, H., Kuhara, S., Goto, S., Yabuuchi, J.,
Kanohisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hirumatsu, K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus

TITLE
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 21311952
PUBMED 11418146
REFERENCE 2 (bases 1 to 348527)
AUTHORS Ohta, T.
JOURNAL Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohta@tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13874937.
COMMENT
FEATURES
Location/Qualifiers
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/protein_id="BAB56789.1"
/db_xref="GI:14246396"
/translaction="MIQTIHMIISLIIFGIALITCLERLKGPTADRVVTFDT
SAVMSIVGLSVLMGTVPFLSDISMLTAIISFVSSVSIISRTIGGAVNGNKRNLT"
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/gene="SAV0628"
6135..6572
/gene="SAV0628"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="BAB56790.1"
/db_xref="GI:14246397"
/translaction="MEIFKEIFSLAAMLLGSEFALISAIQIVFQDVELNSHAT
KSTLSVLTLLIGVLIYIVNTGFFSVRLLSLIVFINTSPVGGHLVRAAYRVGAM
YRINDATHASILLSSNEQSTEQALQRAKREHRKRWQND"
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6912..8954
/gene="SAV0629"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="BAB56791.1"
/db_xref="GI:14246398"
/translaction="MEIFETLIFAVVILSSVHTFIPKVPPLAQIFLQMLLETP
IPQVFNDELPMVTAPLPLFVGVNWSVHLRYIPVMMALGLVITTVIGVGF
IHMTWPLDIGAEFALIAIICPTDAVAVQITKGVLKPGAMTILEGSLNDAGII
SEKIAVEVLGATSLVDVQVLEFASIGAVVGLIGALIVFRLLIMRGYENIM
FTIOLTFEVYILAELEFASGIIAAVAGLVHGFEDRIKQVROQNSYNTNNTI
LCVINGPFSISLGEVPEYIKIITERNPLIFIGITTVAAALVTLREVVYVLY
PYTLAISFPQRMKTKNDDMPTTKPKRSIYALIMTLGVGHITSLAIALTLPFL
AGHIAFYNDLLEFLASGVNLSLVVAVLPLLRPAKTVIGNSFRVARIYITLQ
VIDLQKSTFETSEKGVNKEVHDKLAEKTVKEDNSKELEKQIFNVEKRT
LESIVDEQITNSVLENYMRYAERTQVROASLIRMTVLIRGALKRQVOTRVNSAS
SLSVTNDIMELNKINKLVHNNVSRISKETTKNTLEIGVCCGYLMRIENLPNSNF
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/protein_id="BAB56792.1"

Query Match 79.3%; Score 128.4; DB 1; Length 348527;
Best Local Similarity 87.0%; Pred. No. 16-26;
Matches 141; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Search completed: October 14, 2004, 16:00:32
Job time : 035.506 secs

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 07:30:59 ; Search time 108 Seconds

(without alignments)
6372.297 Million cell updates/sec

Title: US-09-407-804A-7
 Perfect score: 162
 Sequence: 1 atgagcaacattataaag.....atgcttttccaagataa 162

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: geneseq_293und.*
2: geneseq_1980s.*
3: geneseq_1990s.*
4: geneseq_2000s.*
5: geneseq_2001a.*
6: geneseq_2001b.*
7: geneseq_2002s.*
8: geneseq_2003a.*
9: geneseq_2003b.*
10: geneseq_2003c.*
11: geneseq_2004s.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	162	100.0	162	3	AA668251	AA668251 Bacteriophage
2	162	100.0	41708	3	AA668247	AA668247 Bacteriophage
3	162	100.0	41708	4	AA68106	AA68106 Complete
4	144.4	89.1	43576	3	AA66609	AA66609 Bacteriophage
c	142.8	88.1	1408	2	AAV74851	AAV74851 Stephiylus
5	141.4	87.3	159	7	ACF73074	ACF73074 Stephiylus
7	138.2	85.3	159	7	AA11900	AA11900 Pathogen

XX	Staphylococcus aureus; bacteriophage 77.
OS	
XX	
XX	W0200032825-A2.
PN	
XX	
XX	08-JUN-2000.
PD	
XX	
XX	
PE	03-DEC-1999; 99MO-IB002040.
PR	
PR	03-DEC-1999; 98US-0110992P.
PR	03-JUN-1999; 99US-00326144.
PR	28-SEP-1999; 99US-00407604.
PR	30-SEP-1999; 99US-0157218P.
PR	01-DEC-1999; 99US-0168771P.
PR	02-DEC-1999; 99US-00454252.
XX	
PA	(PHAG-) PHAGETECH INC.
XX	
PI	Pelletier J, Gros P, Dubow M;
DR	
DR	WPI: 2000-412361/35.
XX	
DR	P-PSDB: AAB16526.
XX	
PT	Identifying a bacteriophage coding region for treating bacterial
PT	infections comprises identifying a nucleic acid encoding a product that
XX	inhibits bacteria when a bacteriophage infects a bacterium.
XX	
PS	Disclosure; Page 159; 456pp; English.
XX	
XX	The present invention describes a method for identifying a bacteriophage
CC	coding region encoding a product active on an essential bacterial target.
CC	The method comprises identifying a nucleic acid sequence encoding a gene
CC	product that provides a bacteria-inhibiting function when an
CC	uncharacterised bacteriophage infects a pathogenic bacterium. The
CC	compound active on a target of a bacteriophage inhibitor protein in a
CC	bacteria is used to treat or prevent a bacterial infection in an animal.
CC	AAAB69423 to AAAB69442 and AAB16523 to AAB16934 represent bacteriophage
CC	nucleotide and protein sequences which are used in the exemplification of
CC	

XX

Query Match	100.0%	Score 162	DB 3	Length 162
Best Local Similarity	100.0%	Pred. No. 8.9e-42		
Matches 162	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGACCAACATTTATATAAGCTACTAGTAGCAGATTATGCTTCACAGCTTACGATT	60	
Db	1	ATGACCAACATTTATATAAGCTACTAGTAGCAGATTATGCTTCACAGCTTACGATT	60	
QY	61	GATCTTATGCGCTTTCTATACCTACACAGCATGTCATTTGCGGGATTCGCAAGATC	120	
Db	61	GATCTTATGCGCTTTCTATACCTACACAGCATGTCATTTGCGGGATTCGCAAGATC	120	
QY	121	GCAACTTACATGACTACAAAGATGCTTTTCAAGATATA	162	

DB 121 GCACATTCATGTACTACAAAGATGCTTTTCCAAAGATTA 162

RESULT 2

AAA68247

ID AAA68247 standard; DNA; 41708 BP.

XX

AC AAA68247;

XX

DT 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX

DE Bacteriophage 77 complete genome sequence.

XX

KW Bacteriophage; antimicrobial; genome; identification; antibacterial;

KW bacterial growth inhibition; bacterial infection; de.

XX

OS Staphylococcus aureus; bacteriophage 77.

XX

PN WO200032825-A2.

XX

PD 08-JUN-2000.

XX

PE 03-DEC-1999; 99WO-1B002040.

XX

PR 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00454252.

XX

PA (PHAG-) PHAGETECH INC.

XX

PI Pelletier J, Gros P, Dubow M;

XX

DR WPI; 2000-412361/35.

XX

PT Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

PT inhibits bacteria when a bacteriophage infects a bacterium.

XX

PS Example 3; Page 141-151; 456pp; English.

XX

CC The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.

CC The method comprises identifying a nucleic acid sequence encoding a gene

CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a

CC bacterium is used to treat or prevent a bacterial infection in an animal.

CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

CC nucleotide and protein sequences which are used in the exemplification of

CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)

CC

XX

SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 162; DB 3; Length 41708;

Best Local Similarity 100.0%; Pred. No. 4e-41;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1 ATGAGCACATTATATAAGCTACCTAGTAGCAGATATATGCTTACAGTCTTAGCATT 60

DB 29051 ATGAGCACATTATATAAGCTACCTAGTAGCAGATATATGCTTACAGTCTTAGCATT 29110

OY 61 GTACTATGCCGTTTCTATCTACTGACACGATGTCATTGCCGATTCGCAAGTATC 120

DB 29111 GTACTATGCCGTTTCTATCTACTGACACGATGTCATTGCCGATTCGCAAGTATC 29170

OY 121 GCACATTCATGTACTACAAAGATGCTTTTCCAAAGATTA 162

DB 29171 GCACATTCATGTACTACAAAGATGCTTTTCCAAAGATTA 29212

RESULT 3

AAC86106

ID AAC86106 standard; cDNA; 41708 BP.

XX

AC AAC86106;

XX

DT 06-AUG-2003 (revised)

DT 29-AUG-2001 (first entry)

XX

DE Complete genome of bacteriophage 77.

XX

KW Dnal1 S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;

KW screening assay; ss.

XX

OS Bacteriophage.

XX

PN WO200146383-A2.

XX

PD 28-JUN-2001.

XX

PR 21-DEC-2000; 2000WO-US035180.

PR 22-DEC-1999; 99US-00470512.

PR 12-OCT-2000; 2000US-00689952.

XX

PA (PHAG-) PHAGETECH INC.

PA (WILLIAMS K M.

XX

PI Pelletier J, Gros P, Dubow M;

XX

DR WPI; 2001-418052/44.

XX

PT Novel Dnal polypeptides useful for treating and diagnosing microbial,

PT preferably bacterial, diseases such as those caused by Staphylococcus

PT aureus.

XX

PS Disclosure; Fig 2; 107pp; English.

XX

CC This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from *S.*
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially Staphylococcal, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX

Seq Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 162; DB 4; Length 41708;

Best Local Similarity 100.0%; Pred. No. 4e-41;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAATTATTAAGGCTAGTACGATGATGCTTCAAGCTTACGAGT 60

DB 29051 ATGAGCAATTATTAAGGCTAGTACGATGATGCTTCAAGCTTACGAGT 29110

QY 61 GTACTTATGCCGTTTCTATCTCACTACAGCATGTCGCGGATTCGCAAGTATC 120

DB 29111 GTACTTATGCCGTTTCTATCTCACTACAGCATGTCGCGGATTCGCAAGTATC 29170

QY 121 GCAACATTCATGCTACTACAAAGATGCTTTTCAAGATTA 162

DB 29171 GCAACATTCATGCTACTACAAAGATGCTTTTCAAGATTA 29212

RESULT 4

AAA66609
ID AAA66609 standard; DNA; 43576 BP.

XX AAA66609;

AC 15-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 27-OCT-2000 (first entry)

XX Bacteriophage 96 complete genome sequence.

XX Bacteriophage; antimicrobial; genome; identification; antibacterial;

OS Staphylococcus aureus; bacteriophage 96.

XX WO200032825-A2.

XX 08-JUN-2000.

PF 03-DEC-1999; 99WO-1B002040.

PR 03-DEC-1999; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

PR 02-DEC-1999; 99US-00454252.

XX (PHAG-) PHAGETECH INC.

XX Pelletier J, Gros P, Dubow M;

XX WPI; 2000-412361/35.

XX Identifying a bacteriophage coding region for treating bacterial

PT infections comprises identifying a nucleic acid encoding a product that

XX inhibits bacteria when a bacteriophage infects a bacterium.

XX Disclosure; Page 190-198; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage

XX coding region encoding a product active on an essential bacterial target.

XX The method comprises identifying a nucleic acid sequence encoding a gene

XX product that provides a bacteria-inhibiting function when an

XX uncharacterized bacteriophage infects a pathogenic bacterium. The

XX compound active on a target of a bacteriophage inhibitor protein in a

XX bacteria is used to treat or prevent a bacterial infection in an animal.

XX AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage

XX nucleotide and protein sequences which are used in the exemplification of

XX the present invention. (Updated on 06-AUG-2003 to correct OS field.)

XX (Updated on 15-SEP-2003 to standardise OS field.)

XX Sequence 43576 BP; 16057 A; 6485 C; 8769 G; 12265 T; 0 U; 0 Other;

XX Query Match 89.1%; Score 144.4; DB 3; Length 43576;

XX Best Local Similarity 93.2%; Pred. No. 1.6e-35;

XX Matches 151; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGAGCAATTATTAAGGCTAGTACGATGATGCTTCAAGCTTACGAGT 60

DB 4438 ATGAGCAATTATTAAGGCTAGTACGATGATGCTTCAAGCTTACGAGT 4497

QY 61 GTACTTATGCCGTTTCTATCTCACTACAGCATGTCGCGGATTCGCAAGTATC 120

DB 4498 GTACTTATGCCGTTTCTATCTCACTACAGCATGTCGCGGATTCGCAAGTATC 4557

QY 121 GCAACATTCATGCTACTACAAAGATGCTTTTCAAGATTA 162

DB 4558 GCAACATTCATGCTACTACAAAGATGCTTTTCAAGATTA 4599

RESULT 5

AAV74851/C

XX AAV74851 standard; DNA; 1408 BP.

XX AAV74851;

XX 16-MAR-1999 (first entry)

XX Staphylococcus aureus contig SEQ ID #540.

XX Computer readable medium; vaccine; S. aureus infection; immunodetection;

XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

XX

CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel *S. aureus* genes of the invention
XX

SQ Sequence 159 BP; 51 A; 30 C; 26 G; 52 T; 0 U; 0 Other;

Query Match 87.3%; Score 141.4; DB 7; Length 159;
Best Local Similarity 93.1%; Pred. No. 3.2e-35;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGAGCAACATTATTAAGCTACCTAGTAGCAGTATTGCTTCACAGTCTTAGCGATT 60
DB 1 ATGAGTAACATTATTAAGCTACCTAGTAGCAGTATTGCTTCACAGTCTTAGCGATT 60
QY 61 GTACTTATGCCGTTTCTATACCTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
DB 61 GTACTTATGCCGTTTCTATACCTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
QY 121 GCAACATTCATGTACTACAAAGATGCTTTTCAAGAA 159
DB 121 GCAACATTCATGTACTATTAAGAAATCTTTTATGAAGA 159

RESULT 7
ABT14900
ID ABT14900 standard; DNA; 159 BP.

XX ABT14900;
DT 06-MAR-2003 (first entry)

XX Pathogen specific antigen related staphylococcal DNA SEQ ID No 45.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW auto-immune diseases; HIV; hepatitis; gene; ds.

XX Staphylococcus sp.

XX W0200259148-A2.

XX 01-AUG-2002.

XX 21-JAN-2002; 2002WD-EP000546.

XX 26-JAN-2001; 2001AT-00000130.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

PI Melnke A, Negy E, Von Ahnson U, Klade C, Herlitz T, Zauner W;
PI Mlnh DB, Vycvycka O, Ecz H, Dryle A, Weichhart T, Hafner M;
PI Tempelmeier B;
XX WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens

PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX

PS Example 7; Page 152; 252pp; English.

CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against *S. aureus* or *S. epidermidis*. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC polynucleotide sequence represents staphylococcal DNA relating to the
CC method for identifying and producing pathogen specific antigens of the
CC invention
XX

SQ Sequence 159 BP; 52 A; 31 C; 26 G; 50 T; 0 U; 0 Other;

Query Match 85.3%; Score 138.2; DB 7; Length 159;
Best Local Similarity 91.8%; Pred. No. 3.4e-34;
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGAGCAACATTATTAAGCTACCTAGTAGCAGTATTGCTTCACAGTCTTAGCGATT 60
DB 1 ATGAGCAACATTATTAAGCTACCTAGTAGCAGTATTGCTTCACAGTCTTAGCGATT 60
QY 61 GTACTTATGCCGTTTCTATACCTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
DB 61 GTACTTATGCCGTTTCTATACCTCACTACAGCATGGTCATTGGCGGATTGCCAAGTATC 120
QY 121 GCAACATTCATGTACTACAAAGATGCTTTTCAAGAA 159
DB 121 GCAACATTCATGTACTATTAAGAAATCTTTTATGAAGA 159

Search completed: October 14, 2004, 12:48:17

Job time : 111 secs

OM nucleole - nucleole search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 736.65 Seconds

(without alignments)
6393.544 Million cell updates/sec

SUMMARIES

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

28: gb_gss1:.*
29: gb_gss2:.*

Title: US-09-407-804A-7
Perfect score: 162
Sequence: 1 atgagacacattcacaaga.....aatgcttttcagaagaataa 162
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries
Database :
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1: em_estba:.*
2: em_esthum:.*
3: em_estlin:.*
4: em_estm:.*
5: em_estcov:.*
6: em_estpl:.*
7: em_estro:.*
8: em_hnc:.*
9: gb_est1:.*
10: gb_est2:.*
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12: gb_est3:.*
13: gb_est4:.*
14: gb_est5:.*
15: em_estfun:.*
16: em_estom:.*
17: em_gss_hum:.*
18: em_gss_inv:.*
19: em_gss_pln:.*
20: em_gss_vrc:.*
21: em_gss_fun:.*
22: em_gss_man:.*
23: em_gss_mus:.*
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25: em_gss_rnd:.*
26: em_gss_phg:.*
27: em_gss_vrl:.*

Result No.	Score	Query Match	Length	ID	Description
1	37.8	23.3	592	29	CC962715
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3	37.8	23.3	746	29	CC965697
4	36.2	22.3	598	28	BH733956
5	36.2	22.3	637	29	CC951970
6	36.2	22.3	685	28	BH432658
7	36.2	22.3	821	28	BH496295
8	34.6	21.4	694	28	B2043339
9	34.6	21.4	694	28	B2043339
10	34.6	21.4	828	29	CC942125
11	34	21.0	899	29	CC9825379
12	33.8	20.9	332	28	A2017923
13	33.6	20.7	636	28	B2138306
14	33.2	20.5	441	12	BM933696
15	33.2	20.5	441	12	BM933696
16	33.2	20.5	448	10	BE993185
17	33.2	20.5	654	10	BB475101
18	33.2	20.5	807	12	BJ403671
19	33	20.4	521	12	B0377935
20	33	20.4	643	13	BX507709
21	32.8	20.2	502	13	BX558882
22	32.6	20.1	347	29	CG765378
23	32.6	20.1	585	28	CC113035
24	32.6	20.1	694	28	B2389867
25	32.4	20.0	661	12	B0374708
26	32.4	20.0	724	28	BH567725
27	32.2	19.9	675	28	B2015314
28	32	19.8	235	12	BM939055
29	32	19.8	723	28	A2656529
30	32	19.8	1518	28	CC185828
31	31.8	19.6	461	28	AQ587116
32	31.8	19.6	526	13	BY708493
33	31.8	19.6	645	29	CC955595
34	31.8	19.6	834	28	BH687466
35	31.8	19.6	2525	11	BC036519
36	31.6	19.5	1201	29	CNS0150V
37	31.4	19.4	386	28	AQ133541
38	31.4	19.4	488	9	A1240366
39	31.4	19.4	681	12	BJ570871
40	31.4	19.4	741	28	BH460398
41	31.4	19.4	777	28	BH725123
42	31.4	19.4	806	14	CD826219
43	31.4	19.4	811	12	BM007305
44	31.4	19.4	1201	13	BX379698
45	31.2	19.3	360	13	BX550058

Search completed: October 14, 2004, 18:55:16
Job time : 760.65 secs

OM nucleic - nucleic search, using sm model

Run on: October 14, 2004, 19:00:14 ; Search time 816.257 Seconds
(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159
Sequence: 1 atgttaaccagaagaattttt.....ccgctacgtcgaaatttaa 159

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:
1: gb_ba: +
2: gb_hg: +
3: gb_in: +
4: gb_ov: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_sts: +
12: gb_sy: +
13: gb_un: +
14: gb_vl: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_sts: +

28: em_un: +
29: em_vl: +
30: em_hg_hum: +
31: em_hg_inv: +
32: em_hg_other: +
33: em_hg_mus: +
34: em_hg_pln: +
35: em_hg_red: +
36: em_hg_mam: +
37: em_hg_vrt: +
38: em_sy: +
39: em_higo_hum: +
40: em_higo_mus: +
41: em_higo_other: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	159	100.0	159	6	BD245279	BD245279 Develo
2	159	100.0	159	6	AR368771	AR368771 Sequence
3	159	100.0	41708	6	BD245281	BD245281 Develo
4	159	100.0	41708	6	AR368770	AR368770 Sequence
5	62	39.0	348527	1	AP003360	AP003360 Staphyloc
6	60	37.7	42942	7	AB045978	AB045978 Staphyloc
7	42	26.4	42722	7	AF424783	AF424783 Staphyloc
8	25	15.7	232473	2	AC114212	AC114212 Rattus no
9	23	14.5	178469	2	BX248504	BX248504 Danto rer
10	22	13.8	188989	2	AC125363	AC125363 Rattus no
11	22	13.8	224661	2	AC098164	AC098164 Rattus no
12	21	13.2	757	1	MC210	Z33151 H. capricolu
13	21	13.2	141704	9	AC007993	AC007993 Homo sapl
14	21	13.2	142163	9	AC061975	AC061975 Homo sapl
15	21	13.2	196421	2	AC078837	AC078837 Homo sapl
16	21	13.2	215705	9	AL589931	AL589931 Human DNA
17	21	13.2	246441	2	AC098542	AC098542 Rattus no
18	20	12.6	45636	7	AB044554	AB044554 Staphyloc
19	20	12.6	77028	9	AC093716	AC093716 Homo sapl
20	20	12.6	86829	9	AC011382	AC011382 Homo sapl
21	20	12.6	109710	9	HSBA46E17	AL050402 Human DNA
22	20	12.6	138376	8	AP003578	AP003578 Oryza sat
23	20	12.6	145491	8	AP002883	AP002883 Oryza sat
24	20	12.6	148202	10	AC125108	AC125108 Mus muscu
25	20	12.6	148326	10	AL732503	AL732503 Mouse DNA
26	20	12.6	155415	2	AC108886	AC108886 Rattus no
27	20	12.6	166712	2	AC118065	AC118065 Rattus no
28	20	12.6	188932	2	AC011150	AC011150 Homo sapl
29	20	12.6	192499	2	AC133913	AC133913 Homo sapl
30	20	12.6	193514	2	AC121674	AC121674 Rattus no
31	20	12.6	200769	2	AC137118	AC137118 Mus muscu
32	20	12.6	204632	2	AC097583	AC097583 Rattus no
33	20	12.6	216490	10	AC100953	AC100953 Mus muscu

c	34	20	12.6	224659	10	AL1806518	AL1806518 Mouse DNA	c	91	19	11.9	188894	9	AC108675	AC108675 Homo sapi
c	35	20	12.6	232901	2	AC121540	AC121540 Mus muscu	c	92	19	11.9	190066	10	AL1596025	AL1596025 Mouse DNA
c	36	20	12.6	234728	2	AC126570	AC126570 Rattus no	c	93	19	11.9	191261	2	AC074304	AC074304 Mus muscu
c	37	20	12.6	234804	2	AC133409	AC133409 Rattus no	c	94	19	11.9	195161	9	AC013464	AC013464 Homo sapi
c	38	20	12.6	235079	2	AC124475	AC124475 Mus muscu	c	95	19	11.9	195969	2	AC140240	AC140240 Mus muscu
c	39	20	12.6	237263	2	AC097686	AC097686 Rattus no	c	96	19	11.9	200058	2	AC084378	AC084378 Mus muscu
c	40	20	12.6	253127	2	AC094585	AC094585 Rattus no	c	97	19	11.9	203514	10	AC114007	AC114007 Homo sapi
c	41	20	12.6	255861	2	AC106603	AC106603 Rattus no	c	98	19	11.9	210861	2	AC073734	AC073734 Mus muscu
c	42	20	12.6	268850	2	AC110949	AC110949 Rattus no	c	99	19	11.9	218366	9	AC016734	AC016734 Homo sapi
c	43	20	12.6	274799	2	AC109721	AC109721 Rattus no	c	100	19	11.9	230674	10	AL731732	AL731732 Mouse DNA
c	44	19	11.9	504	6	AR394629	AR394629 Sequence	c	101	19	11.9	231135	2	AC099426	AC099426 Rattus no
c	45	19	11.9	673	6	BD194110	BD194110 Enterococ	c	102	19	11.9	233135	2	AC110102	AC110102 Rattus no
c	46	19	11.9	10476	1	AE014951	AE014951 Streptococ	c	103	19	11.9	233625	2	AC079994	AC079994 Homo sapi
c	47	19	11.9	15671	1	AF343914	AF343914 Campyloba	c	104	19	11.9	235328	2	AC094823	AC094823 Rattus no
c	48	19	11.9	32129	3	CER23F11	Z6343 Caenorhabd	c	105	19	11.9	236573	2	AC095450	AC095450 Rattus no
c	49	19	11.9	43487	3	AF016420	AF016420 Caenorhab	c	106	19	11.9	239665	2	AC133279	AC133279 Rattus no
c	50	19	11.9	48993	9	AC133605	AC133605 Homo sapi	c	107	19	11.9	240491	2	AC107412	AC107412 Rattus no
c	51	19	11.9	51952	6	AR110591	AR110591 Sequence	c	108	19	11.9	242331	2	AC122854	AC122854 Mus muscu
c	52	19	11.9	51953	8	LEU81378	U81378 Lycoparico	c	109	19	11.9	253050	1	AL596167	AL596167 Listeria
c	53	19	11.9	54149	10	AL833772	AL833772 Mouse DNA	c	110	19	11.9	256584	2	AC135734	AC135734 Rattus no
c	54	19	11.9	72054	5	AC140935	AC140935 Gallus ga	c	111	19	11.9	260991	2	AC125947	AC125947 Rattus no
c	55	19	11.9	79923	9	AL596178	AL596178 Human DNA	c	112	19	11.9	263020	6	AK417040	AK417040 Sequence
c	56	19	11.9	93177	9	AC098678	AC098678 Homo sapi	c	113	19	11.9	264078	2	AC112829	AC112829 Rattus no
c	57	19	11.9	104948	9	AC015751	AC015751 Homo sapi	c	114	19	11.9	267290	2	AC098041	AC098041 Rattus no
c	58	19	11.9	110000	2	AC096086	AC096086 Rattus no	c	115	19	11.9	267697	2	AC094212	AC094212 Rattus no
c	59	19	11.9	112732	2	AC092367	AC092367 Homo sapi	c	116	19	11.9	268564	2	AC091428	AC091428 Mus muscu
c	60	19	11.9	113060	2	AC121133	AC121133 Mus muscu	c	117	19	11.9	302132	1	AE016955	AE016955 Enterococ
c	61	19	11.9	122613	9	AL596462	AL596462 Human DNA	c	118	19	11.9	349980	6	AK417043	AK417043 Sequence
c	62	19	11.9	131056	2	AC137985	AC137985 Medicago	c	119	18	11.3	343	4	AY461844	AY461844 Bartonell
c	63	19	11.9	135964	9	AC005914	AC005914 Homo sapi	c	120	18	11.3	373	6	AF006409	AF006409 Lynx cana
c	64	19	11.9	139773	2	AC067806	AC067806 Homo sapi	c	121	18	11.3	418	1	AF314054	AF314054 Rhizobium
c	65	19	11.9	145242	9	AC013457	AC013457 Homo sapi	c	122	18	11.3	536	6	AX789619	AX789619 Sequence
c	66	19	11.9	145353	2	AC034177	AC034177 Homo sapi	c	123	18	11.3	575	11	GB8718	GB8718 S208P643RA
c	67	19	11.9	149224	2	AC022753	AC022753 Homo sapi	c	124	18	11.3	931	6	AX794162	AX794162 Sequence
c	68	19	11.9	150312	9	CNS01N13	AL163613 Human chr	c	125	18	11.3	1185	6	BD092877	BD092877 Identifc
c	69	19	11.9	150350	2	CNS01DMV	AL138839 Human chr	c	126	18	11.3	1254	6	AX608631	AX608631 Sequence
c	70	19	11.9	151171	2	AC020775	AC020775 Homo sapi	c	127	18	11.3	1994	10	AF117382	AF117382 Mus muscu
c	71	19	11.9	151673	10	AC087102	AC087102 Rattus no	c	128	18	11.3	3136	8	AK069473	AK069473 Oryza sat
c	72	19	11.9	152186	2	AC084284	AC084284 Homo sapi	c	129	18	11.3	3893	8	AK103512	AK103512 Oryza sat
c	73	19	11.9	154396	2	AC068930	AC068930 Homo sapi	c	130	18	11.3	4490	10	AK129266	AK129266 Mus muscu
c	74	19	11.9	159981	9	AC016817	AC016817 Homo sapi	c	131	18	11.3	15079	1	AE001180	AE001180 Borrelia
c	75	19	11.9	160521	2	AC127728	AC127728 Rattus no	c	132	18	11.3	15617	1	AE000559	AE000559 Helicobac
c	76	19	11.9	160810	9	AC009953	AC009953 Homo sapi	c	133	18	11.3	21781	2	AE014229	AE014229 Streptococ
c	77	19	11.9	162721	10	AC079638	AC079638 Genomic s	c	134	18	11.3	28235	2	AC014089	AC014089 Drosophil
c	78	19	11.9	166014	9	AC022538	AC022538 Homo sapi	c	135	18	11.3	29072	6	AX602188	AX602188 Sequence
c	79	19	11.9	168065	9	CNS05TC6	AL355072 Human chr	c	136	18	11.3	32144	3	CERK337	CERK337 Arabidops
c	80	19	11.9	169266	2	AC102458	AC102458 Mus muscu	c	137	18	11.3	35238	8	AB025612	AB025612 Arabidops
c	81	19	11.9	169514	2	AC064869	AC064869 Homo sapi	c	138	18	11.3	36863	3	U64848	U64848 Caenorhabd
c	82	19	11.9	170511	2	AC116263	AC116263 Homo sapi	c	139	18	11.3	39859	9	AL365449	AL365449 Human DNA
c	83	19	11.9	171051	2	AC023528	AC023528 Homo sapi	c	140	18	11.3	40699	3	CERK637	CERK637 Homo sapi
c	84	19	11.9	173728	9	AL365496	AL365496 Human DNA	c	141	18	11.3	41322	9	AC004076	AC004076 Homo sapi
c	85	19	11.9	174537	9	AC027233	AC027233 Homo sapi	c	142	18	11.3	55217	2	AC101358	AC101358 Mus muscu
c	86	19	11.9	183773	9	AC119299	AC119299 Rattus no	c	143	18	11.3	56080	8	AF003838	AF003838 Oryza sat
c	87	19	11.9	185156	9	HSBB212L9	AL121823 Human DNA	c	144	18	11.3	60858	9	AL512592	AL512592 Human DNA
c	88	19	11.9	185636	2	AC027109	AC027109 Homo sapi	c	145	18	11.3	61095	2	AC101023	AC101023 Mus muscu
c	89	19	11.9	186479	2	AC118083	AC118083 Rattus no	c	146	18	11.3	64318	2	AC100364	AC100364 Mus muscu
c	90	19	11.9	188826	9	AL359380	AL359380 Human DNA	c	147	18	11.3	69028	9	AC087493	AC087493 Homo sapi

148	18	11.3	73390	9	AC012938	AC012938 Homo sapi	205	18	11.3	135569	2	AC073997	AC073997 Homo sapi
149	18	11.3	73484	2	AC133630	AC133630 Homo sapi	206	18	11.3	135934	2	AC018925	AC018925 Homo sapi
150	18	11.3	77910	2	AP000452	AP000452 Homo sapi	207	18	11.3	139266	2	AC068747	AC068747 Homo sapi
151	18	11.3	78331	9	AC098692	AC098692 Homo sapi	208	18	11.3	139357	9	AC010907	AC010907 Homo sapi
152	18	11.3	80485	9	AB026899	AB026899 Homo sapi	209	18	11.3	140935	9	AC025173	AC025173 Homo sapi
153	18	11.3	83547	2	AC022890	AC022890 Homo sapi	210	18	11.3	141771	2	AC16512	AC16512 Homo sapi
154	18	11.3	84731	2	AC068885	AC068885 Homo sapi	211	18	11.3	141977	10	AL844482	AL844482 Mouse DNA
155	18	11.3	90136	9	HS330012	AL031731 Human DNA	212	18	11.3	142273	9	AL391994	AL391994 Mouse DNA
156	18	11.3	90864	8	AP004949	AP004949 Letus cor	213	18	11.3	143861	10	AL929070	AL929070 Mouse DNA
157	18	11.3	91587	1	AE016970	AE016970 Mycoplasma	214	18	11.3	144449	2	AC067926	AC067926 Mus muscu
158	18	11.3	93521	2	AC135555	AC135555 Gallus ga	215	18	11.3	145795	2	AC025548	AC025548 Homo sapi
159	18	11.3	96312	2	AP005554	AP005554 Oryza sat	216	18	11.3	145866	9	AC104771	AC104771 Homo sapi
160	18	11.3	97234	9	AL137859	AL137859 Human DNA	217	18	11.3	146960	2	AC101960	AC101960 Homo sapi
161	18	11.3	99479	9	AL136089	AL136089 Human DNA	218	18	11.3	147418	10	AL451054	AL451054 Homo sapi
162	18	11.3	100090	10	AL772162	AL772162 Mouse DNA	219	18	11.3	148179	9	AC093677	AC093677 Homo sapi
163	18	11.3	100170	9	AL161743	AL161743 Human DNA	220	18	11.3	148179	9	AC093677	AC093677 Homo sapi
164	18	11.3	104762	2	AC108086	AC108086 Homo sapi	221	18	11.3	148753	2	AC141202	AC141202 Homo sapi
165	18	11.3	107909	9	AL359847	AL359847 Human DNA	222	18	11.3	149214	2	AC026535	AC026535 Homo sapi
166	18	11.3	108785	9	AL354682	AL354682 Human DNA	223	18	11.3	150792	5	EX004972	EX004972 Homo sapi
167	18	11.3	110000	2	AC091229_09	Continuation (10 o	224	18	11.3	150891	2	EX640520	EX640520 Danio rer
168	18	11.3	110000	2	AC091360_3	Continuation (4 of	225	18	11.3	150891	2	AC121621	AC121621 Rattus no
169	18	11.3	110000	2	AC092921_3	Continuation (4 of	226	18	11.3	152548	2	AC100741	AC100741 Mus muscu
170	18	11.3	110000	2	AC095121_1	Continuation (3 of	227	18	11.3	152586	9	AC016968	AC016968 Homo sapi
171	18	11.3	110000	2	AC095121_2	Continuation (2 of	228	18	11.3	152632	2	AC145246	AC145246 Homo sapi
172	18	11.3	110000	2	AC095631_1	Continuation (4 of	229	18	11.3	152861	9	AC104772	AC104772 Homo sapi
173	18	11.3	110000	2	AC106241_3	Continuation (5 of	230	18	11.3	153803	2	AC055722	AC055722 Homo sapi
174	18	11.3	110000	2	AC106241_4	Continuation (2 of	231	18	11.3	153929	2	AC011883	AC011883 Homo sapi
175	18	11.3	110000	2	AC106552_0	Continuation (2 of	232	18	11.3	154889	2	AL511842	AL511842 Homo sapi
176	18	11.3	110000	2	AC106552_1	Continuation (2 of	233	18	11.3	154931	2	AL356781	AL356781 Homo sapi
177	18	11.3	110000	2	AC114698_0	AC114698 Rattus no	234	18	11.3	155491	9	AC068339	AC068339 Homo sapi
178	18	11.3	110000	2	AC115185_0	AC115185 Rattus no	235	18	11.3	155666	9	AC068696	AC068696 Homo sapi
179	18	11.3	110000	2	AC126728_1	Continuation (2 of	236	18	11.3	155670	3	AC012097	AC012097 Drosophila
180	18	11.3	110000	2	AC126909_1	Continuation (3 of	237	18	11.3	157043	2	AC013692	AC013692 Homo sapi
181	18	11.3	110000	2	AL360016_2	Continuation (3 of	238	18	11.3	157428	10	AL606832	AL606832 Mouse DNA
182	18	11.3	110000	2	AL713858_2	AR409405 Sequence	239	18	11.3	157533	9	AL354709	AL354709 Human DNA
183	18	11.3	110000	6	AR409405_0	BD061520 Genome DN	240	18	11.3	157568	9	AB005138	AB005138 Homo sapi
184	18	11.3	110000	6	BD061520_0	AC097470 Homo sapi	241	18	11.3	158121	2	AC026594	AC026594 Homo sapi
185	18	11.3	110702	9	AC097470	AP003179 Homo sapi	242	18	11.3	158170	5	EX005472	EX005472 Zebrafish
186	18	11.3	112998	9	AP003179	AL590702 Human DNA	243	18	11.3	158497	2	AC139517	AC139517 Rattus no
187	18	11.3	113587	9	AL590702	AL590628 Human DNA	244	18	11.3	158596	2	AL353192	AL353192 Homo sapi
188	18	11.3	113797	9	AL590628	AL031589 Human DNA	245	18	11.3	158780	9	AP003034	AP003034 Homo sapi
189	18	11.3	115932	9	HS1107	AC146562 Medicago	246	18	11.3	159689	10	AC124387	AC124387 Homo sapi
190	18	11.3	116425	2	AC146562	AC003658 Homo sapi	247	18	11.3	160035	2	EX465852	EX465852 Danio rer
191	18	11.3	119393	9	AC003658	AC004006 Homo sapi	248	18	11.3	160901	9	CNS01DMW	AL137228 Human chr
192	18	11.3	119453	9	AC004006	AC034240 Homo sapi	249	18	11.3	160920	2	AC027087	AC027087 Homo sapi
193	18	11.3	121245	9	AC034240	AC008924 Homo sapi	250	18	11.3	161602	9	AC022634	AC022634 Homo sapi
194	18	11.3	122042	9	AC008924	AC127383 Homo sapi	251	18	11.3	162043	2	AC018803	AC018803 Homo sapi
195	18	11.3	122168	9	AC127383	AL935155 Mouse DNA	252	18	11.3	162322	2	AC093027	AC093027 Homo sapi
196	18	11.3	123205	10	AL935155	AL512484 Human DNA	253	18	11.3	162387	2	AC021213	AC021213 Homo sapi
197	18	11.3	124446	9	AL512484	AC141355 Tetradon	254	18	11.3	162450	6	AB211792	AB211792 Sequence
198	18	11.3	125765	2	AC141355	AC133558 Rattus no	255	18	11.3	162450	6	BD21862	BD21862 Mus muscu
199	18	11.3	129705	2	AC133558	AC135415 Medicago	256	18	11.3	162641	2	AC143910	AC143910 Mus muscu
200	18	11.3	130040	8	AC135415	AL078644 Human DNA	257	18	11.3	162930	2	AC147599	AC147599 Canis fam
201	18	11.3	130177	9	HSB27987	AC092658 Homo sapi	258	18	11.3	163249	2	AC133590	AC133590 Mus muscu
202	18	11.3	130932	9	AC092658	AC192226 Homo sapi	259	18	11.3	163348	10	AC119236	AC119236 Homo sapi
203	18	11.3	132444	9	AC092658	AC129971 Felis cat	260	18	11.3	163520	9	AL391259	AL391259 Human DNA
204	18	11.3	133468	2	AC129971		261	18	11.3	163531	2	AC102289	AC102289 Mus muscu

c 262	18	11.3	163973	9	AL1359854	Human DNA	c 319	18	11.3	180778	9	AL1355596	Human DNA
c 263	18	11.3	163623	9	AP005203	Homo sapi	c 320	18	11.3	181016	2	AC073129	Homo sapi
c 264	18	11.3	163731	9	AC008949	Homo sapi	c 321	18	11.3	181467	10	AL844586	Mouse DNA
c 265	18	11.3	164310	2	AC016156	Homo sapi	c 322	18	11.3	182184	2	AC022891	Mouse sapi
c 266	18	11.3	165147	2	AC021342	Homo sapi	c 323	18	11.3	182440	1	AP000094	Theropila
c 267	18	11.3	165459	9	AC090587	Homo sapi	c 324	18	11.3	182481	9	AC007056	Homo sapi
c 268	18	11.3	165789	2	AL1591029	Homo sapi	c 325	18	11.3	182608	2	BK530059	Danio rer
c 269	18	11.3	165957	9	AC113558	Homo sapi	c 326	18	11.3	182618	9	AC095349	Homo sapi
c 270	18	11.3	166192	9	AC096737	Homo sapi	c 327	18	11.3	183391	2	AC147319	Pan trogl
c 271	18	11.3	166588	2	AC021870	Homo sapi	c 328	18	11.3	183461	9	AC006121	Homo sapi
c 272	18	11.3	166876	2	AL356864	Homo sapi	c 329	18	11.3	183976	9	AC100821	Homo sapi
c 273	18	11.3	166913	2	AC013708	Homo sapi	c 330	18	11.3	184106	9	AC060812	Homo sapi
c 274	18	11.3	167050	1	SAG766847	Streptococ	c 331	18	11.3	184111	9	AC006821	Homo sapi
c 275	18	11.3	167263	9	AC092417	Homo sapi	c 332	18	11.3	184119	2	AC133424	Homo sapi
c 276	18	11.3	167778	2	AC132618	Mus muscu	c 333	18	11.3	184555	9	AC025427	Homo sapi
c 277	18	11.3	168026	9	AL445670	Human DNA	c 334	18	11.3	184557	10	AC116657	Human sapi
c 278	18	11.3	168205	2	AC058819	Homo sapi	c 335	18	11.3	184560	2	AC021124	Homo sapi
c 279	18	11.3	168741	2	AC013573	Homo sapi	c 336	18	11.3	185229	9	AL157762	Homo sapi
c 280	18	11.3	168947	9	AC009453	Homo sapi	c 337	18	11.3	185598	2	AC132909	Human DNA
c 281	18	11.3	169371	2	AC125014	Mus muscu	c 338	18	11.3	186360	9	AC007982	Homo sapi
c 282	18	11.3	169457	2	AC009216	Drosophil	c 339	18	11.3	186748	3	AC012163	Homo sapi
c 283	18	11.3	169771	9	AC079163	Homo sapi	c 340	18	11.3	187914	9	AC104126	Homo sapi
c 284	18	11.3	169775	9	AL139120	Human DNA	c 341	18	11.3	187993	2	AC139292	Homo sapi
c 285	18	11.3	170026	2	AC016421	Homo sapi	c 342	18	11.3	188303	2	AC115256	Homo sapi
c 286	18	11.3	170070	2	BK548039	Danio rer	c 343	18	11.3	188373	9	AC145920	Homo sapi
c 287	18	11.3	170163	2	AC064844	Homo sapi	c 344	18	11.3	189196	10	AL603804	Mouse DNA
c 288	18	11.3	170233	2	AC147091	Pan trogl	c 345	18	11.3	189217	10	AC122858	Homo sapi
c 289	18	11.3	171073	9	AC074254	Homo sapi	c 346	18	11.3	190173	10	AC110573	Homo sapi
c 290	18	11.3	171515	9	AC068389	Homo sapi	c 347	18	11.3	190690	9	HSN324122	Homo sapi
c 291	18	11.3	171619	9	AC008082	Homo sapi	c 348	18	11.3	190802	10	AC124424	Homo sapi
c 292	18	11.3	171726	2	AC136269	Rattus no	c 349	18	11.3	191122	2	AL357669	Homo sapi
c 293	18	11.3	172022	2	AC145440	Bos tauru	c 350	18	11.3	191452	2	AC118966	Homo sapi
c 294	18	11.3	172144	4	AC092497	Sus scrofa	c 351	18	11.3	191841	2	AC118287	Homo sapi
c 295	18	11.3	172157	2	BK571898	Danio rer	c 352	18	11.3	192670	9	AC008592	Homo sapi
c 296	18	11.3	173012	2	AC013728	Homo sapi	c 353	18	11.3	192712	2	BK537285	Danio rer
c 297	18	11.3	174040	2	AC073950	Homo sapi	c 354	18	11.3	193625	2	AP001194	Homo sapi
c 298	18	11.3	174640	2	AC024479	Homo sapi	c 355	18	11.3	193867	2	AC105512	Homo sapi
c 299	18	11.3	174712	4	AC091624	Canis fam	c 356	18	11.3	194247	2	AC128060	Homo sapi
c 300	18	11.3	174790	2	AC134864	Canis fam	c 357	18	11.3	194250	2	AC140094	Bos tauru
c 301	18	11.3	175263	9	AC023102	Homo sapi	c 358	18	11.3	194541	2	AC011119	Homo sapi
c 302	18	11.3	175454	9	AP003303	Homo sapi	c 359	18	11.3	194663	2	BK890578	Homo sapi
c 303	18	11.3	175946	9	AP002088	Homo sapi	c 360	18	11.3	195066	10	AC122215	Mus muscu
c 304	18	11.3	176468	2	AC102928	Mus muscu	c 361	18	11.3	195665	2	BK322638	Danio rer
c 305	18	11.3	177056	2	AC132579	Mus muscu	c 362	18	11.3	196492	3	AC139725	Danio rer
c 306	18	11.3	177136	2	AC103584	Bos tauru	c 363	18	11.3	196873	9	AC063947	Homo sapi
c 307	18	11.3	177268	2	AC145486	Homo sapi	c 364	18	11.3	197013	2	AC079552	Homo sapi
c 308	18	11.3	177417	2	AC133160	Mus muscu	c 365	18	11.3	197437	2	AF303736	Homo sapi
c 309	18	11.3	177470	9	AL357140	Human DNA	c 366	18	11.3	198647	2	AC023056	Homo sapi
c 310	18	11.3	177552	2	BK510351	Danio rer	c 367	18	11.3	198656	2	AC108431	Homo sapi
c 311	18	11.3	178210	2	AC023884	Homo sapi	c 368	18	11.3	198693	2	AC113912	Homo sapi
c 312	18	11.3	178254	2	AC125160	Mus muscu	c 369	18	11.3	199016	2	HS48612	Human DNA
c 313	18	11.3	178679	2	AC113946	Mus muscu	c 370	18	11.3	199315	2	AC087801	Homo sapi
c 314	18	11.3	178914	9	AL590807	Human DNA	c 371	18	11.3	200306	2	AC128157	Rattus no
c 315	18	11.3	179505	9	AC008507	Homo sapi	c 372	18	11.3	201673	2	AC099747	Bos tauru
c 316	18	11.3	179462	2	AC079507	Mus muscu	c 373	18	11.3	202370	2	AC102899	Homo sapi
c 317	18	11.3	179942	2	AP003051	Homo sapi	c 374	18	11.3	202726	5	AL773593	Zebrafish
c 318	18	11.3	180137	2	AC023081	Homo sapi	c 375	18	11.3				

376	18	11.3	203279	9	AL354826	AL354826 Human DNA	c 433	18	11.3	259599	2	AC123087	AC123087 Rattus no
377	18	11.3	203524	2	AC012159	AC012159 Drosophila	c 434	18	11.3	264412	2	AC128074	AC128074 Rattus no
378	18	11.3	205830	5	AP006193	AP006193 Homo sapi	c 435	18	11.3	266461	2	AC120718	AC120718 Rattus no
379	18	11.3	205870	5	BX088695	BX088695 Zebrafish	c 436	18	11.3	268583	2	AC111344	AC111344 Rattus no
380	18	11.3	206436	2	AC112605	AC112605 Rattus no	c 437	18	11.3	274480	2	AC115513	AC115513 Rattus no
c 381	18	11.3	209326	2	AC106407	AC106407 Rattus no	c 438	18	11.3	276049	2	AC128259	AC128259 Rattus no
382	18	11.3	209643	10	AC080018	AC080018 Mus muscu	c 439	18	11.3	285256	2	AC118492	AC118492 Rattus no
c 383	18	11.3	209901	2	AC102707	AC102707 Mus muscu	c 440	18	11.3	286008	2	AC134828	AC134828 Mus muscu
c 384	18	11.3	210740	2	AC120321	AC120321 Rattus no	c 441	18	11.3	286395	2	AC125732	AC125732 Rattus no
c 385	18	11.3	216571	9	AC009961	AC009961 Homo sapi	c 442	18	11.3	290633	2	AC099180	AC099180 Rattus no
c 386	18	11.3	217916	2	AC099190	AC099190 Rattus no	c 443	18	11.3	292171	2	AC091244	AC091244 Rattus no
c 387	18	11.3	219488	2	AC095440	AC095440 Rattus no	c 444	18	11.3	298532	2	AC129468	AC129468 Rattus no
c 388	18	11.3	220084	2	AL445221	AL445221 Homo sapi	c 445	18	11.3	299804	3	AE003507	AE003507 Rattus no
c 389	18	11.3	220216	9	AC021019	AC021019 Homo sapi	c 446	18	11.3	300355	1	AE01162	AE01162 Drosophila
c 390	18	11.3	220231	2	AC125358	AC125358 Rattus no	c 447	18	11.3	301697	2	AC133490	AC133490 Rattus no
391	18	11.3	220248	10	AL772385	AL772385 Mouse DNA	c 448	18	11.3	302960	1	AE016935	AE016935 Bacteroid
392	18	11.3	220320	2	AC132527	AC132527 Rattus no	c 449	18	11.3	304642	2	AC123398	AC123398 Rattus no
393	18	11.3	221787	2	AC073690	AC073690 Mus muscu	c 450	18	11.3	322781	2	AC110396	AC110396 Rattus no
394	18	11.3	221969	2	AC139955	AC139955 Rattus no	c 451	18	11.3	324462	2	AC137263	AC137263 Rattus no
395	18	11.3	221974	2	AC099118	AC099118 Rattus no	c 452	18	11.3	326700	2	AC134362	AC134362 Rattus no
396	18	11.3	222570	2	AC103895	AC103895 Rattus no	c 453	18	11.3	327812	2	AC115555	AC115555 Rattus no
397	18	11.3	222975	2	AC130905	AC130905 Rattus no	c 454	18	11.3	331314	2	AC125550	AC125550 Rattus no
398	18	11.3	223366	2	AC091366	AC091366 Rattus no	c 455	18	11.3	333622	2	AC111475	AC111475 Rattus no
c 399	18	11.3	225118	2	AC117168	AC117168 Rattus no	c 456	18	11.3	340899	2	AC095219	AC095219 Rattus no
400	18	11.3	225216	10	AL844888	AL844888 Mouse DNA	c 457	18	11.3	341944	2	AC079158	AC079158 Homo sapi
401	18	11.3	225651	2	AC106065	AC106065 Rattus no	c 458	18	11.3	345434	2	AC098412	AC098412 Rattus no
402	18	11.3	226450	2	BX088714	BX088714 Danto fer	c 459	18	11.3	345992	2	AC107197	AC107197 Rattus no
403	18	11.3	226872	2	AC108645	AC108645 Rattus no	c 460	18	11.3	346354	2	AC095850	AC095850 Rattus no
404	18	11.3	227457	2	AC129997	AC129997 Rattus no	c 461	18	11.3	346865	2	AC097921	AC097921 Rattus no
c 405	18	11.3	227876	2	AC097192	AC097192 Rattus no	c 462	18	11.3	346865	2	AC097921	AC097921 Rattus no
c 406	18	11.3	228353	2	AL445283	AL445283 Homo sapi	c 463	18	11.3	347550	1	AB001118	AB001118 Buchnera
407	18	11.3	228655	2	AC096829	AC096829 Rattus no	c 464	18	11.3	348650	1	AE003364	AE003364 Staphyloc
408	18	11.3	230378	2	AC102893	AC102893 Mus muscu	c 465	18	11.3	348650	1	HS69D11F	HS69D11F Z62451 H.sapiens C
409	18	11.3	230575	2	AC128992	AC128992 Rattus no	c 466	17	10.7	303	11	BV048861	BV048861 S212P6034
410	18	11.3	231529	2	AC125102	AC125102 Mus muscu	c 467	17	10.7	358	3	EZAS06154	EZAS06154 Euscorpili
411	18	11.3	232552	2	AC103111	AC103111 Rattus no	c 468	17	10.7	375	8	ATHS23814	ATHS23814 Arabidops
412	18	11.3	233562	2	AC130670	AC130670 Mus muscu	c 469	17	10.7	375	8	ATHS23827	ATHS23827 Arabidops
413	18	11.3	233645	2	AC097282	AC097282 Rattus no	c 470	17	10.7	375	8	ATHS23827	ATHS23827 Arabidops
c 414	18	11.3	234072	2	AC099135	AC099135 Rattus no	c 471	17	10.7	425	6	AX431960	AX431960 Sequence
c 415	18	11.3	236629	2	AC120586	AC120586 Rattus no	c 472	17	10.7	445	8	AJ592834	AJ592834 Arabidops
c 416	18	11.3	236676	2	AC115491	AC115491 Rattus no	c 473	17	10.7	486	6	AX311732	AX311732 Sequence
c 417	18	11.3	238009	2	AC103650	AC103650 Mus muscu	c 474	17	10.7	534	11	BV029827	BV029827 S212P6020
418	18	11.3	239113	2	AC094034	AC094034 Rattus no	c 475	17	10.7	594	9	HSN34265	HSN34265 Homo sapi
c 419	18	11.3	240830	2	AC095615	AC095615 Rattus no	c 476	17	10.7	629	6	AX371038	AX371038 Sequence
c 420	18	11.3	241407	2	AC130827	AC130827 Mus muscu	c 477	17	10.7	641	11	BV001915	BV001915 S208P6122
c 421	18	11.3	242269	10	AC125187	AC125187 Mus muscu	c 478	17	10.7	759	6	AR348254	AR348254 Sequence
422	18	11.3	249987	2	AC098279	AC098279 Rattus no	c 479	17	10.7	760	4	AY285283	AY285283 Sus scrofa
423	18	11.3	251645	2	AC105549	AC105549 Rattus no	c 480	17	10.7	811	6	AX136583	AX136583 Sequence
424	18	11.3	251766	2	AC106117	AC106117 Rattus no	c 481	17	10.7	848	8	AT022	AT022 Secretory
425	18	11.3	252402	2	BX005425	BX005425 Danto fer	c 482	17	10.7	868	11	BV056539	BV056539 S212P6790
426	18	11.3	252632	2	AC123197	AC123197 Rattus no	c 483	17	10.7	906	8	AF362487	AF362487 Arabidops
c 428	18	11.3	253589	2	AC113741	AC113741 Rattus no	c 485	17	10.7	972	8	AF207978	AF207978 Ipomopsis
c 429	18	11.3	253638	2	AC102537	AC102537 Mus muscu	c 486	17	10.7	1014	8	AF362486	AF362486 Arabidops
c 430	18	11.3	254114	2	AC129431	AC129431 Rattus no	c 487	17	10.7	1050	3	LD138021	LD138021 Apotestatin
c 431	18	11.3	254437	9	AP000500	AP000500 Homo sapi	c 488	17	10.7	1147	5	AF1300147	AF1300147 Lopnutra d
c 432	18	11.3	258789	2	AC113921	AC113921 Rattus no	c 489	17	10.7	1232	3	DNMC70F	DNMC70F D.melanogaster

c 490	17	10.7	1438	6	AX154644	Sequence	c 547	17	10.7	5683	6	AX825986	AX825986
c 491	17	10.7	1463	6	AX136329	Sequence	c 548	17	10.7	5683	6	AX826114	AX826114
c 492	17	10.7	1463	6	BD123617	Secretary	c 549	17	10.7	5880	6	AX251085	AX251085
c 493	17	10.7	1463	6	AK075525	Homo sapi	c 550	17	10.7	5880	6	AX323563	AX323563
c 494	17	10.7	1565	3	AK113875	AK113875	c 551	17	10.7	6076	6	AX251418	AX251418
c 495	17	10.7	1799	10	AY082332	AY082332	c 552	17	10.7	6301	6	AX344953	AX344953
c 496	17	10.7	1827	10	BC050206	BC050206	c 553	17	10.7	6316	6	AX251105	AX251105
c 497	17	10.7	1831	3	DROGACATRA	DROGACATRA	c 554	17	10.7	6316	6	AX251866	AX251866
c 498	17	10.7	1905	1	AF056335	AF056335	c 555	17	10.7	6316	6	AX344256	AX344256
c 499	17	10.7	1968	1	AY128680	AY128680	c 556	17	10.7	6321	6	AX348647	AX348647
c 500	17	10.7	1969	7	BADLGADH	BADLGADH	c 557	17	10.7	6321	6	AX458547	AX458547
c 501	17	10.7	1992	6	BC040869	BC040869	c 558	17	10.7	6475	6	AX347150	AX347150
c 502	17	10.7	2000	6	AKS09766	AKS09766	c 559	17	10.7	6534	6	AX277948	AX277948
c 503	17	10.7	2087	9	AK093752	AK093752	c 560	17	10.7	6534	6	AX323637	AX323637
c 504	17	10.7	2153	3	AY069651	AY069651	c 561	17	10.7	6534	6	AX344776	AX344776
c 505	17	10.7	2246	6	AR395926	AR395926	c 562	17	10.7	6534	6	AX346328	AX346328
c 506	17	10.7	2261	6	AX544449	AX544449	c 563	17	10.7	6950	2	AC014419	AC014419
c 507	17	10.7	2400	1	AF092086	AF092086	c 564	17	10.7	7262	9	HSMB06281	HSMB06281
c 508	17	10.7	2447	8	AY114653	AY114653	c 565	17	10.7	7888	6	AX278015	AX278015
c 509	17	10.7	2398	8	AY227363S2	AY227363S2	c 566	17	10.7	8588	6	AX323712	AX323712
c 510	17	10.7	2612	8	AY062594	AY062594	c 567	17	10.7	9265	6	AX339183	AX339183
c 511	17	10.7	2682	8	CAU64206	CAU64206	c 568	17	10.7	9265	6	AX347055	AX347055
c 512	17	10.7	2814	10	BC023094	BC023094	c 569	17	10.7	10279	6	AX279995	AX279995
c 513	17	10.7	2882	6	AX747740	AX747740	c 570	17	10.7	10279	6	AX346492	AX346492
c 514	17	10.7	2882	9	AK092806	AK092806	c 571	17	10.7	10279	6	AX356451	AX356451
c 515	17	10.7	3360	1	STXSAU3A1M	STXSAU3A1M	c 572	17	10.7	10279	6	AX356451	AX356451
c 516	17	10.7	3360	6	AT7958	AT7958	c 573	17	10.7	10988	1	AE007626	AE007626
c 517	17	10.7	3478	8	SCYOR273C	SCYOR273C	c 574	17	10.7	11147	6	AX598807	AX598807
c 518	17	10.7	3759	3	DMJ18386	DMJ18386	c 575	17	10.7	11147	6	AX598853	AX598853
c 519	17	10.7	3776	1	LAJ10153	LAJ10153	c 576	17	10.7	11196	1	AE006318	AE006318
c 520	17	10.7	4043	9	HSMB06088	HSMB06088	c 577	17	10.7	11279	1	AE009840	AE009840
c 521	17	10.7	4300	8	AF279129	AF279129	c 578	17	10.7	11502	9	ACT138607	ACT138607
c 522	17	10.7	4313	3	DM068563	DM068563	c 579	17	10.7	11964	6	AX458509	AX458509
c 523	17	10.7	4353	6	AX252138	AX252138	c 580	17	10.7	12203	3	AE016653	AE016653
c 524	17	10.7	4353	6	AX344498	AX344498	c 581	17	10.7	12221	1	AE015001	AE015001
c 525	17	10.7	4353	6	AX348905	AX348905	c 582	17	10.7	12523	1	AE010575	AE010575
c 526	17	10.7	4915	9	HSMB07057	HSMB07057	c 583	17	10.7	13377	8	AF341860511	AF341860511
c 527	17	10.7	5031	6	AX085162	AX085162	c 584	17	10.7	13779	3	DMAS5042	DMAS5042
c 528	17	10.7	5031	6	AX085359	AX085359	c 585	17	10.7	14147	6	AX251501	AX251501
c 529	17	10.7	5142	6	AX367152	AX367152	c 586	17	10.7	14147	6	AX347392	AX347392
c 530	17	10.7	5218	9	HSMB06829	HSMB06829	c 587	17	10.7	14147	6	AX349113	AX349113
c 531	17	10.7	5236	6	AX345252	AX345252	c 588	17	10.7	14147	6	AX657806	AX657806
c 532	17	10.7	5278	6	AX251130	AX251130	c 589	17	10.7	14147	6	AX659080	AX659080
c 533	17	10.7	5278	6	AX345725	AX345725	c 590	17	10.7	14147	6	AX767435	AX767435
c 534	17	10.7	5360	6	AX281201	AX281201	c 591	17	10.7	14147	6	AX795753	AX795753
c 535	17	10.7	5360	6	AX346839	AX346839	c 592	17	10.7	14147	6	AX825901	AX825901
c 536	17	10.7	5360	6	AX356472	AX356472	c 593	17	10.7	14147	6	AX795869	AX795869
c 537	17	10.7	5683	6	AX281480	AX281480	c 594	17	10.7	14147	6	AX822261	AX822261
c 538	17	10.7	5683	6	AX346709	AX346709	c 595	17	10.7	14147	6	AX822385	AX822385
c 539	17	10.7	5683	6	AX348832	AX348832	c 596	17	10.7	14147	6	AX825901	AX825901
c 540	17	10.7	5683	6	AX795708	AX795708	c 597	17	10.7	14147	6	AX826029	AX826029
c 541	17	10.7	5683	6	AX795834	AX795834	c 598	17	10.7	14287	6	AX344624	AX344624
c 542	17	10.7	5683	6	AX795950	AX795950	c 599	17	10.7	14946	8	AF362474	AF362474
c 543	17	10.7	5683	6	AX822161	AX822161	c 600	17	10.7	15479	6	AX348350	AX348350
c 544	17	10.7	5683	6	AX822346	AX822346	c 601	17	10.7	15548	6	AX347057	AX347057
c 545	17	10.7	5683	6	AX822474	AX822474	c 602	17	10.7	15549	8	AF362475	AF362475
c 546	17	10.7	5683	6	AX825801	AX825801	c 603	17	10.7	18611	10	AF330048	AF330048

604	17	10.7	19000	3	CEK05D4	292804 Caenorhabdi	c 661	17	10.7	61469	2	AC107910	AC107910 Homo sapi
605	17	10.7	19605	9	AC103746	AC103746 Homo sapi	c 662	17	10.7	61818	2	AC106008	AC106008 Homo sapi
606	17	10.7	20720	3	CEC0762	Z33840 Caenorhabdi	c 663	17	10.7	61824	2	AC101450	AC101450 Mus muscu
607	17	10.7	20723	3	AC024639	AC024639 Caenorhab	c 664	17	10.7	62880	2	AC026926	AC026926 Homo sapi
608	17	10.7	20723	3	AC024639	AC024639 Caenorhab	c 665	17	10.7	63142	9	AP000279	AP000279 Homo sapi
609	17	10.7	20941	1	AE000976	AE000976 Archaeogl	c 666	17	10.7	63266	9	AL607038	AL607038 Homo sapi
610	17	10.7	23552	8	T15D22	AC012189 Arabidops	c 667	17	10.7	63918	9	AL672104	AL672104 Human DNA
611	17	10.7	23992	9	AC110298	AC110298 Homo sapi	c 668	17	10.7	64524	2	AC087195	AC087195 Homo sapi
612	17	10.7	26726	9	AY194117	AY194117 Homo sapi	c 669	17	10.7	64550	2	AC125427	AC125427 Homo sapi
613	17	10.7	30051	9	AL732446	AL732446 Human DNA	c 670	17	10.7	65361	2	AC091863	AC091863 Homo sapi
614	17	10.7	30060	2	AC017401	AC017401 Drosophila	c 671	17	10.7	65752	2	AC018627	AC018627 Homo sapi
615	17	10.7	31226	3	U39998	U39998 Caenorhabdi	c 672	17	10.7	65838	2	AC115758	AC115758 Mus muscu
616	17	10.7	32919	2	CEH37L19	Z92836 Caenorhabdi	c 673	17	10.7	66009	2	AC101250	AC101250 Mus muscu
617	17	10.7	33399	3	CEC09H6	Z81466 Caenorhabdi	c 674	17	10.7	66152	2	AC137709	AC137709 Homo sapi
618	17	10.7	34101	3	U64837	U64837 Caenorhabdi	c 675	17	10.7	66686	2	AC087669	AC087669 Homo sapi
619	17	10.7	35503	3	CEW09D6	Z82078 Caenorhabdi	c 676	17	10.7	66833	2	AC101655	AC101655 Mus muscu
620	17	10.7	36242	9	AL360228	AL360228 Human DNA	c 677	17	10.7	66874	9	AC069130	AC069130 Homo sapi
621	17	10.7	37467	3	DMC14E2	Z98254 Drosophila	c 678	17	10.7	66959	9	AL591214	AL591214 Human DNA
622	17	10.7	37672	8	SCVCSMCN	X89633 S. cerevisia	c 679	17	10.7	67179	2	AC084787	AC084787 Homo sapi
623	17	10.7	38020	9	AC122131	AC122131 Homo sapi	c 680	17	10.7	67340	2	AC113954	AC113954 Mus muscu
624	17	10.7	38225	3	CEP13611	Z83317 Caenorhabdi	c 681	17	10.7	67575	9	HSBR211L9	HSBR211L9 Homo sapi
625	17	10.7	39057	3	AF078788	AF078788 Caenorhab	c 682	17	10.7	68480	9	AC026426	AC026426 Homo sapi
626	17	10.7	39550	9	HSU85B5	Z69724 Human DNA	c 683	17	10.7	68648	9	HS635G19	HS635G19 Homo sapi
627	17	10.7	39982	6	AR308846	AR308846 Sequence	c 684	17	10.7	68986	2	AC020283	AC020283 Homo sapi
628	17	10.7	40198	9	HS1261H12	Z54072 Human DNA	c 685	17	10.7	70687	8	AP006376	AP006376 Homo sapi
629	17	10.7	40873	2	CEH04109	Z92846 Caenorhabdi	c 686	17	10.7	71118	9	AL390375	AL390375 Homo sapi
630	17	10.7	41509	2	AC140536	AC140536 Homo sapi	c 687	17	10.7	71327	8	AP001300	AP001300 Homo sapi
631	17	10.7	41735	9	AC134050	AC134050 Homo sapi	c 688	17	10.7	74515	9	AL355482	AL355482 Homo sapi
632	17	10.7	42042	3	CEC34B4	Z78059 Caenorhabdi	c 689	17	10.7	75551	3	AC005111	AC005111 Homo sapi
633	17	10.7	42065	3	CBR902E15	AC084480 Caenorhab	c 690	17	10.7	78446	9	AL358392	AL358392 Homo sapi
634	17	10.7	42141	3	CEV54G9A	AL032648 Caenorhab	c 691	17	10.7	78241	9	AL358392	AL358392 Homo sapi
635	17	10.7	42612	2	CEY54G9A	AC091825 Mus muscu	c 692	17	10.7	78689	9	AC108668	AC108668 Homo sapi
636	17	10.7	43585	3	U97593	U97593 Caenorhabdi	c 693	17	10.7	81278	9	AC091062	AC091062 Homo sapi
637	17	10.7	43785	7	LBA131519	AJ131519 Lactobaci	c 694	17	10.7	82168	9	AC092769	AC092769 Homo sapi
638	17	10.7	43955	2	AC100238	AC100238 Mus muscu	c 695	17	10.7	82415	8	AB005244	AB005244 Homo sapi
639	17	10.7	44443	9	HSU72E5	Z68328 Human DNA	c 696	17	10.7	82422	9	AL138763	AL138763 Homo sapi
640	17	10.7	44722	9	AC107396	AC107396 Homo sapi	c 697	17	10.7	82453	9	AC004558	AC004558 Homo sapi
641	17	10.7	45983	9	BX004861	BX004861 Human DNA	c 698	17	10.7	82646	10	AL928620	AL928620 Mouse DNA
642	17	10.7	49137	2	AC106018	AC106018 Homo sapi	c 699	17	10.7	83391	6	AX458577	AX458577 Sequence
643	17	10.7	49137	2	AC106018	AC106018 Homo sapi	c 700	17	10.7	85836	2	AC108384	AC108384 Pan trogl
644	17	10.7	49349	9	AL451134	AL451134 Human DNA	c 701	17	10.7	86203	9	AC017116	AC017116 Homo sapi
645	17	10.7	49349	9	AF184110	AF184110 Homo sapi	c 702	17	10.7	87243	9	AC117497	AC117497 Homo sapi
646	17	10.7	49743	2	AC017211	AC017211 Drosophila	c 703	17	10.7	87347	9	AC133530	AC133530 Homo sapi
647	17	10.7	50572	2	AC023899	AC023899 Mus muscu	c 704	17	10.7	88783	9	AC026398	AC026398 Homo sapi
648	17	10.7	51070	9	AC116303	AC116303 Homo sapi	c 705	17	10.7	88900	2	AC020204	AC020204 Homo sapi
649	17	10.7	51921	9	AC016145	AC016145 Homo sapi	c 706	17	10.7	89089	9	HS260B21	HS260B21 Homo sapi
650	17	10.7	54161	9	BX276189	BX276189 Human DNA	c 707	17	10.7	89354	9	AC008957	AC008957 Homo sapi
651	17	10.7	54626	2	AC103762	AC103762 Homo sapi	c 708	17	10.7	89690	8	AC079374	AC079374 Homo sapi
652	17	10.7	55335	9	AL592227	AL592227 Human DNA	c 709	17	10.7	90599	8	AC130275	AC130275 Homo sapi
653	17	10.7	56287	8	AP002060	AP002060 Arabidops	c 710	17	10.7	90940	9	AC104052	AC104052 Homo sapi
654	17	10.7	57493	9	AC004505	AC004505 Homo sapi	c 711	17	10.7	91516	9	AL731577	AL731577 Homo sapi
655	17	10.7	58484	9	AL37160	AL37160 Human DNA	c 712	17	10.7	91722	8	AP004976	AP004976 Homo sapi
656	17	10.7	58749	2	AC139006	AC139006 Homo sapi	c 713	17	10.7	92250	9	AC026693	AC026693 Homo sapi
657	17	10.7	59266	2	AC131282	AC131282 Homo sapi	c 714	17	10.7	93214	2	AC013107	AC013107 Homo sapi
658	17	10.7	60036	2	AC009610	AC009610 Homo sapi	c 715	17	10.7	93974	9	AC084421	AC084421 Homo sapi
659	17	10.7	60565	2	AC023852	AC023852 Homo sapi	c 716	17	10.7	94038	8	AC004401	AC004401 Arabidops
660	17	10.7	61404	9	AL513546	AL513546 Human DNA	c 717	17	10.7	95214	8	AC006526	AC006526 Arabidops

c 718	17	10.7	95337	2	AC138691	AC138691 Homo sapi	c 775	17	10.7	110811	8	AP004520	AP004520 Lotus cor
c 719	17	10.7	95302	9	AC010380	AC010380 Homo sapi	c 776	17	10.7	110907	14	AY229987	AY229987 Cryptoph
c 720	17	10.7	96726	2	HS1178F13	AL118500 Homo sapi	c 777	17	10.7	111104	9	AC117389	AC117389 Homo sapi
c 721	17	10.7	97101	2	AL450308	AL450308 Homo sapi	c 778	17	10.7	111255	8	AC125478	AC125478 Medicago
c 722	17	10.7	97434	9	AC087882	AC087882 Homo sapi	c 779	17	10.7	112088	9	AC005216	AC005216 Homo sapi
c 723	17	10.7	99332	9	HSJ298J18	AL096764 Homo sapi	c 780	17	10.7	112656	9	AC112253	AC112253 Homo sapi
c 724	17	10.7	100000	9	AP000038	AP000038 Homo sapi	c 781	17	10.7	114688	9	AC125437	AC125437 Homo sapi
c 725	17	10.7	100000	9	AP000106	AP000106 Homo sapi	c 782	17	10.7	115038	10	AL929270	AL929270 Mouse sapi
c 726	17	10.7	100000	9	AP000182	AL353912 Arabidops	c 783	17	10.7	115279	9	AC114744	AC114744 Arabidops
c 727	17	10.7	100028	8	ATF3C22	AL929178 Mouse sapi	c 784	17	10.7	115512	9	AC114744	AC114744 Arabidops
c 728	17	10.7	100057	10	AL929178	AC103866 Homo sapi	c 785	17	10.7	115568	9	AC1092120	AC1092120 Homo sapi
c 729	17	10.7	101324	9	AC010386	AC024810 Caenorhab	c 786	17	10.7	115626	9	AC010631	AC010631 Homo sapi
c 730	17	10.7	101640	3	AC024810	AC024810 Caenorhab	c 787	17	10.7	115626	9	AC010631	AC010631 Homo sapi
c 731	17	10.7	101640	3	AC024810	AC024810 Caenorhab	c 788	17	10.7	115626	9	AC010631	AC010631 Homo sapi
c 732	17	10.7	102307	9	HSJ328N14	AL109938 Homo sapi	c 789	17	10.7	117303	8	AT1211	AT1211 Homo sapi
c 733	17	10.7	103787	9	HSJ328N14	AL109938 Homo sapi	c 790	17	10.7	117406	9	AC010792	AC010792 Homo sapi
c 734	17	10.7	103820	5	AL929560	AL929560 Zebrafish	c 791	17	10.7	118080	10	AL844550	AL844550 Mouse sapi
c 735	17	10.7	103822	9	AL929560	AL929560 Zebrafish	c 792	17	10.7	118280	9	HSJ75305	HSJ75305 Homo sapi
c 736	17	10.7	103952	9	AC008852	AC008852 Homo sapi	c 793	17	10.7	118696	2	AC108843	AC108843 Homo sapi
c 737	17	10.7	104246	2	AC084785	AC084785 Arabidops	c 794	17	10.7	119065	2	AC136141	AC136141 Homo sapi
c 738	17	10.7	104972	2	AC025176	AC025176 Homo sapi	c 795	17	10.7	119077	9	AL354982	AL354982 Homo sapi
c 739	17	10.7	105391	2	AC144728	AC144728 Medicago	c 796	17	10.7	119753	8	AC006248	AC006248 Arabidops
c 740	17	10.7	105643	9	AC005629	AC005629 Homo sapi	c 797	17	10.7	120316	2	AC025984	AC025984 Homo sapi
c 741	17	10.7	105960	9	HS209A6	AL035401 Human sapi	c 798	17	10.7	120461	2	AC131654	AC131654 Homo sapi
c 742	17	10.7	106710	9	HSB711C4	AL035401 Human sapi	c 799	17	10.7	120586	9	AL590322	AL590322 Human sapi
c 743	17	10.7	106773	9	AL590012	AL590012 Human sapi	c 800	17	10.7	120921	8	AC139336	AC139336 Homo sapi
c 744	17	10.7	107100	9	AC117377	AC117377 Homo sapi	c 801	17	10.7	121151	9	HS705D16	HS705D16 Homo sapi
c 745	17	10.7	107341	2	AC136973	AC136973 Medicago	c 802	17	10.7	121289	2	AC145851	AC145851 Homo sapi
c 746	17	10.7	107895	9	AC078929	AC078929 Homo sapi	c 803	17	10.7	121372	2	AC145851	AC145851 Homo sapi
c 747	17	10.7	108681	8	AC002391	AC002391 Arabidops	c 804	17	10.7	121524	8	AC008468	AC008468 Homo sapi
c 748	17	10.7	108933	2	AC146692	AC146692 Medicago	c 805	17	10.7	122371	2	BK255908	BK255908 Homo sapi
c 749	17	10.7	109450	2	AC019498	AC019498 Drosophila	c 806	17	10.7	122371	2	BK255908	BK255908 Homo sapi
c 750	17	10.7	109588	9	AC093059	AC093059 Homo sapi	c 807	17	10.7	123209	8	ATF4F15	ATF4F15 Homo sapi
c 751	17	10.7	109588	9	AC010461	AC010461 Homo sapi	c 808	17	10.7	123291	9	AC104070	AC104070 Homo sapi
c 752	17	10.7	110000	2	AC095363_1	AC095363_1 Rattus no	c 809	17	10.7	124211	8	AC126787	AC126787 Homo sapi
c 753	17	10.7	110000	2	AC095857_0	AC095857_0 Rattus no	c 810	17	10.7	126154	10	AL935159	AL935159 Mouse sapi
c 754	17	10.7	110000	2	AC099211_2	AC099211_2 Rattus no	c 811	17	10.7	126270	9	AC005439	AC005439 Homo sapi
c 755	17	10.7	110000	2	AC110868_2	AC110868_2 Rattus no	c 812	17	10.7	126270	9	AC005439	AC005439 Homo sapi
c 756	17	10.7	110000	2	AC111335_0	AC111335_0 Rattus no	c 813	17	10.7	126414	9	AC108084	AC108084 Homo sapi
c 757	17	10.7	110000	2	AC111335_1	AC111335_1 Rattus no	c 814	17	10.7	126761	2	AC084129	AC084129 Homo sapi
c 758	17	10.7	110000	2	AC114447_1	AC114447_1 Rattus no	c 815	17	10.7	126803	9	AC007032	AC007032 Homo sapi
c 759	17	10.7	110000	2	AC117022_3	AC117022_3 Rattus no	c 816	17	10.7	127703	9	AL357034	AL357034 Homo sapi
c 760	17	10.7	110000	2	AC118422_0	AC118422_0 Rattus no	c 817	17	10.7	128428	2	AC144889	AC144889 Homo sapi
c 761	17	10.7	110000	2	AC120234_0	AC120234_0 Rattus no	c 818	17	10.7	128554	9	AL162500	AL162500 Homo sapi
c 762	17	10.7	110000	2	AC125151_2	AC125151_2 Rattus no	c 819	17	10.7	128856	2	AC126779	AC126779 Homo sapi
c 763	17	10.7	110000	2	AC125156_1	AC125156_1 Rattus no	c 820	17	10.7	129196	10	BK005080	BK005080 Homo sapi
c 764	17	10.7	110000	2	AC125548_2	AC125548_2 Rattus no	c 821	17	10.7	129708	4	AC145407	AC145407 Homo sapi
c 765	17	10.7	110000	2	AC130479_1	AC130479_1 Rattus no	c 822	17	10.7	129802	2	AC136701	AC136701 Homo sapi
c 766	17	10.7	110000	2	AC132284_1	AC132284_1 Rattus no	c 823	17	10.7	129819	9	AC104049	AC104049 Homo sapi
c 767	17	10.7	110000	2	AL390202_04	Continuation (2 of	c 824	17	10.7	129858	10	AL772272	AL772272 Homo sapi
c 768	17	10.7	110000	2	BK255915_0	Continuation (3 of	c 825	17	10.7	129989	9	AC005681	AC005681 Homo sapi
c 769	17	10.7	110000	2	BK255915_0	Continuation (3 of	c 826	17	10.7	129996	2	AC133462	AC133462 Homo sapi
c 770	17	10.7	110000	2	PFMAL13_21	BK255915 Danto rer	c 827	17	10.7	130878	9	AL450063	AL450063 Homo sapi
c 771	17	10.7	110000	2	PFMAL13P2_0	AL049185 Plasmodu	c 828	17	10.7	131355	2	AC139655	AC139655 Homo sapi
c 772	17	10.7	110000	2	PFMAL13P2_0	Continuation (2 of	c 829	17	10.7	131402	10	AL773583	AL773583 Homo sapi
c 773	17	10.7	110312	10	AF131866	Continuation (2 of	c 830	17	10.7	131743	8	AC004561	AC004561 Homo sapi
c 774	17	10.7	110520	9	AL603757	AL603757 Human sapi	c 831	17	10.7	131944	8	AC097659	AC097659 Homo sapi
c 774	17	10.7	110626	9	AC005541	AC005541 Homo sapi							

c 832	17	10.7	132473	8	AC136651	AC136651 Medicago	c 889	17	10.7	146742	2	AC016275	AC016275 Homo sapi
c 833	17	10.7	132501	9	AC107613	AC107613 Homo sapi	c 890	17	10.7	146921	9	AC007992	AC007992 Homo sapi
c 834	17	10.7	132641	9	AP00679-	AP00679 Homo sapi	c 891	17	10.7	147002	2	AC126914	AC126914 Rattus no
c 835	17	10.7	134043	2	AC146717	AC146717 Rattus no	c 892	17	10.7	147047	9	AL353778	AL353778 Human DNA
c 836	17	10.7	134457	9	AC001231	AC001231 Homo sapi	c 893	17	10.7	147179	2	AC117937	AC117937 Canis fam
c 837	17	10.7	134825	10	AC108420	AC108420 Mus muscu	c 894	17	10.7	147250	2	AC011778	AC011778 Homo sapi
c 838	17	10.7	134878	9	AC140847	AC140847 Homo sapi	c 895	17	10.7	147260	2	AC016340	AC016340 Homo sapi
c 839	17	10.7	135240	9	AL136362	AL136362 Human DNA	c 896	17	10.7	147595	2	AC136834	AC136834 Rattus no
c 840	17	10.7	135280	5	BX296520	BX296520 Zebrafish	c 897	17	10.7	147810	9	AL353730	AL353730 Human DNA
c 841	17	10.7	135638	1	SYCSLNG	D64005 Synchocyst	c 898	17	10.7	148293	9	AC087730	AC087730 Pan trogl
c 842	17	10.7	135862	10	AC132576	AC132576 Mus muscu	c 899	17	10.7	148317	5	BX649477	BX649477 Zebrafish
c 843	17	10.7	135966	2	AL356007	AL356007 Homo sapi	c 900	17	10.7	148328	10	AL808410	AL808410 Mouse DNA
c 844	17	10.7	136311	2	AC146972	AC146972 Medicago	c 901	17	10.7	148338	2	AC022831	AC022831
c 845	17	10.7	136372	9	AC103828	AC103828 Homo sapi	c 902	17	10.7	148380	2	AL139325	AL139325 Homo sapi
c 846	17	10.7	136485	10	BX294008	BX294008 Mouse DNA	c 903	17	10.7	148438	9	AC019072	AC019072 Homo sapi
c 847	17	10.7	136723	9	AC074000	AC074000 Homo sapi	c 904	17	10.7	148498	2	AC034225	AC034225 Homo sapi
c 848	17	10.7	136943	9	AL359842	AL359842 Human DNA	c 905	17	10.7	148504	2	AC138732	AC138732
c 849	17	10.7	137343	9	AP000946	AP000946 Homo sapi	c 906	17	10.7	148573	2	AC066693	AC066693 Homo sapi
c 850	17	10.7	137484	10	AC126021	AC126021 Mus muscu	c 907	17	10.7	148641	9	HS111909	HS111909
c 851	17	10.7	137580	2	AC146553	AC146553 Medicago	c 908	17	10.7	148751	2	AC144694	AC144694 Sus scrof
c 852	17	10.7	137890	9	AB045364	AB045364 Homo sapi	c 909	17	10.7	148915	9	AC005030	AC005030 Homo sapi
c 853	17	10.7	137897	9	AL161913	AL161913 Human DNA	c 910	17	10.7	149050	9	AC024697	AC024697 Homo sapi
c 854	17	10.7	138007	2	AC141282	AC141282 Homo sapi	c 911	17	10.7	149059	9	AC027779	AC027779 Homo sapi
c 855	17	10.7	138209	9	HS044211	AL078597 Human DNA	c 912	17	10.7	149110	9	AP003692	AP003692
c 856	17	10.7	138215	2	AC023523	AC023523 Homo sapi	c 913	17	10.7	149114	9	AP001172	AP001172 Homo sapi
c 857	17	10.7	138573	9	AL354211	AL354211 Pan trogl	c 914	17	10.7	149769	9	HS3323A24	HS3323A24 Homo sapi
c 858	17	10.7	139056	2	AC141691	AC141691 Apis mell	c 915	17	10.7	149981	2	AC011929	AC011929 Homo sapi
c 859	17	10.7	139189	10	AL935138	AL935138 Mouse DNA	c 916	17	10.7	150001	9	AC006063	AC006063 Homo sapi
c 860	17	10.7	139881	9	AL160254	AL160254 Human DNA	c 917	17	10.7	150136	9	BS000056	BS000056 Pan trogl
c 861	17	10.7	140506	2	AC137198	AC137198 Rattus no	c 918	17	10.7	150136	9	AC000056	AC000056 Pan trogl
c 862	17	10.7	140869	2	AC116515	AC116515 Mus muscu	c 919	17	10.7	150375	10	AC124404	AC124404 Mus muscu
c 863	17	10.7	141000	9	AC121756	AC121756 Homo sapi	c 920	17	10.7	150375	10	AC124404	AC124404 Mus muscu
c 864	17	10.7	141582	2	AC138465	AC138465 Medicago	c 921	17	10.7	150489	2	AC069491	AC069491 Homo sapi
c 865	17	10.7	141620	2	AC068008	AC068008 Homo sapi	c 922	17	10.7	150951	10	RN52A6	RN52A6
c 866	17	10.7	141913	9	AL512452	AL512452 Human DNA	c 923	17	10.7	150966	2	AC146246	AC146246 Pan trogl
c 867	17	10.7	142800	9	BS000037	BS000037 Pan trogl	c 924	17	10.7	151494	2	AC132989	AC132989 Rattus no
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c 871	17	10.7	143527	9	AC011553	AC011553 Homo sapi	c 928	17	10.7	151923	10	AL845499	AL845499 Human DNA
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c 873	17	10.7	144290	9	AC098866	AC098866 Homo sapi	c 930	17	10.7	152205	2	AC041037	AC041037 Homo sapi
c 874	17	10.7	144301	9	AC010467	AC010467 Homo sapi	c 931	17	10.7	152248	2	AC027522	AC027522 Homo sapi
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c 880	17	10.7	145256	9	AL360182	AL360182 Human DNA	c 937	17	10.7	153203	2	AL359812	AL359812 Homo sapi
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c 883	17	10.7	145726	2	AC021807	AC021807 Homo sapi	c 940	17	10.7	154019	10	AL671885	AL671885 Mouse DNA
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c 887	17	10.7	146267	2	AC008815	AC008815 Homo sapi	c 944	17	10.7	154618	2	AC094013	AC094013 Papio anu
c 888	17	10.7	146410	9	AC006575	AC006575 Homo sapi	c 945	17	10.7	154640	9	AC096659	AC096659 Homo sapi

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	JOURNAL	COMMENT
BD245279	BD245279	Development of novel antibiotics based on bacteriophage genomics.	BD245279	1	GI:33055049	JP 2002531107-A/14.	unidentified	1 (bases 1 to 159)	Pelletier,J., Gros,P. and Dubow,M.	Development of novel antibiotics based on bacteriophage genomics	Patent: JP 2002531107-A 14 24-SEP-2002;
							unclassified.				PHARTECH INC
											OS Staphylococcus aureus bacteriophage 77
											PN JP 2002531107-A/14
											PD 24-SEP-2002
											PR 03-DEC-1999 JP 2000585456
											PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/32614 PR
											28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
											01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
											PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
											PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005, PC C12M1/00,
											PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC C12N15/00,
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RESULT 2
LOCUS AR368771 159 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6376652.
ACCESSION AR368771
VERSION AR368771.1 GI:34603078
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential staphylococcus aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 4 23-SEP-2002;
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source Location/Qualifiers
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Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055051
KEYWORDS JP 2002531107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 16 24-SEP-2002;
PHARTECH INC

COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992, 03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804, 30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777, 02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K45/00, A61P31/04, C07K14/009, PC
C12M1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT /organism="Staphylococcus aureus bacteriophage 77".

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source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 7.6e-79;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTCTAGATGAGGCAAGGCGATGAATAAGTTGTACGACCTATTATCAAAAATT 120
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Db 34453 CTCTAGATGAGGCAAGGCGATGAATAAGTTGTACGACCTATTATCAAAAATT 34512
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Db 34513 GCAGAACGTCAACACCCCGCTATGTCGAATTTAA 34551

RESULT 4
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LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential staphylococcus aureus gene and its encoded protein

JOURNAL Patent: US 6376652-A 3 23-APR-2002;
FEATURES Location/Qualifiers
source 1..41708
/organism="unknown"
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Query Match 100.0%; Score 159; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 7,66-79;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTAACCAAGATTTTAACTAACTGAGTTCAGATATGTAAGCTCAGAA 60
DB 34393 ATGGTAACCAAGATTTTAACTAACTGAGTTCAGATATGTAAGCTCAGAA 34452
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DB 34453 CTCATGATGAGGCAAGGCGCATGAAATAGGTGTACACACTATTATCAAAACT 34512
QY 121 GCAGAACGTCAACACGCGCGCTATGCTGCAATATTA 159
DB 34513 GCAGAACGTCAACACGCGCGCTATGCTGCAATATTA 34551
RESULT 5
LOCUS AP003360 348527 bp DNA linear BCT 07-FEB-2002
DEFINITION Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
ACCESSION AP003360 BA000017
VERSION AP003360.2 GI:14246388
KEYWORDS
SOURCE Staphylococcus aureus subsp. aureus Mu50
ORGANISM Staphylococcus aureus subsp. aureus Mu50
REFERENCE
AUTHORS 1
Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Iian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hoshiyama,A.,
Mitsunaga-Uji,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kato,C.,
Sekiinzu,K., Hirakawa,H., Kuzura,S., Goto,S., Yabuzaki,J.,
Koshida,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
TITLE Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 2131952
PUBMED 11418146
REFERENCE 2 (bases 1 to 348527)
AUTHORS Ohta,T.
TITLE Direct Submision
SUMMARY Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology/ 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohts@tsakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
COMMENT On May 29, 2001 this sequence version replaced gi:13674937.

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DEFINITION	Staphylococcus aureus temperate phage phiSLT genomic DNA, complete sequence.			
ACCESSION	AB045978			
VERSION	AB045978.1	GI:12697822		
KEYWORDS	Staphylococcus aureus temperate phage phiSLT			
ORGANISM	Staphylococcus aureus temperate phage phiSLT			
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AUTHORS	Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J. and Kamio,Y.			
TITLE	Phage conversion of Panton-Valentine leukocidin in Staphylococcus aureus: molecular analysis of a PVL-converting phage, phiSLT			
JOURNAL	Gene 266 (1-2), 195-206 (2001)			
MEDLINE	21261936			
PUBMED	11368915			
REFERENCE	2 (base 1 to 42942)			
AUTHORS	Kaneko,J., Narita,S. and Kamio,Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate School of Agricultural Science, 1-1 Tsurumidori Azaamiyamachi, Sendai, Miyagi 981-8535, Japan (E-mail:j.kaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781, Fax:81-22-747-8780)			
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 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 100 GACCTATTTATCCAAAACCTGCGAAGCGTCATACAGCCCGCGCTATCGTCGATATTAA 159
 DB 11997 GACCTATTTATCCAAAACCTGCGAAGCGTCATACAGCCCGCGCTATCGTCGATATTAA 12056

RESULT 7
 AF424783

LOCUS AF424783 42722 bp DNA linear PHG 10-JUN-2002

DEFINITION Staphylococcus aureus phage phi 13, complete genome.

ACCESSION AF424783

VERSION AF424783.1 GI:18920591

KEYWORDS

ORGANISM Staphylococcus aureus phage phi 13

SOURCE Staphylococcus aureus phage phi 13

REFERENCE 1 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.

AUTHORS Iandolo, J., Worrell, V., Grochev, K.H., Qian, Y., Tian, R., Kenton, S., Dorman, A., Ji, H., Lin, S., Loh, P., Qi, S., Zhu, H. and Roe, B. A.

TITLE Comparative analysis of the genomes of the temperate bacteriophages phi11, phi12 and phi13 of Staphylococcus aureus 8325

JOURNAL Gene 289 (1-2), 109-118 (2002)

MEDLINE 22032962

PUBMED 12036589

REFERENCE 2 (bases 1 to 42722)

AUTHORS Iandolo, J., Worrell, V., Roe, B., Qian, Y., Dorman, A., Tian, R., Lin, S. and Ji, H.

TITLE Direct Submission

JOURNAL Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City, OK 73190, USA

FEATURES

source

1. 42722 Location/Qualifiers

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/specific_host="Staphylococcus aureus strain 8325"

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Best Local Similarity 100.0%; Pident.No. 1.9e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 TAAACTGAGTTCAGATATGATGCTCAGAACTCATAGA 68
Db 11433 TAAACTGAGTTCAGATATGATGCTCAGAACTCATAGA 11474
RESULT 8
AC114212/c
LOCUS AC114212 232473 bp DNA linear HTG 11-OCT-2002
DEFINITION Rattus norvegicus clone CH230-313016, *** SEQUENCING IN PROGRESS

AC114212
VERSION AC114212.3 GI:23634343
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 232473)
Muzny,D,Marle,J, Metzger,M,Lee,J, Abramson,S, Adams,C, Alder,J,
Allen,C, Allen,H, Albrooks,S, Anin,A, Angilano,D,
Ayala-Jeancot,V, Ayoubi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benaimed,F,

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JOURNAL
Submitted (11-Oct-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 11, 2002 this sequence version replaced g1:21738321.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/ra/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: Q2W
Center clone name: CH230-313016
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 181733 bases at least Q40
Consensus quality: 185734 bases at least Q40
Consensus quality: 188537 bases at least Q20
Estimated insert size: 192613; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
  1 234473: contig of 232473 bp in length.
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site:hoel
end_sequence:RANB92TV"
45821..48619
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misc_feature 79031..80632
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ORIGIN

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Best Local Similarity 100.0%; Pred.No. 0.0091;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTAAACTAACTGAGTGT 40
|||||
DB 129782 TTTTAAACTAACTGAGTGT 129758

Search completed: October 15, 2004, 03:32:43
Job time : 879.423 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: October 14, 2004, 18:55:29 ; Search time 106.071 Seconds
(without alignments)
6368.040 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159

Sequence: 1 atcgttaaccacagaatttc.....ccgcatcgcgaatactaa 159

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_29Jan04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001s:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003as:
8: geneseqn2003bs:
9: geneseqn2003cs:
10: geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	3	AA68252 Bacterioph
2	159	100.0	159	4	AA68107 Bacterioph
3	159	100.0	41708	3	AA68247 Bacterioph
4	159	100.0	41708	4	AA68106 Complete
5	45	28.3	1134	2	AA68398 DNA encod
6	19	11.9	673	2	AA61364 Enterococ
7	19	11.9	673	6	AB599436 Enterococ

8	19	11.9	51952	2	ANV26084	ANv26084 Tomato pe	c	65	17	10.7	5278	6	AB132823	AB132823 Human imm	
c	9	19	11.9	110000	6	ABv69245_10	Continuation (11 o	c	66	17	10.7	5360	6	AB133937	AB133937 Human imm
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c	11	18	11.3	383	4	AAK60738	Human imm	c	68	17	10.7	5360	6	AB149366	AB149366 Human pol
c	12	18	11.3	405	8	ACH18258	Human adu	c	69	17	10.7	5683	6	AB133807	AB133807 Human imm
c	13	18	11.3	536	6	ABK66443	Hollicobac	c	70	17	10.7	5683	6	AB134591	AB134591 Human met
c	14	18	11.3	931	6	ABX70380	Hollicobac	c	71	17	10.7	5683	6	AB170400	AB170400 Human met
c	15	18	11.3	1185	2	AAK14577	H. pylori	c	72	17	10.7	5683	6	ADBS5397	ADBS5397 THBS1 gen
c	16	18	11.3	1351	6	ABv68272	Streptococ	c	73	17	10.7	5683	9	ADBS4310	ADBS4310 Preteroste
c	17	18	11.3	3424	6	ABX13901	CDNA enco	c	74	17	10.7	5880	4	AAK28177	AAK28177 DNA trans
c	18	18	11.3	5031	4	AB11822	Drosophi	c	75	17	10.7	5880	6	AA54664	AA54664 Tumor su
c	19	18	11.3	6790	7	ABZ67443	Human sec	c	76	17	10.7	6076	4	AB132053	AB132053 Human imm
c	20	18	11.3	6790	7	ABZ73864	Secreted	c	77	17	10.7	6301	6	AA54631	AA54631 Tumor su
c	21	18	11.3	24934	4	AAK78433	Human imm	c	78	17	10.7	6316	6	ABK31260	ABK31260 SIgnal tr
c	22	18	11.3	24934	4	AAK71542	Human imm	c	79	17	10.7	6316	6	AA570215	AA570215 Chemical
c	23	18	11.3	110000	2	AAK20248_00	Borrelia	c	80	17	10.7	6321	6	ABv67063	ABv67063 Human ang
c	24	18	11.3	110000	6	ABN71527_07	Continuation (8 of	c	81	17	10.7	6475	6	AB134248	AB134248 Human imm
c	25	18	11.3	110000	6	ABA92787_0	Buchnera	c	82	17	10.7	6534	4	AA545404	AA545404 Chemical
c	26	18	11.3	162450	3	AAZ68667	Retinobla	c	83	17	10.7	6534	6	AB133426	AB133426 Human imm
c	27	17	10.7	325	4	AA182650	Human pol	c	84	17	10.7	6534	6	ABK28251	ABK28251 DNA trans
c	28	17	10.7	375	4	AA186131	Human pol	c	85	17	10.7	8588	4	AA545470	AA545470 Chemical
c	29	17	10.7	425	6	ABK73084	Bacillus	c	86	17	10.7	9265	6	AB134153	AB134153 Human imm
c	30	17	10.7	468	4	AAK66136	Human imm	c	87	17	10.7	9265	6	AA563355	AA563355 Chemical
c	31	17	10.7	468	4	AAK66137	Human imm	c	88	17	10.7	9642	4	AB119832	AB119832 Drosophi
c	32	17	10.7	468	6	ABN77412	Human ORF	c	89	17	10.7	9642	4	AB129856	AB129856 Drosophi
c	33	17	10.7	609	6	ABv90422	N. capsul	c	90	17	10.7	10279	6	AB133590	AB133590 Human imm
c	34	17	10.7	629	6	ABK33453	Human eos	c	91	17	10.7	10279	6	AB192276	AB192276 Chemical
c	35	17	10.7	759	9	ADC93238	E. faecul	c	92	17	10.7	11147	7	ABZ10007	ABZ10007 Haematopo
c	36	17	10.7	811	5	AAE94071	AAE94071 Primer sp	c	93	17	10.7	11147	7	ABZ10153	ABZ10153 Haematopo
c	37	17	10.7	913	4	ABK43483	DNA enco	c	94	17	10.7	11964	6	ABv67025	ABv67025 Human ang
c	38	17	10.7	1438	5	AAE90472	Candida a	c	95	17	10.7	12025	4	AB129856	AB129856 Drosophi
c	39	17	10.7	1463	5	AAE93869	Human CDN	c	96	17	10.7	14147	4	AA546743	AA546743 Tumor su
c	40	17	10.7	1713	7	AAZ28856	Prokaryot	c	97	17	10.7	14147	6	ABK33955	ABK33955 Human DNA
c	41	17	10.7	2000	6	ABZ16656	Prokaryot	c	98	17	10.7	14147	7	ADZ20386	ADZ20386 Prostate
c	42	17	10.7	2010	7	ACA46947	Prokaryot	c	99	17	10.7	14147	9	ADZ84193	ADZ84193 Human ren
c	43	17	10.7	2222	6	ABN92180	Streptococ	c	100	17	10.7	14147	9	ADBS4225	ADBS4225 Preteroste
c	44	17	10.7	2218	4	AAH41248	Human ATP	c	101	17	10.7	14147	9	ADBS4097	ADBS4097 Preteroste
c	45	17	10.7	2241	5	AA572846	DNA enco	c	102	17	10.7	14287	6	ABN80032	ABN80032 Human che
c	46	17	10.7	2261	6	ABZ66869	Arabidops	c	103	17	10.7	15479	6	ABK33964	ABK33964 Human che
c	47	17	10.7	2751	7	ACA32896	Prokaryot	c	104	17	10.7	28011	4	AAK81639	AAK81639 Human imm
c	48	17	10.7	2793	4	AA553045	Enterococ	c	105	17	10.7	39982	7	ADZ67093	ADZ67093 Human enz
c	49	17	10.7	2851	4	AB109564	Drosophi	c	106	17	10.7	83391	6	ABX08336_08	ABX08336_08 Continuation (8 of
c	50	17	10.7	2882	9	ADB63111	Human CDN	c	107	17	10.7	110000	6	ABX08336_07	ABX08336_07 Continuation (9 of
c	51	17	10.7	3360	2	AAQ15130	DNA contg	c	108	17	10.7	110000	6	AA561639	AA561639 Human imm
c	52	17	10.7	3411	4	AB110700	Drosophi	c	109	17	10.7	110000	8	AD13411_0	AD13411_0 Human tfa
c	53	17	10.7	3936	4	AB119833	Drosophi	c	110	17	10.7	185695	7	AA55693	AA55693 Human THB
c	54	17	10.7	3961	4	AA103517	Human rep	c	111	17	10.7	185695	7	AA55693	AA55693 Human THB
c	55	17	10.7	3961	4	AA103518	Human rep	c	112	17	10.7	185695	7	AA55693	AA55693 Human THB
c	56	17	10.7	4353	6	ABK31502	SIgnal tr	c	113	17	10.7	185695	7	AA55693	AA55693 Human THB
c	57	17	10.7	4353	6	AB170473	Chemical	c	114	17	10.7	185695	7	AA55693	AA55693 Human THB
c	58	17	10.7	4353	6	AA561436	Human gen	c	115	17	10.7	185695	7	AA55693	AA55693 Human THB
c	59	17	10.7	4432	4	AB129655	Prokaryot	c	116	17	10.7	185695	7	AA55693	AA55693 Human THB
c	60	17	10.7	5031	4	AAE76068	Human MAD	c	117	17	10.7	185695	7	AA55693	AA55693 Human THB
c	61	17	10.7	5031	5	AAE76655	Malize ZmM	c	118	17	10.7	185695	7	AA55693	AA55693 Human THB
c	62	17	10.7	5142	6	ABA94934	Human Zne	c	119	17	10.7	185695	7	AA55693	AA55693 Human THB
c	63	17	10.7	5236	6	AB132350	Human imm	c	120	17	10.7	185695	7	AA55693	AA55693 Human THB
c	64	17	10.7	5278	4	AA546576	Tumour su	c	121	17	10.7	185695	7	AA55693	AA55693 Human THB

c 122	17	10.7	198285	6	ABK84699	Abv84699 Human cDN	179	16	10.1	686	2	AAV28637	AAV28637 Human che
c 123	17	10.7	198285	5	ABN97319	Abn97319 Gene #381	c 180	16	10.1	700	4	AAH92500	AAH92500 Human inf
c 124	17	10.7	240823	9	ADP69391	Adp69391 Human PG-	c 181	16	10.1	700	4	AAH92499	AAH92499 Human inf
c 125	17	10.7	240825	4	AAE24497	Aae24497 Human PG-	c 182	16	10.1	750	2	AAH75257	AAH75257 Nucleotid
c 126	17	10.7	240825	6	ABQ81802	Abq81802 Human PG-	183	16	10.1	756	7	ACD19379	ACD19379 Human onco
c 127	16	10.1	25	8	ACK03529	Ack03529 Human mic	184	16	10.1	756	3	AAZ32843	AAZ32843 Human che
c 128	16	10.1	111	3	AAA42720	Aaa42720 Human sec	185	16	10.1	759	6	ABN94845	ABN94845 Human bet
c 129	16	10.1	142	6	AAI68888	Aai68888 ActiVated	186	16	10.1	768	4	AAI196382	AAI196382 Human neu
c 130	16	10.1	187	2	AAI26147	Aai26147 Human gen	c 187	16	10.1	776	4	AAI20017	AAI20017 Human bre
c 131	16	10.1	252	3	AAI0747	Aai0747 Human sec	c 188	16	10.1	844	2	AAZ33455	AAZ33455 Human bre
c 132	16	10.1	295	5	ABV61570	Abv61570 Human pro	189	16	10.1	860	7	ADH70262	Adh70262 Rice gene
c 133	16	10.1	300	2	AAI67744	Aai67744 H. pylori	190	16	10.1	893	6	ABX65548	ABX65548 Helicobac
c 134	16	10.1	300	2	AAI77424	Aai77424 H. pylori	191	16	10.1	966	2	AAH7430	AAH7430 Human cDN
c 135	16	10.1	307	7	ABK35303	Abk35303 Bovine ES	192	16	10.1	966	2	AAH7430	AAH7430 Human cDN
c 136	16	10.1	330	6	ABK65644	Abk65644 Helicobac	193	16	10.1	966	3	ADC38645	ADC38645 Human cDN
c 137	16	10.1	372	6	ABJ84125	Abj84125 Human ova	194	16	10.1	1024	6	ABX65475	ABX65475 Helicobac
c 138	16	10.1	398	4	AAK92935	Aak92935 Human cDN	195	16	10.1	1024	6	ABX67004	ABX67004 Helicobac
c 139	16	10.1	402	7	ABK43585	Abk43585 Bovine ES	196	16	10.1	1029	7	ACA30227	ACA30227 Prokaryot
c 140	16	10.1	414	8	ACH16292	Ach16292 Human adu	197	16	10.1	1043	9	ADB37435	ADB37435 Human can
c 141	16	10.1	420	8	ACH48626	Ach48626 Human leu	198	16	10.1	1077	6	ABN93333	ABN93333 Staphyloc
c 142	16	10.1	422	9	ADD33185	Add33185 Human mlt	199	16	10.1	1083	7	ACA30327	ACA30327 Prokaryot
c 143	16	10.1	428	7	ABK3597	Abk3597 Bovine ES	200	16	10.1	1086	7	ABZ81912	ABZ81912 Tobacco D
c 144	16	10.1	431	5	ABV17652	Abv17652 Human pro	c 201	16	10.1	1104	2	AAV75129	AAV75129 Staphyloc
c 145	16	10.1	437	7	ABK50178	Abk50178 Bovine ES	202	16	10.1	1111	3	AAA09306	AAA09306 Human alp
c 146	16	10.1	442	6	ABJ78441	Abj78441 Human ova	203	16	10.1	1111	5	AAH76472	AAH76472 CDNA code
c 147	16	10.1	452	8	ABV19176	Abv19176 Human pro	204	16	10.1	1111	6	ABJ61814	ABJ61814 Colon ade
c 148	16	10.1	455	8	ACH24294	Ach24294 Human adu	205	16	10.1	1111	6	ABJ92125	ABJ92125 Human tum
c 149	16	10.1	475	6	ABJ37743	Abj37743 Human col	206	16	10.1	1111	7	ACD19378	ACD19378 Human cDN
c 150	16	10.1	479	5	AAH81583	Aah81583 Human dlf	207	16	10.1	1111	7	ABX72050	ABX72050 DNA enco
c 151	16	10.1	482	5	ABV48952	Abv48952 Human pro	208	16	10.1	1111	7	ACE12940	ACE12940 Human cor
c 152	16	10.1	499	5	ABV47446	Abv47446 Human pro	209	16	10.1	1193	3	AAH59711	AAH59711 Human sec
c 153	16	10.1	515	9	ADD59601	Add59601 Human pdc	210	16	10.1	1198	4	AAH31383	AAH31383 Human sec
c 154	16	10.1	522	9	ADB37434	Adb37434 Human can	211	16	10.1	1354	2	AAH7431	AAH7431 C1one H17
c 155	16	10.1	528	2	AAV86461	Aav86461 EST clone	212	16	10.1	1354	3	AAA30224	AAA30224 Human non
c 156	16	10.1	532	4	AAH92665	Aah92665 Human inf	213	16	10.1	1354	3	ADC38647	ADC38647 Human cDN
c 157	16	10.1	544	5	ABV55726	Abv55726 Human pro	214	16	10.1	1371	2	AAH33332	AAH33332 Human CXC
c 158	16	10.1	546	4	AAK78241	Aak78241 Human tum	215	16	10.1	1445	2	AAH74176	AAH74176 Human che
c 159	16	10.1	576	2	AAI68039	Aai68039 H. pylori	216	16	10.1	1481	9	ADB25640	ADB25640 Human cDN
c 160	16	10.1	600	5	ABV53353	Abv53353 Human pro	217	16	10.1	1493	6	ABT07758	ABT07758 Breast ca
c 161	16	10.1	600	5	ABV50792	Abv50792 Human pro	218	16	10.1	1493	7	ACC72819	ACC72819 Human can
c 162	16	10.1	602	5	ABV58326	Abv58326 Human pro	219	16	10.1	1493	7	ACC51010	ACC51010 Human bla
c 163	16	10.1	620	2	AAZ24594	Aaz24594 Human lun	220	16	10.1	1493	7	ABX76375	ABX76375 Lung can
c 164	16	10.1	620	2	AAZ24646	Aaz24646 Human lun	221	16	10.1	1493	9	ADC78926	ADC78926 Human PRO
c 165	16	10.1	620	3	AAI65833	Aai65833 Human lun	c 222	16	10.1	1518	4	AAH16511	AAH16511 Human cDN
c 166	16	10.1	620	3	AAI65885	Aai65885 Human lun	223	16	10.1	1539	2	AAH75304	AAH75304 Nucleotid
c 167	16	10.1	620	6	ABJ49052	Abj49052 Human lun	224	16	10.1	1556	3	AAI66427	AAI66427 Human sec
c 168	16	10.1	620	6	ABJ49104	Abj49104 Human lun	225	16	10.1	1641	3	AAI681126	AAI681126 Human sec
c 169	16	10.1	620	6	ABQ92290	Abq92290 Human lun	226	16	10.1	1725	8	ADA26332	ADA26332 Human HSP
c 170	16	10.1	620	6	ABQ92238	Abq92238 Human lun	227	16	10.1	1741	3	AAI76623	AAI76623 Human ORF
c 171	16	10.1	620	8	ADA28653	Ada28653 Human lun	228	16	10.1	1747	3	AAH64872	AAH64872 Human sec
c 172	16	10.1	620	8	ADA28239	Ada28239 Human lun	c 229	16	10.1	1757	4	AAH78964	AAH78964 Human D-H
c 173	16	10.1	620	9	ADH53613	Adh53613 Human lun	c 230	16	10.1	1849	4	AAI59812	AAI59812 Human pol
c 174	16	10.1	620	9	ADH53444	Adh53444 Human lun	231	16	10.1	1881	4	AAI58026	AAI58026 Human pol
c 175	16	10.1	645	6	ABQ57035	Abq57035 Human col	232	16	10.1	1896	7	ACA43105	ACA43105 Prokaryot
c 176	16	10.1	646	6	ABX66909	Abx66909 Helicobac	233	16	10.1	2036	4	ABJ11823	ABJ11823 Drosophila
c 177	16	10.1	664	6	ABX66273	Abx66273 Helicobac	c 234	16	10.1	2115	4	AAH13699	AAH13699 Human cDN
c 178	16	10.1	684	3	AAI79836	Aai79836 Human sec	235	16	10.1	2196	6	ABJ99480	ABJ99480 Mouse 1sc

236	16	10.1	2226	3	AACT7875	Aac77875 Human can	293	16	10.1	6306	6	ABL49350	Ab149350 Human pol
237	16	10.1	2248	6	AA62481	Aa62481 cDNA sequ	c 294	16	10.1	6385	4	AA545353	Aa545353 Chemical
c 238	16	10.1	2254	5	AA344401	Aa344401 Human DNA	c 295	16	10.1	6385	6	ABK28186	ABK28186 DNA trans
239	16	10.1	2263	9	AD672974	Ad672974 Human end	c 296	16	10.1	6418	6	ABL32322	Ab132322 Human imm
240	16	10.1	2289	4	AA553785	Aa553785 Helicobac	c 297	16	10.1	6418	6	AA561073	Aa561073 Human gen
241	16	10.1	2289	7	ACA34700	Ac34700 Prokaryot	c 298	16	10.1	6636	6	AAB80022	Ab80022 Human gen
242	16	10.1	2395	4	AAH78432	AaH78432 Nucleotid	c 299	16	10.1	6664	6	AA561368	Aa561368 Human che
243	16	10.1	2396	3	AA663334	Aa663334 Human cel	c 300	16	10.1	6664	6	AD854321	Ad854321 Human gen
c 244	16	10.1	2492	4	ABL21854	Ab121854 Drosophi1	c 301	16	10.1	6664	9	AD854193	Ad854193 Pretreate
c 245	16	10.1	2532	4	ABL21826	Ab121826 Drosophi1	c 302	16	10.1	6736	2	AAV68471	AaV68471 A. pleuro
246	16	10.1	2656	5	AA567350	Aa567350 DNA encod	c 303	16	10.1	6736	2	AAV68471	AaV68471 A. pleuro
247	16	10.1	2678	7	ACC75521	Ac75521 Clostridi	c 304	16	10.1	6863	4	AA546518	AA546518 Human dig
248	16	10.1	2811	7	ABX34595	Abx34595 Human mcd	c 305	16	10.1	7297	4	AAK89535	AAK89535 Human dig
249	16	10.1	2859	7	ABK62811	Abk62811 Human act	c 306	16	10.1	7544	4	AA545301	AA545301 Chemical
c 250	16	10.1	2875	3	AA26857	Aa26857 Essential	c 307	16	10.1	8323	6	ABK28140	ABK28140 DNA trans
c 251	16	10.1	2875	3	AA91539	Aa91539 Stephyloc	c 308	16	10.1	8323	6	ABK28140	ABK28140 DNA trans
c 252	16	10.1	2875	4	AA508008	Aa508008 Stephyloc	c 309	16	10.1	8420	4	AAK89536	AAK89536 Human dig
c 253	16	10.1	2875	9	ADD67386	Ad67386 Antibacte	c 310	16	10.1	10417	7	AD851192	Ad851192 Human imm
c 254	16	10.1	2875	9	ADE73610	Ad673610 Mutant ba	c 311	16	10.1	10417	7	AD851192	Ad851192 BAC fragm
c 255	16	10.1	3154	4	AB118228	Ab118228 Drosophi1	c 312	16	10.1	10417	7	AD851192	Ad851192 Human sec
c 256	16	10.1	3202	4	AAH94410	AaH94410 S. epider	c 313	16	10.1	10717	6	ABK33695	ABK33695 Human imm
257	16	10.1	3288	7	ACC72030	Ac72030 BCU571 g	c 314	16	10.1	10717	6	AAZ80211	AaZ80211 Human che
258	16	10.1	3636	8	ADA32554	Ad32554 DNA encod	c 315	16	10.1	10754	2	AAZ82836	AaZ82836 Human ade
259	16	10.1	3652	4	AAH16223	AaH16223 Human cin	c 316	16	10.1	10754	5	AAK90294	AAK90294 Nucleotid
260	16	10.1	3660	2	AAV74483	AaV74483 Stephyloc	c 317	16	10.1	10754	5	AAK90294	AAK90294 Nucleotid
c 261	16	10.1	3706	3	AA293312	Aa293312 Sequence	c 318	16	10.1	11327	4	AA546432	AA546432 Tumour su
262	16	10.1	3736	6	AB235271	Ab235271 Human gen	c 319	16	10.1	11899	7	ACC69142	Ac69142 M. genital
263	16	10.1	3764	4	ABL23312	Ab123312 Drosophi1	c 320	16	10.1	12889	4	ABA07412	AbA07412 Human pan
264	16	10.1	3785	6	AA98640	Aa98640 Wheat car	c 321	16	10.1	12889	4	AAK91143	AAK91143 Human dig
265	16	10.1	3814	10	ADE77089	Ade77089 Human cin	c 322	16	10.1	13024	4	AAK91143	AAK91143 Human dig
c 266	16	10.1	4050	9	ADB53325	Ad53325 Primary r	c 323	16	10.1	13024	4	ABL97644	AbL97644 Human tes
267	16	10.1	4055	7	ACC69144	Ac69144 M. genital	c 324	16	10.1	13919	6	ABL97644	AbL97644 Human tes
268	16	10.1	4169	3	AAK09331	AaK09331 Human can	c 325	16	10.1	14143	4	ABA07413	AbA07413 Human pan
269	16	10.1	4169	9	ADC35131	AdC35131 Human bre	c 326	16	10.1	14143	4	AAK91144	AAK91144 Human dig
270	16	10.1	4344	6	ABN95256	Abn95256 Gene #175	c 327	16	10.1	15016	2	AAK99560	AaK99560 Nucleic a
271	16	10.1	4388	2	AAT75302	AA75302 Nucleotid	c 328	16	10.1	15018	7	ACA52817	AcA52817 Prokaryot
c 272	16	10.1	4544	5	ABA15386	Ab15386 Human ner	c 329	16	10.1	15069	4	ABL08378	AbL08378 Drosophi1
273	16	10.1	4563	7	ABK62910	Abk62910 Human act	c 330	16	10.1	15282	6	ABL70190	AbL70190 Human gen
274	16	10.1	4870	4	AAH57564	AaH57564 Human bra	c 331	16	10.1	15282	6	AA561140	AA561140 Human gen
275	16	10.1	4870	7	ABK63121	Abk63121 Human cin	c 332	16	10.1	15649	4	AA545397	AA545397 Chemical
276	16	10.1	5265	6	ABK28419	AbK28419 DNA trans	c 333	16	10.1	15649	6	ABK28242	ABK28242 DNA trans
c 277	16	10.1	5267	6	ABK67043	AbK67043 Human ang	c 334	16	10.1	15866	4	AAK90892	AAK90892 Human dig
c 278	16	10.1	5282	4	AA561407	Aa561407 Human gen	c 335	16	10.1	17249	4	AAK71137	AAK71137 Human imm
279	16	10.1	5581	4	AAK80802	AaK80802 Human imm	c 336	16	10.1	17848	6	AAK45323	AAK45323 Chemical
280	16	10.1	5581	4	AAK80803	AaK80803 Human imm	c 337	16	10.1	17848	6	AAK39976	AAK39976 Human che
281	16	10.1	5602	4	AAK80801	AaK80801 Human arc	c 338	16	10.1	17848	6	ABK28164	ABK28164 DNA trans
c 282	16	10.1	5717	9	ADD14637	Ad14637 Human arc	c 339	16	10.1	17959	6	ABL32575	AbL32575 Human imm
c 283	16	10.1	5718	5	AA564495	Aa564495 DNA encod	c 340	16	10.1	17959	6	ABL54342	AbL54342 Chemical
284	16	10.1	5728	6	ABL32100	Ab132100 Human imm	c 341	16	10.1	17970	4	AAK80740	AAK80740 Human imm
c 285	16	10.1	5788	6	ABK39942	Abk39942 Human che	c 342	16	10.1	19635	6	ABL33335	AbL33335 Human imm
c 286	16	10.1	5864	6	ABK33440	Abk33440 Human imm	c 343	16	10.1	19802	4	AAK90894	AAK90894 Human dig
c 287	16	10.1	5864	6	ABK34361	AbK34361 Chemical	c 344	16	10.1	19802	4	AAK04554	AAK04554 Human rep
c 288	16	10.1	5883	6	ABL33733	Ab133733 Human imm	c 345	16	10.1	19802	4	ABL97477	AbL97477 Human tes
c 289	16	10.1	5931	4	AA546702	Aa546702 Tumour su	c 346	16	10.1	19966	3	AAZ30355	AaZ30355 Nucleotid
c 290	16	10.1	6015	4	AA546684	Aa546684 Chemical	c 347	16	10.1	19966	3	AAZ42528	AaZ42528 DNA encod
c 291	16	10.1	6203	4	AA545475	Aa545475 Chemical	c 348	16	10.1	21358	4	AAK90363	AAK90363 Human dig
c 292	16	10.1	6203	6	ABK28399	AbK28399 DNA trans	c 349	16	10.1	21358	4	AAK73090	AAK73090 Human imm

350	16	10.1	21358	4	AAK87446	AAK87446	Human	Imm	407	16	10.1	143068	6	AB168124	AB168124	Ovary	can
c 351	16	10.1	21358	4	AAK87558	AAK87558	Human	Imm	408	16	10.1	143068	6	AB111034	AB111034	Human	bire
352	16	10.1	21358	4	AA106419	AA106419	Human	rep	409	16	10.1	143068	7	AB296966	AB296966	Human	nuc
353	16	10.1	21358	8	AA339919	AA339919	Genomic s		410	16	10.1	143068	7	AB296966	AB296966	Human	nuc
354	16	10.1	21358	8	AD832879	AD832879	Human	nov	c 411	16	10.1	144460	3	AA293815	AA293815	Olfactory	
c 355	16	10.1	21403	4	AAK90893	AAK90893	Human	dig	412	16	10.1	148412	3	AA335151	AA335151	Human	ade
c 356	16	10.1	21403	4	AA104555	AA104555	Human	rep	413	16	10.1	152740	3	AA212173	AA212173	Human	low
c 357	16	10.1	21403	4	AB197478	AB197478	Human	tes	414	16	10.1	152740	7	AA296967	AA296967	Human	nuc
c 358	16	10.1	21676	4	AAK90362	AAK90362	Human	dig	415	16	10.1	154465	6	AA28763	AA28763	Human	nuc
c 359	16	10.1	21676	4	AAK87549	AAK87549	Human	Imm	416	16	10.1	158245	6	AA28763	AA28763	Human	nuc
c 360	16	10.1	21676	4	AAK73081	AAK73081	Human	Imm	417	16	10.1	161425	4	AAH02340	AAH02340	Human	AKA
361	16	10.1	21676	4	AAK87445	AAK87445	Human	Imm	418	16	10.1	162025	4	AAH02339	AAH02339	Human	AKA
362	16	10.1	21676	4	AA106418	AA106418	Human	rep	419	16	10.1	162025	6	AA28763	AA28763	Human	AKA
363	16	10.1	21676	4	AA339918	AA339918	Genomic s		c 420	16	10.1	162025	6	AA28763	AA28763	Human	AKA
364	16	10.1	21676	8	AD832878	AD832878	Human	nov	c 421	16	10.1	162025	6	AA28763	AA28763	Human	AKA
365	16	10.1	23241	4	AAK87225	AAK87225	Human	Imm	422	16	10.1	169998	7	AA28763	AA28763	Human	AKA
366	16	10.1	23241	4	AAK84291	AAK84291	Human	Imm	423	16	10.1	183337	6	ABQ77402	ABQ77402	Human	EDN
c 367	16	10.1	23263	4	AAK90895	AAK90895	Human	dig	424	16	10.1	188888	6	ABQ77402	ABQ77402	Human	EDN
c 368	16	10.1	23763	4	AA104558	AA104558	Human	rep	c 425	16	10.1	197496	6	ABH85584	ABH85584	Human	EGF
c 369	16	10.1	23763	4	AB197481	AB197481	Human	tes	426	16	10.1	198161	6	ABH85584	ABH85584	Human	EGF
370	16	10.1	23592	4	AAK82159	AAK82159	Human	Imm	427	16	10.1	302250	6	AB167703	AB167703	Human	CDN
371	16	10.1	32185	4	AA136806	AA136806	Human	mus	c 428	16	10.1	322101	9	AA258431	AA258431	Human	PAO
372	16	10.1	32185	7	ABK59794	ABK59794	cDNA	emco	c 429	16	10.1	334462	9	AD24763	AD24763	Human	PAO
c 373	16	10.1	32885	4	AB119560	AB119560	Drosophila		c 430	16	10.1	335913	5	AA161371	AA161371	Human	wil
c 374	16	10.1	33053	6	ABQ67006	ABQ67006	Human	ang	c 431	16	10.1	349901	6	AD24763	AD24763	Human	PAO
c 375	16	10.1	50000	3	AA644140	AA644140	Nucleotid		c 432	16	10.1	349901	6	AD24763	AD24763	Human	PAO
c 376	16	10.1	56423	9	AD85728	AD85728	Human	GPC	c 433	16	10.1	349901	6	AD24763	AD24763	Human	PAO
377	16	10.1	57248	6	ABR83563	ABR83563	Human	CDN	c 434	16	10.1	349901	6	AD24763	AD24763	Human	PAO
378	16	10.1	65787	8	AD802603	AD802603	Mouse	112	c 435	15	9.4	116	6	ABR86236	ABR86236	Human	PAO
379	16	10.1	65787	9	AD872241	AD872241	Mouse	112	c 436	15	9.4	173	3	AA202917	AA202917	Human	sec
380	16	10.1	84539	8	AB164158	AB164158	Stomach	c	c 437	15	9.4	187	6	AB176872	AB176872	Human	ova
c 381	16	10.1	84539	8	ADN03068	ADN03068	Human	PPP	c 438	15	9.4	216	6	AB176872	AB176872	Human	ova
c 382	16	10.1	96395	9	AD872806	AD872806	Human	PPP	c 439	15	9.4	240	2	AA169263	AA169263	Human	me
c 383	16	10.1	96396	8	AD866352	AD866352	Human	Egr	c 440	15	9.4	240	2	AA169263	AA169263	Human	me
384	16	10.1	96399	9	AD865298	AD865298	Human	Egr	c 441	15	9.4	252	6	ABH66415	ABH66415	Streptococ	
385	16	10.1	96600	8	ADA02819	ADA02819	Mouse	Sos	c 442	15	9.4	270	4	AAK61270	AAK61270	Human	Imm
386	16	10.1	96600	8	AD872557	AD872557	Mouse	Sos	443	15	9.4	276	6	ABH03058	ABH03058	Human	bire
c 387	16	10.1	97662	4	AA183908	AA183908	Genomic s		444	15	9.4	279	7	AB122531	AB122531	Human	sec
c 388	16	10.1	100543	6	AB552816	AB552816	Genomic D		c 445	15	9.4	299	3	AA203407	AA203407	Human	sec
389	16	10.1	106746	3	AA110225	AA110225	Human	PCT	c 446	15	9.4	312	3	AA244770	AA244770	Human	sec
c 390	16	10.1	110000	2	AA158840	AA158840	Myocoplasm		c 447	15	9.4	317	7	AB552277	AB552277	Bovine	ES
391	16	10.1	110000	2	AA158840	AA158840	Myocoplasm		c 448	15	9.4	321	7	AA244770	AA244770	Human	sec
c 392	16	10.1	110000	2	AA158840	AA158840	Myocoplasm		c 449	15	9.4	321	7	AA244770	AA244770	Human	sec
c 393	16	10.1	110000	2	AA158840	AA158840	Myocoplasm		c 450	15	9.4	325	3	AA203407	AA203407	Human	sec
c 394	16	10.1	110000	6	AB21209_04	AB21209_04	Continuation (5 of		c 451	15	9.4	335	3	AA444083	AA444083	Human	sec
395	16	10.1	110000	6	AB21209_04	AB21209_04	Continuation (5 of		c 452	15	9.4	341	8	AA444083	AA444083	Human	sec
c 396	16	10.1	110000	6	AB21209_04	AB21209_04	Continuation (5 of		c 453	15	9.4	341	8	AA444083	AA444083	Human	sec
397	16	10.1	110000	7	ACF42745_0	ACF42745_0	Continuation (29 of		c 454	15	9.4	344	8	AA444083	AA444083	Human	sec
c 398	16	10.1	110000	7	AB083210_1	AB083210_1	Continuation (2 of		c 455	15	9.4	350	5	AA255076	AA255076	Human	bon
399	16	10.1	110000	7	AB083210_1	AB083210_1	Continuation (2 of		c 456	15	9.4	351	5	AA255076	AA255076	Human	bon
400	16	10.1	113306	9	AD866354	AD866354	Human	GPC	c 457	15	9.4	353	4	AAH93666	AAH93666	Human	pro
c 401	16	10.1	113315	6	AB134175	AB134175	Human	Imm	c 458	15	9.4	355	5	AAH93666	AAH93666	Human	pro
402	16	10.1	113624	2	AAV52850	AAV52850	Human	eye	c 459	15	9.4	356	7	AAH93666	AAH93666	Human	pro
403	16	10.1	143068	3	AA34983	AA34983	Human	eye	c 460	15	9.4	357	8	AAH93666	AAH93666	Human	pro
404	16	10.1	143068	3	AA34983	AA34983	Human	eye	c 461	15	9.4	360	5	AB115418	AB115418	Human	ner
405	16	10.1	143068	3	AA34983	AA34983	Human	eye	c 462	15	9.4	363	3	AA216990	AA216990	Human	sec
406	16	10.1	143068	3	AA212172	AA212172	Human	low	c 463	15	9.4	364	4	AA185003	AA185003	Human	pol

464	15	9.4	366	7	ACA22929	Ac22929	Prokaryot	521	15	9.4	459	4	AAK67407	AAK67407	Human imm
c 465	15	9.4	370	8	ACB31547	Ac31547	Human bon	522	15	9.4	463	4	AAK87996	AAK87996	Human dig
466	15	9.4	372	4	AAK74731	AAK74731	Human imm	523	15	9.4	464	4	AAK56121	AAK56121	Human imm
467	15	9.4	372	7	ABK55205	Abk55205	Bovine ES	c 524	15	9.4	464	8	ACH45481	ACH45481	Human foe
468	15	9.4	376	7	ABK54968	Abk54968	Bovine ES	525	15	9.4	467	2	AAT83836	AAT83836	Human imm
469	15	9.4	377	4	AA189286	AA189286	Human pol	526	15	9.4	467	4	AA535283	AA535283	DNA encod
470	15	9.4	381	7	ABK39567	Abk39567	Bovine ES	527	15	9.4	467	9	ABE45362	ABE45362	Human car
471	15	9.4	388	4	AA185553	AA185553	Human pol	528	15	9.4	468	6	AB191329	AB191329	Human car
472	15	9.4	394	5	ABV17897	Abv17897	Human pro	529	15	9.4	469	4	AA198762	AA198762	Human exc
c 473	15	9.4	398	4	AA187937	AA187937	Human pol	530	15	9.4	469	5	AA163158	AA163158	Human kid
c 474	15	9.4	398	8	ACH31014	ACH31014	Human bon	531	15	9.4	470	6	ABQ96387	ABQ96387	Human kid
475	15	9.4	399	6	ABN16543	Abn16543	Human ORF	532	15	9.4	470	8	ACH50808	ACH50808	Human kid
476	15	9.4	399	7	ABK40689	Abk40689	Bovine ORF	533	15	9.4	471	8	ACH37766	ACH37766	Human mam
c 477	15	9.4	401	4	AAK95891	AAK95891	Human ES	534	15	9.4	474	4	AA139334	AA139334	Human end
478	15	9.4	401	4	AAK93866	AAK93866	Human neu	c 535	15	9.4	474	6	ABQ90253	ABQ90253	Probe #80
479	15	9.4	401	4	AAK97359	AAK97359	Human neu	c 536	15	9.4	475	8	ACH48413	ACH48413	Human leu
c 480	15	9.4	401	4	AAK97384	AAK97384	Human neu	537	15	9.4	480	6	ABQ96391	ABQ96391	Human leu
c 481	15	9.4	401	6	ABT00661	Abt00661	Human neu	c 538	15	9.4	493	4	AA161679	AA161679	Human bre
482	15	9.4	401	6	ABT00636	Abt00636	Human neu	539	15	9.4	493	6	ABQ96390	ABQ96390	Human bre
c 483	15	9.4	401	6	ABT02154	Abt02154	Human neu	c 540	15	9.4	494	4	AAK57130	AAK57130	Human su
484	15	9.4	401	6	ABT02129	Abt02129	Human neu	c 541	15	9.4	500	3	AAK95176	AAK95176	Human imm
485	15	9.4	401	7	ABK55085	Abk55085	Bovine ES	c 542	15	9.4	502	6	ACH39323	ACH39323	Cat flea
c 486	15	9.4	403	4	AA190677	AA190677	Human pol	c 543	15	9.4	502	7	ACM11652	ACM11652	DNA encod
487	15	9.4	403	7	ABK37575	Abk37575	Bovine ES	c 544	15	9.4	502	7	ACM02838	ACM02838	Human lun
c 488	15	9.4	406	5	ABV51599	Abv51599	Human pro	c 545	15	9.4	502	7	ACM02838	ACM02838	Lung canc
489	15	9.4	408	4	AB115789	Ab115789	Drosophill	c 546	15	9.4	512	5	ABK20924	ABK20924	Human ner
c 490	15	9.4	409	4	AA111114	AA111114	Probe #10	c 547	15	9.4	512	5	ABK20925	ABK20925	Human ner
c 491	15	9.4	409	4	ABK52773	Abk52773	Human foe	c 548	15	9.4	512	5	ABA20927	ABA20927	Human ner
c 492	15	9.4	409	4	AA132379	AA132379	Probe #10	549	15	9.4	512	7	ABK25894	ABK25894	Human ner
c 493	15	9.4	409	4	ABK42347	Abk42347	Human bre	550	15	9.4	512	7	ABK25894	ABK25894	Asporegill
c 494	15	9.4	409	4	ABK22558	Abk22558	Probe #10	c 551	15	9.4	513	3	AAA45955	AAA45955	Human nov
c 495	15	9.4	409	4	AAK26684	AAK26684	Human bon	552	15	9.4	517	5	ABV47716	ABV47716	Human met
c 496	15	9.4	409	4	AAK01026	AAK01026	Human bra	553	15	9.4	521	9	ADE81244	ADE81244	Human pro
c 497	15	9.4	409	4	ABK26076	Abk26076	Human liv	554	15	9.4	530	5	ABV07485	ABV07485	Human pro
c 498	15	9.4	409	5	AA101032	AA101032	Probe #10	555	15	9.4	532	2	AAQ24835	AAQ24835	Human pro
c 499	15	9.4	409	6	ABK01074	Abk01074	Human gen	556	15	9.4	532	3	AAZ98840	AAZ98840	Peroxidase
500	15	9.4	414	5	ABV47687	Abv47687	Human pro	c 557	15	9.4	534	5	ABV12105	ABV12105	Horrearedi
c 501	15	9.4	416	5	ABV17926	Abv17926	Human pro	558	15	9.4	535	6	ABK60606	ABK60606	Human pro
c 502	15	9.4	417	4	AAK72248	AAK72248	Human imm	559	15	9.4	546	6	ABK87699	ABK87699	Human can
c 503	15	9.4	417	5	ABV45814	Abv45814	Human pro	560	15	9.4	550	9	ADD19049	ADD19049	Human can
c 504	15	9.4	418	4	AAK79731	AAK79731	Human imm	561	15	9.4	555	6	ABQ50104	ABQ50104	Human dis
c 505	15	9.4	419	6	ABQ98581	Abq98581	Human ORF	c 562	15	9.4	555	8	ABQ50105	ABQ50105	Oligonuc
c 506	15	9.4	420	8	ACH18985	ACH18985	Human adu	563	15	9.4	555	8	ACH41943	ACH41943	Human foe
c 507	15	9.4	421	3	AAK32214	AAK32214	Human sec	c 564	15	9.4	563	5	ABV57035	ABV57035	Human foe
508	15	9.4	421	7	ABK43038	Abk43038	Bovine ES	565	15	9.4	585	4	AAH12711	AAH12711	Human pro
509	15	9.4	428	7	ABK35359	Abk35359	Bovine ES	566	15	9.4	590	4	AAH13368	AAH13368	Human cin
510	15	9.4	429	7	ABK42396	Abk42396	Bovine ES	567	15	9.4	597	6	ABQ24336	ABQ24336	Human cin
c 511	15	9.4	432	4	AA183048	AA183048	Human pol	c 568	15	9.4	597	6	ABQ24337	ABQ24337	Oligonuc
c 512	15	9.4	438	5	ABV58602	Abv58602	Human pro	c 569	15	9.4	603	5	ABV19942	ABV19942	Human pro
513	15	9.4	438	8	ABQ96389	ABQ96389	Tumour su	c 570	15	9.4	612	6	ABK64177	ABK64177	Human can
514	15	9.4	440	8	ACH49504	ACH49504	Human leu	c 571	15	9.4	616	5	ABV55734	ABV55734	Human can
c 515	15	9.4	444	6	ABE12607	ABE12607	Arabidops	c 572	15	9.4	621	5	ABV49703	ABV49703	Human pro
c 516	15	9.4	446	5	AA571285	AA571285	DNA encod	573	15	9.4	633	5	AAH17671	AAH17671	Human pro
517	15	9.4	451	8	ACH17490	ACH17490	Human adu	574	15	9.4	633	7	ACH37372	ACH37372	Prokaryot
518	15	9.4	453	4	AA186781	AA186781	Human pol	575	15	9.4	638	4	AA124154	AA124154	Human bre
519	15	9.4	456	6	ABQ96388	ABQ96388	Tumour su	c 576	15	9.4	648	6	ABK92382	ABK92382	Stephyloc
520	15	9.4	457	9	ADK84923	ADK84923	Farnesyl	c 577	15	9.4	656	6	ABK65878	ABK65878	Human can

c 578	15	9.4	669	6	AB065847	Ab065847 Arabidops	635	15	9.4	942	6	AB069793	Ab069793 Listeria
c 579	15	9.4	674	7	ACF63950	Acf63950 Photornab	636	15	9.4	942	7	ACB36897	AcB36897 Prokaryot
c 580	15	9.4	676	7	ACF63950	Acf63950 Photornab	637	15	9.4	953	6	AB088911	AB088911 Human pro
c 581	15	9.4	686	7	ACF65977	Acf65977 Photornab	638	15	9.4	969	7	ACF71302	ACF71302 Photornab
c 582	15	9.4	691	7	ACF67187	Acf67187 Photornab	639	15	9.4	993	2	AAV24131	AAV24131 Homo sapi
c 583	15	9.4	693	3	ACA73555	AcA73555 Arabidops	640	15	9.4	1002	6	ABW70409	ABW70409 Streptoco
c 584	15	9.4	696	3	ACA52659	AcA52659 Arabidops	641	15	9.4	1002	6	ABW67791	ABW67791 Streptoco
c 585	15	9.4	704	4	AA122125	AA122125 Human bre	642	15	9.4	1004	4	AAW71074	AAW71074 Protilfara
c 586	15	9.4	720	4	AA555682	AA555682 Streptoco	643	15	9.4	1009	9	ADBE60651	ADBE60651 Human gen
c 587	15	9.4	720	7	ACA98366	AcA98366 Prokaryot	644	15	9.4	1035	2	AAV14487	AAV14487 H. pylori
c 588	15	9.4	727	4	AAK69198	AAK69198 Human dig	645	15	9.4	1068	7	ACB28004	ACB28004 Prokaryot
c 589	15	9.4	738	4	AB049427	Ab049427 Human sec	646	15	9.4	1092	5	ABV24326	ABV24326 Human pro
c 590	15	9.4	740	6	AB015471	Abq15470 Oligonuc	647	15	9.4	1116	8	ADA31719	ADA31719 DNA encod
c 591	15	9.4	741	5	AA580147	AA580147 DNA encod	648	15	9.4	1119	3	AA53578	AA53578 Arabidops
c 592	15	9.4	744	6	ABN67508	Abn67508 Streptoco	649	15	9.4	1119	7	ACA54060	ACA54060 Prokaryot
c 593	15	9.4	744	7	ACA37136	AcA37136 Prokaryot	650	15	9.4	1155	8	AA294444	AA294444 DNA encod
c 594	15	9.4	751	4	AA194977	AA194977 Human neu	651	15	9.4	1173	6	AA242107	AA242107 Human P1B
c 595	15	9.4	753	4	AAH90835	AAH90835 ZCFE 26 c	652	15	9.4	1217	4	ABL20053	ABL20053 Drosophil
c 596	15	9.4	761	4	AA125022	AA125022 Human bre	653	15	9.4	1230	7	ACB30168	ACB30168 Prokaryot
c 597	15	9.4	765	4	AA124460	AA124460 Human rep	654	15	9.4	1235	3	AA252509	AA252509 Human sec
c 598	15	9.4	766	4	AA105794	AA105794 Human tes	655	15	9.4	1254	6	AB216066	AB216066 Arabidops
c 599	15	9.4	766	4	AB198358	Ab198358 Human cin	656	15	9.4	1262	2	AAV13696	AAV13696 Enterococ
c 600	15	9.4	772	4	AAH07018	AAH07018 Human cin	657	15	9.4	1272	6	ABN92417	ABN92417 Enterococ
c 601	15	9.4	773	3	AAH08009	AAH08009 Human cin	658	15	9.4	1276	3	AA252509	AA252509 Staphyloc
c 602	15	9.4	775	3	AA17164	AA17164 Arabidops	659	15	9.4	1301	6	AAH63930	AAH63930 DNA encod
c 603	15	9.4	776	4	AA12045	AA12045 Prokaryot	660	15	9.4	1303	7	AAH48387	AAH48387 Human c-m
c 604	15	9.4	788	6	ABV95106	ABV95106 Human pan	661	15	9.4	1303	7	AB210096	AB210096 Haematopo
c 605	15	9.4	798	4	AAH33098	AAH33098 Human col	662	15	9.4	1303	7	AB210036	AB210036 Haematopo
c 606	15	9.4	800	2	AA930757	AA930757 Avian int	663	15	9.4	1303	6	AAH48387	AAH48387 Human c-m
c 607	15	9.4	801	6	ABK63731	ABK63731 Ret seque	664	15	9.4	1303	6	AAH48387	AAH48387 Human c-m
c 608	15	9.4	801	9	ADBS2803	ADBS2803 Primary r	665	15	9.4	1303	7	AB210036	AB210036 Haematopo
c 609	15	9.4	801	9	ADBS2803	ADBS2803 Primary r	666	15	9.4	1303	7	AB210036	AB210036 Haematopo
c 610	15	9.4	801	9	ADBS2803	ADBS2803 Primary r	667	15	9.4	1303	7	AB210036	AB210036 Haematopo
c 611	15	9.4	801	9	ADBS2803	ADBS2803 Primary r	668	15	9.4	1303	7	AB210036	AB210036 Haematopo
c 612	15	9.4	802	2	AA20466	AA20466 Human sec	669	15	9.4	1303	7	AB210242	AB210242 Haematopo
c 613	15	9.4	802	9	ADP90250	ADP90250 Novel hum	670	15	9.4	1307	4	AB107035	AB107035 Drosophil
c 614	15	9.4	804	4	AA126418	AA126418 Human bre	671	15	9.4	1308	7	AAH50274	AAH50274 Human nuc
c 615	15	9.4	807	6	ABN67122	ABN67122 Streptoco	672	15	9.4	1326	6	ABN99422	ABN99422 Human nuc
c 616	15	9.4	811	7	ACB46087	ACB46087 Human dlt	673	15	9.4	1332	8	ADA32711	ADA32711 DNA encod
c 617	15	9.4	824	6	ABQ36600	ABQ36600 Oligonuc	674	15	9.4	1399	1	AAH80507	AAH80507 Gene enc
c 618	15	9.4	824	6	ABQ36601	ABQ36601 Oligonuc	675	15	9.4	1411	4	AAH13981	AAH13981 Human cin
c 619	15	9.4	845	6	AA166947	AA166947 Chicken 1	676	15	9.4	1426	4	AAK74696	AAK74696 Human lim
c 620	15	9.4	845	6	ABN87700	ABN87700 Human pro	677	15	9.4	1432	6	AB134259	AB134259 Human lim
c 621	15	9.4	861	8	AA79732	AA79732 Human cin	678	15	9.4	1438	9	ADBE2888	ADBE2888 Human MDD
c 622	15	9.4	867	8	ADBS1855	ADBS1855 Human cin	679	15	9.4	1468	4	AAAC91700	AAAC91700 Mouse fat
c 623	15	9.4	876	6	ABQ54672	ABQ54672 Human ova	680	15	9.4	1480	6	AB189965	AB189965 Human fat
c 624	15	9.4	876	7	ACA30332	ACA30332 Prokaryot	681	15	9.4	1492	5	AAH94440	AAH94440 Human foe
c 625	15	9.4	881	2	AA556828	AA556828 Mouse pmd	682	15	9.4	1492	5	AAH94440	AAH94440 Human foe
c 626	15	9.4	891	7	ACA22829	ACA22829 Prokaryot	683	15	9.4	1496	2	AAV33362	AAV33362 Nucleotid
c 627	15	9.4	892	7	AAK79612	AAK79612 Human lim	684	15	9.4	1502	2	AAV33362	AAV33362 Nucleotid
c 628	15	9.4	894	4	AAK79612	AAK79612 Human lim	685	15	9.4	1502	2	AAV33362	AAV33362 Nucleotid
c 629	15	9.4	899	6	ABQ38187	ABQ38187 Oligonuc	686	15	9.4	1502	2	AAV33362	AAV33362 Nucleotid
c 630	15	9.4	899	6	ABQ38186	ABQ38186 Oligonuc	687	15	9.4	1502	2	AAV33362	AAV33362 Nucleotid
c 631	15	9.4	919	4	AAH06453	AAH06453 Human cin	688	15	9.4	1537	6	AB97663	AB97663 Human cin
c 632	15	9.4	935	4	AA106886	AA106886 Human rep	689	15	9.4	1537	6	AB97663	AB97663 Human cin
c 633	15	9.4	935	4	AB08107	AB08107 Human ova	690	15	9.4	1537	6	AB97663	AB97663 Human cin
c 634	15	9.4	942	6	AB068221	AB068221 Listeria	691	15	9.4	1537	6	AB97663	AB97663 Human cin

c 692	15	9.4	1557	3	AAZ97079	AAZ97079 Human sec	749	15	9.4	2403	6	AAZ42109	AAZ42109 Human PIB
c 693	15	9.4	1557	8	ACH6708	ACH6708 Novel hum	750	15	9.4	2408	4	ABL15788	ABL15788 Drosophill
c 694	15	9.4	1576	6	ABQ69006	ABQ69006 Listeria	c 751	15	9.4	2414	4	ABL27894	ABL27894 Drosophill
c 695	15	9.4	1583	6	ABQ14699	ABQ14699 Oligonuc	c 752	15	9.4	2460	7	ACR70439	ACR70439 Phocorhab
c 696	15	9.4	1583	6	ABQ14698	ABQ14698 Oligonuc	753	15	9.4	2468	7	ACD19418	ACD19418 CDNA enco
c 697	15	9.4	1596	6	AAD42108	AAZ42108 Human PIB	c 754	15	9.4	2468	7	ABZ56967	ABZ56967 CDNA enco
c 698	15	9.4	1603	3	AAZ98152	AAZ98152 Human col	c 755	15	9.4	2491	7	ACC44332	ACC44332 CDNA enco
c 699	15	9.4	1630	5	AAZ94470	AAZ94470 DNA enco	c 756	15	9.4	2506	4	AAH14282	AAH14282 Human cDN
c 700	15	9.4	1631	6	ABZ14925	ABZ14925 Arabidops	c 757	15	9.4	2506	7	ABZ23171	ABZ23171 Polynucle
c 701	15	9.4	1662	4	AAH02237	AAH02237 Tetrageno	c 758	15	9.4	2506	7	ABZ23172	ABZ23172 Polynucle
c 703	15	9.4	1663	4	AAH74693	AAH74693 Human imm	c 759	15	9.4	2511	2	AAV71032	AAV71032 Grk5-gree
c 704	15	9.4	1697	4	AAH18581	AAH18581 Human cDN	c 760	15	9.4	2519	9	ACN03892	ACN03892 CDNA upre
c 705	15	9.4	1729	4	AAH99095	AAH99095 Human EST	c 761	15	9.4	2519	9	ACB47372	ACB47372 Human cDN
c 706	15	9.4	1739	3	AAZ36472	AAZ36472 Arabidops	c 762	15	9.4	2529	2	AAV71024	AAV71024 Grk3-gree
c 707	15	9.4	1753	4	AAH191399	AAH191399 Human pol	763	15	9.4	2533	2	AAQ060100	AAQ060100 Sequence
c 708	15	9.4	1796	5	ABA21095	ABA21095 Human ner	764	15	9.4	2541	6	AAI47520	AAI47520 Human rib
c 709	15	9.4	1805	2	AAV52280	AAV52280 Streptoco	765	15	9.4	2552	9	AAZ53667	AAZ53667 Human pro
c 710	15	9.4	1815	6	ABR66231	ABR66231 cDNA enco	c 766	15	9.4	2557	4	AAH24841	AAH24841 Nucloetid
c 711	15	9.4	1817	5	AAZ63219	AAZ63219 Human pur	c 767	15	9.4	2557	6	AAZ36142	AAZ36142 Human G p
c 712	15	9.4	1818	5	ABV28274	ABV28274 Human pro	c 768	15	9.4	2557	6	ABZ49404	ABZ49404 CDNA enco
c 713	15	9.4	1818	5	ABV28500	ABV28500 Human pro	c 769	15	9.4	2557	7	ACA56700	ACA56700 Human sfg
c 714	15	9.4	1880	6	AAZ42110	AAZ42110 Human PIB	c 770	15	9.4	2558	4	ABL25882	ABL25882 Drosophill
c 715	15	9.4	1882	4	ABZ04875	ABZ04875 Drosophill	771	15	9.4	2571	4	AAK52271	AAK52271 Human pol
c 716	15	9.4	1884	4	AAH99130	AAH99130 Human EST	c 772	15	9.4	2577	7	ABZ23173	ABZ23173 Polynucle
c 717	15	9.4	1901	9	ADC27053	ADC27053 Human deu	c 773	15	9.4	2598	7	ACA27473	ACA27473 Prokaryot
c 718	15	9.4	1926	9	ADZ55611	ADZ55611 Human gen	c 774	15	9.4	2599	6	AAZ32333	AAZ32333 Human TRN
c 719	15	9.4	1926	9	ADZ53615	ADZ53615 Human gen	c 775	15	9.4	2605	4	AAH14939	AAH14939 Human cDN
c 720	15	9.4	1944	3	AAZ69015	AAZ69015 Bacterioph	c 776	15	9.4	2627	4	ABZ129318	ABZ129318 Drosophill
c 721	15	9.4	1977	6	ABN66202	ABN66202 Streptoco	c 777	15	9.4	2633	6	ABZ061024	ABZ061024 Human pol
c 722	15	9.4	1984	7	ABZ36115	ABZ36115 Human sec	c 778	15	9.4	2634	3	AAA66001	AAA66001 E. coli p
c 723	15	9.4	1995	7	ACA30619	ACA30619 Prokaryot	c 779	15	9.4	2645	4	ABL27910	ABL27910 Drosophill
c 724	15	9.4	1996	5	AAZ80696	AAZ80696 DNA enco	c 780	15	9.4	2715	6	AAZ42100	AAZ42100 Human pro
c 725	15	9.4	1998	7	AAZ78417	AAZ78417 Human sec	781	15	9.4	2716	2	AAZ12939	AAZ12939 Enterococ
c 726	15	9.4	1998	7	AAZ50608	AAZ50608 Human sec	782	15	9.4	2766	6	ABZ12979	ABZ12979 Arabidops
c 727	15	9.4	1998	8	ADZ71334	ADZ71334 Secreted	c 783	15	9.4	2766	7	AAZ68503	AAZ68503 Human NR6
c 728	15	9.4	1998	8	ADZ91260	ADZ91260 Human sec	c 784	15	9.4	2791	3	AAZ52952	AAZ52952 Human NR6
c 729	15	9.4	1998	9	ADC73677	ADC73677 Human sec	c 785	15	9.4	2831	4	AAZ53179	AAZ53179 Human pol
c 730	15	9.4	2000	6	ABZ17292	ABZ17292 Arabidops	c 786	15	9.4	2839	2	AAQ03742	AAQ03742 Human SKI
c 731	15	9.4	2000	6	ABZ16849	ABZ16849 Arabidops	787	15	9.4	2862	7	ACA45720	ACA45720 Prokaryot
c 732	15	9.4	2000	6	ABZ16044	ABZ16044 Arabidops	788	15	9.4	2864	9	ADB62335	ADB62335 Human cDN
c 733	15	9.4	2000	6	ABZ08383	ABZ08383 Human pro	c 789	15	9.4	2887	3	AAZ294533	AAZ294533 Human cyt
c 734	15	9.4	2000	7	ADA68828	ADA68828 Arabidops	c 790	15	9.4	2887	3	AAZ294533	AAZ294533 Human cyt
c 735	15	9.4	2000	7	ADA72089	ADA72089 Rice gene	c 791	15	9.4	2887	3	AAZ294533	AAZ294533 Human cyt
c 736	15	9.4	2001	5	AAZ88985	AAZ88985 Rice gene	c 792	15	9.4	2887	3	AAZ294533	AAZ294533 Human cyt
c 737	15	9.4	2034	6	ABZ61028	ABZ61028 Transmem	793	15	9.4	2916	8	ABZ44090	ABZ44090 Pasteurel
c 738	15	9.4	2055	5	AAZ82025	AAZ82025 DNA enco	794	15	9.4	2918	9	ADB61936	ADB61936 Human cDN
c 739	15	9.4	2102	4	AAZ81791	AAZ81791 Human sec	795	15	9.4	2937	2	AAZ58857	AAZ58857 Pasteurel
c 740	15	9.4	2112	3	AAZ27448	AAZ27448 P. multoc	796	15	9.4	2937	3	AAZ35589	AAZ35589 P. multoc
c 741	15	9.4	2220	4	AAZ93783	AAZ93783 Human sur	797	15	9.4	2937	9	ADC77478	ADC77478 Pasteurel
c 742	15	9.4	2225	4	AAZ13689	AAZ13689 Gene enco	798	15	9.4	2937	9	ADD93925	ADD93925 Pasteurel
c 743	15	9.4	2234	7	ABZ23174	ABZ23174 Polynucle	799	15	9.4	2979	3	AAA27449	AAA27449 P. multoc
c 744	15	9.4	2272	4	ABZ196184	ABZ196184 Polypept	800	15	9.4	2979	6	ABA05098	ABA05098 Pasteurel
c 745	15	9.4	2291	4	ABZ127734	ABZ127734 Drosophill	c 801	15	9.4	3024	4	ABL07566	ABL07566 Drosophill
c 746	15	9.4	2308	4	AAH18526	AAH18526 Human cDN	c 802	15	9.4	3054	4	AAH54843	AAH54843 S. epider
c 747	15	9.4	2309	4	AAH53255	AAH53255 Human pol	c 803	15	9.4	3080	4	AAZ13357	AAZ13357 Human sec
c 748	15	9.4	2310	2	AAZ25547	AAZ25547 Arabidops	c 805	15	9.4	3080	6	ABL90697	ABL90697 Human pol

806	15	9.4	3086	6	ABN59711	Novel hum	AbN59711	Novel hum	c	863	15	9.4	4308	9	ADCC4175	ADc44175	Human EST
c 807	15	9.4	3102	7	ACG30727	Prokaryot	AcG30727	Prokaryot	c	864	15	9.4	4308	9	ADCC1935	ADc61935	Human EST
c 808	15	9.4	3117	7	ACF71013	Phototrab	AcF71013	Phototrab	c	865	15	9.4	4308	9	ADCC3899	ADc63899	Human EST
c 809	15	9.4	3118	4	AAK51953	Human pol	AAK51953	Human pol	c	866	15	9.4	4308	9	ADCC6999	ADc66999	Human EST
c 810	15	9.4	3132	6	ABK47581	DNA encod	ABK47581	DNA encod	c	867	15	9.4	4308	9	ADCC69123	ADc69123	Human EST
c 811	15	9.4	3140	4	AAO13390	Human sec	AAo13390	Human sec	c	868	15	9.4	4308	9	ADCC31183	ADc63183	Human EST
c 812	15	9.4	3151	6	ABO67143	Human ang	ABo67143	Human ang	c	869	15	9.4	4308	9	ADCC8248	ADc68248	Human EST
c 813	15	9.4	3192	4	ABLO6428	Drosophill	ABlo6428	Drosophill	c	870	15	9.4	4308	9	ADCC1368	ADc61368	Human EST
c 814	15	9.4	3228	4	ABLO4162	Drosophill	ABlo4162	Drosophill	c	871	15	9.4	4308	9	ADCC7623	ADc67623	Human EST
c 815	15	9.4	3242	4	ABLO6414	Drosophill	ABlo6414	Drosophill	c	872	15	9.4	4308	9	ADCC2559	ADc62559	Human EST
c 816	15	9.4	3275	8	ACF25333	Rat cytos	AcF25333	Rat cytos	c	873	15	9.4	4308	9	ADCC42192	ADc42192	Human EST
c 817	15	9.4	3275	8	ADBS8295	Ades8295	Ades8295	Toxicity-	c	874	15	9.4	4308	9	ADBE9561	ADc49561	Human EST
c 818	15	9.4	3305	5	ABV25506	Human pro	ABv25506	Human pro	c	875	15	9.4	4308	9	ADBE5615	ADc45615	Human EST
c 819	15	9.4	3305	5	ABV25506	Human pro	ABv25506	Human pro	c	876	15	9.4	4308	9	ADBE6729	ADc46729	Human EST
c 820	15	9.4	3387	7	ABE236087	Human sec	ABe236087	Human sec	c	877	15	9.4	4308	9	ADDB73344	ADd77344	Human EST
c 821	15	9.4	3434	4	ABLI19863	Drosophill	ABl19863	Drosophill	c	878	15	9.4	4308	9	ADDB72702	ADd72702	Human EST
c 822	15	9.4	3473	4	ABLI17404	Drosophill	ABl17404	Drosophill	c	879	15	9.4	4308	9	ADDE17303	ADd17303	Human EST
c 823	15	9.4	3476	4	ABLI19970	Drosophill	ABl19970	Drosophill	c	880	15	9.4	4308	10	ADDE48861	ADd48861	Human EST
c 824	15	9.4	3509	9	ADDE54086	Human pro	ADe54086	Human pro	c	881	15	9.4	4308	10	ADDE89962	ADd89962	Human EST
c 825	15	9.4	3568	2	AAH17770	Human cDN	AAh17770	Human cDN	c	882	15	9.4	4381	6	ABO70089	ABq70089	listeria
c 826	15	9.4	3586	2	AAO56643	Human tyr	AAo56643	Human tyr	c	883	15	9.4	4384	4	AAI35762	AAI35762	Human mus
c 827	15	9.4	3676	4	ABE23598	Drosophill	ABe23598	Drosophill	c	884	15	9.4	4394	7	ABK58750	ABk58750	cDNA encd
c 828	15	9.4	3691	4	AAK74691	Human imm	AAk74691	Human imm	c	885	15	9.4	4400	7	ABK58751	ABk58751	cDNA encd
c 829	15	9.4	3696	7	ACA21669	Prokaryot	AcA21669	Prokaryot	c	886	15	9.4	4400	7	ABK58751	ABk58751	cDNA encd
c 830	15	9.4	3739	4	AAH14685	Human cDN	AAh14685	Human cDN	c	887	15	9.4	4449	2	AAAI9253	AAi19253	Corn dity
c 831	15	9.4	3746	4	ABK43586	DNA encod	ABk43586	DNA encod	c	888	15	9.4	4467	2	AAAI9253	AAi19253	Corn dity
c 832	15	9.4	3772	3	ABE23233	Drosophill	ABe23233	Drosophill	c	889	15	9.4	4467	2	AAAI9253	AAi19253	Corn dity
c 833	15	9.4	3818	3	ABE23233	Drosophill	ABe23233	Drosophill	c	890	15	9.4	4467	2	AAAI9253	AAi19253	Corn dity
c 834	15	9.4	3837	4	AAH15755	Human cDN	AAh15755	Human cDN	c	891	15	9.4	4733	5	AAH070470	AAh070470	DNA encod
c 835	15	9.4	3844	5	ABV23912	Human pro	ABv23912	Human pro	c	892	15	9.4	4958	4	ABLI19334	ABl19334	Drosophill
c 836	15	9.4	3844	5	ABV29793	Human pro	ABv29793	Human pro	c	893	15	9.4	5005	5	AAAS42428	AAa42428	DNA encod
c 837	15	9.4	3881	3	AAAG1269	Human sec	AAa61269	Human sec	c	894	15	9.4	5072	6	ABNS9669	ABn9669	Novel hum
c 838	15	9.4	3881	7	ADAS5931	Gene encd	AdA55931	Gene encd	c	895	15	9.4	5078	6	ADCC2307	ADc2307	Human nov
c 839	15	9.4	3881	7	ADAS9741	Human sec	AdA59741	Human sec	c	896	15	9.4	5079	4	AAK67674	AAk67674	Human imm
c 840	15	9.4	3897	7	AAK52195	Human pol	ABk1200	cDNA encd	c	897	15	9.4	5126	4	AAH57506	AAh57506	Human kid
c 841	15	9.4	3938	7	ABK11200	cDNA encd	ABk11200	cDNA encd	c	898	15	9.4	5133	6	ABLI33913	ABl33913	Human imm
c 842	15	9.4	3949	4	ABLI33968	Drosophill	ABl33968	Drosophill	c	899	15	9.4	5142	7	ACDD19398	ACd19398	cDNA encd
c 843	15	9.4	3952	6	AAO29901	Bacillus	AAa29901	Bacillus	c	900	15	9.4	5239	6	ADAD3316	ADa3316	Human DTC
c 844	15	9.4	4049	6	AAJ42955	Human cer	AAj42955	Human cer	c	901	15	9.4	5276	4	AAAS6380	AAa6380	Tumour x
c 845	15	9.4	4050	4	ABJ25878	Drosophill	ABj25878	Drosophill	c	902	15	9.4	5276	6	ABLI12827	ABl12827	Human imm
c 846	15	9.4	4130	3	ABJ77406	Human ORF	ABj77406	Human ORF	c	903	15	9.4	5333	3	AAAS7410	AAa7410	DNA seque
c 847	15	9.4	4134	3	ABAI9810	Human nec	ABa19810	Human nec	c	904	15	9.4	5360	6	ABLI3397	ABl3397	Human imm
c 848	15	9.4	4210	4	AA527090	cDNA encd	AAa27090	cDNA encd	c	905	15	9.4	5360	6	ABLI9366	ABl9366	Chemical
c 849	15	9.4	4210	4	ADBS93268	Human cDN	ADb93268	Human cDN	c	906	15	9.4	5360	6	ABLI9366	ABl9366	Human pol
c 850	15	9.4	4308	2	AA234327	Human EST	AAa34327	Human EST	c	907	15	9.4	5467	6	ABLI4108	ABl4108	Human imm
c 851	15	9.4	4308	3	AACT8593	Human EST	AAc78593	Human EST	c	908	15	9.4	5507	7	ABE21005	ABe21005	Human top
c 852	15	9.4	4308	7	ACD42860	Novel hum	ACd42860	Novel hum	c	909	15	9.4	5507	7	ABE21005	ABe21005	Human top
c 853	15	9.4	4308	7	ACA63895	Novel hum	Ac63895	Novel hum	c	910	15	9.4	5514	4	ABLO6604	ABLo6604	Drosophill
c 854	15	9.4	4308	7	ACA72059	Human PRO	Ac72059	Human PRO	c	911	15	9.4	5518	6	ABKR28305	ABkR28305	Drosophill
c 855	15	9.4	4308	7	ABK92699	Human PRO	ABk92699	Human PRO	c	912	15	9.4	5526	6	AAAS61697	AAa61697	lung smal
c 856	15	9.4	4308	8	ADCA6640	Human sec	ADc6640	Human sec	c	913	15	9.4	5583	4	ABLI5146	ABl5146	Drosophill
c 857	15	9.4	4308	8	ADCA25066	Novel hum	ADc25066	Novel hum	c	914	15	9.4	5641	4	AAK51946	AAk51946	Human pol
c 858	15	9.4	4308	8	ACD30041	Novel hum	ACd30041	Novel hum	c	915	15	9.4	5768	6	ABLI41463	ABl41463	Human imm
c 859	15	9.4	4308	8	ADAI12727	Human sec	ADa12727	Human sec	c	916	15	9.4	5815	6	ABKR40024	ABkR40024	Human cne
c 860	15	9.4	4308	8	ADCA29456	Human sec	ADc29456	Human sec	c	917	15	9.4	5828	6	AAK470247	AAk470247	Allergic
c 861	15	9.4	4308	9	ADB74033	Human PRO	ADb74033	Human PRO	c	918	15	9.4	5867	6	ABO67151	ABo67151	Human ang
c 862	15	9.4	4308	9	ADB76749	Human PRO	ADb76749	Human PRO	c	919	15	9.4	5869	9	ADBE2578	ADb62578	Human gen

	977	15	9.4	6929	6	A8134159	Abj134159 Human tum
C	978	15	9.4	7008	4	AAS46531	Aas46531 Tumour su
C	979	15	9.4	7040	4	AAS46440	Aas46440 Tumour su
C	980	15	9.4	7040	6	ABK33964	Abk33964 Human DNA
C	981	15	9.4	7040	7	ABZ10034	Abz10034 Haematopo
C	982	15	9.4	7040	7	ABZ10180	Abz10180 Haematopo
C	983	15	9.4	7040	7	ADJ20349	Adj20349 Prostate
C	984	15	9.4	7040	7	ADA94156	Ada94156 Human ren
C	985	15	9.4	7040	9	ADEB4116	AdeB4116 Human lym
C	986	15	9.4	7040	9	ADEB4192	AdeB4192 Human lym
C	987	15	9.4	7013	6	ABE235416	AbE235416 Human ger
C	988	15	9.4	7117	4	AAD03131	Aad03131 COLE3-CA3
C	989	15	9.4	7158	2	AAT727394	Aat727394 Hepatitis
C	990	15	9.4	7158	2	AAQ65197	Aaq65197 HEV strai
C	991	15	9.4	7168	2	AAV71604	Aav71604 Hepatitis
C	992	15	9.4	7167	6	ABNR8037	AbnR8037 Human che
C	993	15	9.4	7200	7	ACA35000	Aca35000 Prokaryote
C	994	15	9.4	7204	8	ADA50062	Ada50062 SK-HEV-3
C	995	15	9.4	7204	8	ADA50065	Ada50065 Hepatitis
C	996	15	9.4	7204	8	ADA50064	Ada50064 Hepatitis
C	997	15	9.4	7204	8	ADA50063	Ada50063 SK-HEV-2
C	998	15	9.4	7341	6	ABQ67109	Abq67109 Human ang
C	999	15	9.4	7380	4	AAS43360	Aas43360 Chemocali
C	1000	15	9.4	7380	6	ABK28195	Abk28195 DNA trans

ALIGNMENTS

```

RESULT 1
AAA68252
ID AAA68252 standard; DNA; 159 BP.
XX
AC AAA68252;
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 77 77ORF104 nucleotide sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
OS Staphylococcus aureus; bacteriophage 77.
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WO-IB002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 98US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
```

PR 02-DEC-1999; 99US-00454252.
XX (PHAG-) PHAGETECH INC.
XX
XX
PI Polletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR P-PSDB; AAB16527.
XX
XX
PI Identifying a bacteriophage coding region for treating bacterial
PI infections comprises identifying a nucleic acid encoding a product that
PI inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX
PS Disclosure; Page 162; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB6243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
CC
XX (Updated on 15-SEP-2003 to standardise 05 field)
XX
SQ Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 5e-74;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTAACCAAGATTTTAAACTAACTGAGTTCAGATATGAGCTCAGAA 60
DB 1 ATGGTAACCAAGATTTTAAACTAACTGAGTTCAGATATGAGCTCAGAA 60
QY 61 CTCATGATGAGGCAAGGCGATGAAATAGGTTGTACGACCTATTATCCAAAACT 120
DB 61 CTCATGATGAGGCAAGGCGATGAAATAGGTTGTACGACCTATTATCCAAAACT 120
QY 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159
DB 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159

RESULT 2
ID AAC86107 standard; cDNA; 159 BP.
XX
XX AAC86107;
XX
XX 06-AUG-2003 (revised)
XX 29-AUG-2001 (first entry)
XX
XX Bacteriophage 77 ORF 104.

KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW screening assay; ss.
XX
XX Bacteriophage.
XX
XX WO200146383-A2.
XX
XX 28-JUN-2001.
XX
XX
XX 21-DEC-2000; 2000WO-US035180.
XX
XX 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-0068952.
XX
XX (PHAG-) PHAGETECH INC.
XX (WILLIAMS K M.
XX
XX Polletier J, Gros P, Dubow M;
XX WPI; 2001-418052/44.
DR P-PSDB; AAB47318.
XX
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PI preferably bacterial, diseases such as those caused by Staphylococcus
PI aureus.
XX
XX
XX Example 1; Fig 4; 107pp; English.
XX
XX This sequence represents open reading frame (ORF) 104 of Bacteriophage
CC 77. The growth inhibitory gene product of ORF 104 interacts with DnaI
CC derived from S. aureus, to form the basis of a screening assay. DnaI
CC polypeptides and polynucleotides are useful for treating microbial,
CC preferably bacterial, especially staphylococcal, infections. DnaI
CC polypeptides and polynucleotides are useful for biological, diagnostic,
CC prophylactic, clinical and therapeutic use, and as components in
CC databases useful for search analyses as well as in sequence analysis
XX algorithms. (Updated on 06-AUG-2003 to correct 05 field.)
XX
SQ Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 5e-74;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTAACCAAGATTTTAAACTAACTGAGTTCAGATATGAGCTCAGAA 60
DB 1 ATGGTAACCAAGATTTTAAACTAACTGAGTTCAGATATGAGCTCAGAA 60
QY 61 CTCATGATGAGGCAAGGCGATGAAATAGGTTGTACGACCTATTATCCAAAACT 120
DB 61 CTCATGATGAGGCAAGGCGATGAAATAGGTTGTACGACCTATTATCCAAAACT 120
QY 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159
DB 121 GCAGAACGTCATACAGCCGCCCTATGTCGAATATTA 159

RESULT 3
 AAB68247
 ID AAB68247 standard; DNA; 41708 BP.
 XX
 AC AAB68247;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 complete genome sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 OS
 XX Staphylococcus aureus; bacteriophage 77.
 XX
 PN W0200032825-A2.
 PD 08-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-1B002040.
 XX
 PR 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1998; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 PI Pelletier J, Gros P, Dubow M;
 DR WPI; 2000-412361/35.
 XX
 PT Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 XX
 PS Example 3; Page 141-151; 456pp; English.
 XX
 CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an
 CC uncharacterized bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAB68243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 other;
 Query Match 100.0%; Score 159; DB 3; Length 41708;

Best Local Similarity 100.0%; Pred. No. 5.7e-74;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ATGTTACCAAGATTCTTTAAAACTAACTGAGTTCAGATATGTAGCTCAGAA 60
 DB 34393 ATGTTACCAAGATTCTTTAAAACTAACTGAGTTCAGATATGTAGCTCAGAA 34452
 OY 61 CTGATGATGAGGACAGGGGCAATGAAATAGGTTGTAGACCTATTATCCAAACTT 120
 DB 34453 CTGATGATGAGGACAGGGGCAATGAAATAGGTTGTAGACCTATTATCCAAACTT 34512
 OY 121 GCAGAACTGATACAGCCCGCTATGCTCAATATTAA 159
 DB 34513 GCAGAACTGATACAGCCCGCTATGCTCAATATTAA 34551
 RESULT 4
 AAC86106
 ID AAC86106 standard; cDNA; 41708 BP.
 XX
 AC AAC86106;
 XX
 DT 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Complete genome of bacteriophage 77.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 XX
 OS Bacteriophage.
 XX
 EN W0200146383-A2.
 PD 28-JUN-2001.
 XX
 PF 21-DEC-2000; 2000MO-US035180.
 PR 22-DEC-1999; 99US-00470512.
 PR 12-OCT-2000; 2000US-00689952.
 XX
 PA (PHAG-) PHAGETECH INC.
 PA (WILL/) WILLIAMS K M.
 XX
 PI Pelletier J, Gros P, Dubow M;
 DR WPI; 2001-418052/44.
 XX
 PT Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by Staphylococcus
 PT aureus.
 XX
 PS Disclosure; Fig 2; 107pp; English.
 XX
 CC This sequence represents the genome of Bacteriophage 77. The growth
 CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
 CC aureus, to form the basis of a screening assay. DnaI polypeptides and

CC polynucleotides are useful for treating microbial, preferably bacterial, CC especially staphylococcal, infections. DnaI polypeptides and CC polynucleotides are useful for biological, diagnostic, prophylactic, CC clinical and therapeutic use, and as components in databases useful for CC search analyses as well as in sequence analysis algorithms. (Updated on CC 06-NUC-2003 to correct OS field.)

XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 4; Length 41708;
Best Local Similarity 100.0%; Pred. No. 5.7e-74;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTACCAAGATTTTAAACTTAACCTGATGCTGATATGTACGCTCAGAA 60
| | | | |
DB 34393 ATGGTACCAAGATTTTAAACTTAACCTGATGCTGATATGTACGCTCAGAA 34452
| | | | |
QY 61 CTCATGATGAGGACAGGCGATGAAATAGGTTGTACGACCTATTATCCAAAACTT 120
| | | | |
DB 34453 CTCATGATGAGGACAGGCGATGAAATAGGTTGTACGACCTATTATCCAAAACTT 34512
| | | | |
QY 121 GCAGAACTGATACACCCGCCCTATGCTGAAATATTA 159
| | | | |
DB 34513 GCAGAACTGATACACCCGCCCTATGCTGAAATATTA 34551
| | | | |

RESULT 5
AAT83989
ID AAT83989 standard; DNA; 1134 BP.
XX
AC AAT83989;
XX
DT 27-NUC-1998 (first entry)
XX
DE DNA encoding a Staphylococcus aureus protein of unknown function.
XX
KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
KW Staphylococcal gene; regulatory element; bacterial gene expression;
KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
KW toxic shock syndrome; ss.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT CDS 593..946
FT /'tag= a
XX
XX MO9730070-A1.
XX
XX 21-NUC-1997.
XX
XX 19-FEB-1997; 97MO-US002318.
XX
XX 20-FEB-1996; 96US-0011888P.
XX
XX (SMITK) SMITHKLINE BEECHAM CORP.
XX

P1 Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
P1 Pratt JM, Reichard RW, Rosenberg M, Ward JM;
XX
XX WPI; 1997-424969/39.
DR P-PSDB; AAW28036.
XX
XX Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to
PT isolate antimicrobial compounds, and in vaccines against S. aureus
PT infection.
XX
XX Claim 9; Page 797; 989pp; English.
XX
XX The present sequence encodes a Staphylococcus aureus protein of unknown
CC function. The present sequence was isolated from a library of clones of
CC S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in
CC the construction of ribozymes and antisense sequences to control the
CC expression of Staphylococcal genes. The DNA sequence is also useful as a
CC source of regulatory elements for the control of bacterial gene
CC expression. The encoded protein may be used to produce vaccines to enable
CC a host to produce specific antibodies with antibacterial action. These
CC vaccines and antibodies would protect a host against invasion by S.
CC aureus, and conditions relating to Staphylococcal infection, e.g.
CC Staphylococcal food poisoning, scaled skin syndrome, and toxic shock
CC syndrome
XX
SQ Sequence 1134 BP; 407 A; 179 C; 247 G; 290 T; 0 U; 11 Other;

Query Match 28.3%; Score 45; DB 2; Length 1134;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTACCAAGATTTTAAACTTAACCTGATGCTGAT 45
| | | | |
DB 5 ATGGTACCAAGATTTTAAACTTAACCTGATGCTGAT 49
| | | | |

Search completed: October 15, 2004, 00:17:33
Job time : 134.071 secs

OK nucleole - nucleole search, using SW model

Run on: October 14, 2004, 22:42:59 / Search time 743.134 Seconds

(without alignments)
6389.277 Million cell updates/sec

SUMMARIES

28: gb_gsa1: +
29: gb_gsa2: +
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Title:	US-09-407-804A-8
Perfect score:	159
Sequence:	1 atggttaaccaagaattttt.....ccgctatcgctgaattactaa 159
Scoring table:	OLIGO_NUC Gapop 60.0 / Gapext 60.0
Searched:	27513289 seqs, 14931090276 residues
Word size :	0
Total number of hits satisfying chosen parameters:	53026578
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing: Listing first 1000 summaries	
Database :	EST:*
1:	em_gstba:*
2:	em_gsthum:*
3:	em_gstlin:*
4:	em_gstmu:*
5:	em_gstov:*
6:	em_gstpl:*
7:	em_gstiro:*
8:	em_hnc:*
9:	gb_gstcl:*
10:	gb_gstc2:*
11:	gb_hnc:*
12:	gb_gstc3:*
13:	gb_gstc4:*
14:	gb_gstc5:*
15:	em_gstfun:*
16:	em_gstom:*
17:	em_gst_hum:*
18:	em_gst_inv:*
19:	em_gst_pln:*
20:	em_gst_vrt:*
21:	em_gst_fun:*
22:	em_gst_man:*
23:	em_gst_mus:*
24:	em_gst_pro:*
25:	em_gst_rnd:*
26:	em_gst_phg:*
27:	em_gst_vrt:*

1	21	13.2	270	29	CE255312	CE255312 t1gr-gs-
2	21	13.2	357	29	CE691097	CE691097 t1gr-gs-
3	21	13.2	697	29	CE423104	CE423104 t1gr-gs-
4	20	12.6	342	9	AV858453	AV858453 AV858453
5	20	12.6	456	28	AZ232968	AZ232968 RPCT-23-s-
6	20	12.6	546	12	B1610223	B1610223 RH15267.5
7	20	12.6	719	29	CC622177	CC622177 OGMA108TV
8	20	12.6	724	12	BG705867	BG705867 6026693557
9	20	12.6	781	29	CC622172	CC622172 OGMA108TV
10	20	12.6	1179	28	CC264106	CC264106 CH261-577R
11	19	11.9	287	10	AW905496	AW905496 RC4-NM108
12	19	11.9	475	29	CE660226	CE660226 t1gr-gs-
13	19	11.9	561	28	AZ424688	AZ424688 IM020418
14	19	11.9	569	28	AQ420952	AQ420952 RPCT-11-2
15	19	11.9	579	14	CB935098	CB935098 ru02a11.1
16	19	11.9	595	28	AQ368393	AQ368393 HS 5039 J
17	19	11.9	596	9	AL041452	AL041452 DMFE2434E
18	19	11.9	639	12	B1106130	B1106130 60289201
19	19	11.9	685	29	CE297788	CE297788 t1gr-gs-
20	19	11.9	695	29	CE429047	CE429047 t1gr-gs-
21	19	11.9	701	29	AG088522	AG088522 Pan tregd
22	19	11.9	734	28	AZ200805	AZ200805 SP 1011 J
23	19	11.9	854	28	AZ190550	AZ190550 SP 1017 E
24	19	11.9	885	28	CC117791	CC117791 NDLE 517.7
25	19	11.9	1016	29	CNS067W	AL421590 T3 end of
26	18	11.3	165	10	BE841808	BE841808 MK1-SN006
27	18	11.3	168	28	CC170087	CC170087 1194008.6
28	18	11.3	172	28	CC170085	CC170085 1194008.6
29	18	11.3	181	29	CNS07FCZ	AL608561 Anophala
30	18	11.3	199	14	CA812153	CA812153 CNA11N022
31	18	11.3	250	9	AA251660	AA251660 zsa11f05.3
32	18	11.3	260	29	CG668289	CG668289 OST464103
33	18	11.3	263	10	AW832582	AW832582 PM4-CT029
34	18	11.3	285	28	AZ912465	AZ912465 RPCT-24-1
35	18	11.3	316	10	BB395991	BB395991 BB395991
36	18	11.3	317	14	CD567746	CD567746 RK043A1G6
37	18	11.3	320	10	BB255119	BB255119 BB255119
38	18	11.3	341	13	BU360800	BU360800 6037861554
39	18	11.3	362	28	BH373111	BH373111 AG-ND-13762
40	18	11.3	367	14	CB088393	CB088393 1699f12.1
41	18	11.3	369	14	R99699	R99699 vtg2a06.r1
42	18	11.3	370	28	AQ513966	AQ513966 HS 5179.1
43	18	11.3	383	10	BF012226	BF012226 us39g03.1
44	18	11.3	390	10	BF012250	BF012250 us40a06.1
45	18	11.3	391	28	AZ342125	AZ342125 1M0075H01

46	18	11.3	392	12	BJ167771	BJ167771	103	18	11.3	699	29	AG215096	AG215096
47	18	11.3	396	12	BQ865591	BQ865591	104	18	11.3	701	28	BH322345	BH322345
48	18	11.3	407	28	A2512143	A2512143	105	18	11.3	701	28	BH971448	BH971448
49	18	11.3	408	28	AQ104107	AQ104107	106	18	11.3	704	28	BH397547	BH397547
50	18	11.3	438	28	AQ602863	AQ602863	107	18	11.3	710	28	BH992062	BH992062
51	18	11.3	443	28	CC170086	CC170086	108	18	11.3	714	12	BG695502	BG695502
52	18	11.3	451	10	BH679871	BH679871	109	18	11.3	715	14	CB266873	CB266873
53	18	11.3	465	28	AQ441657	AQ441657	110	18	11.3	720	18	BQ771270	BQ771270
54	18	11.3	481	12	BI741223	BI741223	111	18	11.3	723	28	A2854721	A2854721
55	18	11.3	481	12	CA682350	CA682350	112	18	11.3	728	12	B3585672	B3585672
56	18	11.3	485	29	CE726036	CE726036	113	18	11.3	733	29	BX244581	BX244581
57	18	11.3	497	14	CP565756	CP565756	114	18	11.3	741	12	B3605840	B3605840
58	18	11.3	500	12	BP109214	BP109214	115	18	11.3	744	29	CNS017M0	CNS017M0
59	18	11.3	500	12	BP186540	BP186540	116	18	11.3	746	14	CF408079	CF408079
60	18	11.3	504	14	CP538790	CP538790	117	18	11.3	761	14	CF747486	CF747486
61	18	11.3	516	14	CP548998	CP548998	118	18	11.3	763	14	CD299599	CD299599
62	18	11.3	523	14	CP547227	CP547227	119	18	11.3	766	29	CE021679	CE021679
63	18	11.3	529	28	A2765927	A2765927	120	18	11.3	771	13	BU455066	BU455066
64	18	11.3	534	9	AV960850	AV960850	121	18	11.3	776	28	BH545670	BH545670
65	18	11.3	553	13	BQ394219	BQ394219	122	18	11.3	786	14	CF747503	CF747503
66	18	11.3	554	28	BH378082	BH378082	123	18	11.3	790	29	CC527885	CC527885
67	18	11.3	555	14	CP561729	CP561729	124	18	11.3	808	13	BU454610	BU454610
68	18	11.3	560	29	CE653603	CE653603	125	18	11.3	823	14	CF662123	CF662123
69	18	11.3	571	9	AV701220	AV701220	126	18	11.3	826	28	BH262136	BH262136
70	18	11.3	578	14	CA396589	CA396589	127	18	11.3	826	28	BH355686	BH355686
71	18	11.3	578	28	BH059617	BH059617	128	18	11.3	830	28	AQ750378	AQ750378
72	18	11.3	588	28	AQ624968	AQ624968	129	18	11.3	835	14	CD644235	CD644235
73	18	11.3	592	14	CP546392	CP546392	130	18	11.3	840	28	AQ892977	AQ892977
74	18	11.3	592	28	BH317476	BH317476	131	18	11.3	853	28	B2841480	B2841480
75	18	11.3	594	9	AL595905	AL595905	132	18	11.3	860	29	CG117558	CG117558
76	18	11.3	597	28	BH264109	BH264109	133	18	11.3	862	13	BU322661	BU322661
77	18	11.3	602	13	BQ396416	BQ396416	134	18	11.3	875	14	CF239298	CF239298
78	18	11.3	604	9	AL595165	AL595165	135	18	11.3	876	11	CNS09126	CNS09126
79	18	11.3	607	9	AL850869	AL850869	136	18	11.3	889	28	B2252751	B2252751
80	18	11.3	610	29	CC767439	CC767439	137	18	11.3	892	12	BI648511	BI648511
81	18	11.3	614	12	BM940643	BM940643	138	18	11.3	908	28	CC653529	CC653529
82	18	11.3	615	13	BQ526286	BQ526286	139	18	11.3	913	13	EX743864	EX743864
83	18	11.3	618	9	AV845559	AV845559	140	18	11.3	927	14	CA472543	CA472543
84	18	11.3	624	9	AL871043	AL871043	141	18	11.3	956	12	BG423519	BG423519
85	18	11.3	625	9	AL683050	AL683050	142	18	11.3	960	14	CF782339	CF782339
86	18	11.3	634	29	CC736161	CC736161	143	18	11.3	972	14	CF591419	CF591419
87	18	11.3	642	9	AL899906	AL899906	144	18	11.3	988	29	CNS066HF	CNS066HF
88	18	11.3	646	9	AL876497	AL876497	145	18	11.3	1027	28	CC203152	CC203152
89	18	11.3	647	9	AL877431	AL877431	146	18	11.3	1047	29	CNS0530N	CNS0530N
90	18	11.3	650	14	CP599680	CP599680	147	18	11.3	1055	29	CNS055B7	CNS055B7
91	18	11.3	652	12	BQ907416	BQ907416	148	18	11.3	1118	28	B09876	B09876
92	18	11.3	663	10	BH452472	BH452472	149	18	11.3	1124	14	CF994259	CF994259
93	18	11.3	663	28	BH208660	BH208660	150	18	11.3	1163	28	CC186610	CC186610
94	18	11.3	667	28	A2436122	A2436122	151	18	11.3	1201	9	AL534838	AL534838
95	18	11.3	669	28	BH265963	BH265963	152	18	11.3	3095	11	AK083595	AK083595
96	18	11.3	671	9	AL645123	AL645123	153	18	11.3	4349	11	AK028357	AK028357
97	18	11.3	672	29	AG149254	AG149254	154	18	11.3	132	28	A2561648	A2561648
98	18	11.3	683	28	BH268672	BH268672	155	17	10.7	150	13	BU578780	BU578780
99	18	11.3	683	29	AG059187	AG059187	156	17	10.7	150	28	A2774120	A2774120
100	18	11.3	687	28	AQ959888	AQ959888	157	17	10.7	151	9	AF150423	AF150423
101	18	11.3	689	11	CNS09127	CNS09127	158	17	10.7	166	9	AV266112	AV266112
102	18	11.3	689	28	AQ029536	AQ029536	159	17	10.7	170	29	AG026096	AG026096

c 160	17	10.7	207	10	BB200265	c 217	17	10.7	404	13	BY523913
c 161	17	10.7	218	10	BB013168	c 218	17	10.7	406	10	BG044050
c 162	17	10.7	219	9	AU071473	c 219	17	10.7	406	13	BY533393
c 163	17	10.7	224	10	BB031237	c 220	17	10.7	409	29	CE712808
c 164	17	10.7	236	9	AV236694	c 221	17	10.7	410	9	AV976542
c 165	17	10.7	236	10	BF333693	c 222	17	10.7	410	13	BY521034
c 166	17	10.7	236	28	AA539449	c 223	17	10.7	414	12	BI815478
c 167	17	10.7	240	28	BB772326	c 224	17	10.7	417	12	BJ342006
c 168	17	10.7	245	9	AV276093	c 225	17	10.7	417	28	AQ262207
c 169	17	10.7	246	9	AV736438	c 226	17	10.7	418	9	AA067007
c 170	17	10.7	260	10	AW227520	c 227	17	10.7	421	29	CE300363
c 171	17	10.7	263	28	AQ524888	c 228	17	10.7	423	28	AZ299013
c 172	17	10.7	268	9	AL598037	c 229	17	10.7	423	28	AQ203215
c 173	17	10.7	269	9	AV277144	c 230	17	10.7	424	28	AQ596662
c 174	17	10.7	272	10	BB412255	c 231	17	10.7	427	12	BI245048
c 175	17	10.7	272	10	BB577721	c 232	17	10.7	431	10	BE580829
c 176	17	10.7	275	10	BB128300	c 233	17	10.7	434	10	BF986122
c 177	17	10.7	276	10	BB456442	c 234	17	10.7	435	28	AA556737
c 178	17	10.7	277	10	BB434280	c 235	17	10.7	438	12	BI18987
c 179	17	10.7	282	9	AL639159	c 236	17	10.7	439	12	BJ341202
c 180	17	10.7	283	28	AQ999053	c 237	17	10.7	440	13	BY531602
c 181	17	10.7	299	10	BB117660	c 238	17	10.7	441	9	AA183097
c 182	17	10.7	300	10	BB117597	c 239	17	10.7	441	9	AL931574
c 183	17	10.7	312	28	AZ589032	c 240	17	10.7	442	28	AA0813262
c 184	17	10.7	318	13	BB139793	c 241	17	10.7	442	28	AZ818166
c 185	17	10.7	321	10	BB313457	c 242	17	10.7	443	28	AQ338029
c 186	17	10.7	321	12	BB790406	c 243	17	10.7	444	28	AQ275872
c 187	17	10.7	326	10	BB208767	c 244	17	10.7	449	9	AL145286
c 188	17	10.7	326	12	BG988238	c 245	17	10.7	451	10	BG078256
c 189	17	10.7	331	12	BJ398636	c 246	17	10.7	451	10	CE703758
c 190	17	10.7	344	10	BB131569	c 247	17	10.7	454	29	CE533929
c 191	17	10.7	344	13	BY602850	c 248	17	10.7	455	10	BE223544
c 192	17	10.7	346	9	AV732005	c 249	17	10.7	459	12	BI244916
c 193	17	10.7	349	9	AW022843	c 250	17	10.7	460	9	AL550436
c 194	17	10.7	349	12	BJ343683	c 251	17	10.7	467	28	AZ061189
c 195	17	10.7	352	9	AW103146	c 252	17	10.7	470	12	BJ388733
c 196	17	10.7	355	12	BJ438375	c 253	17	10.7	471	28	AZ389317
c 197	17	10.7	360	28	AQ000938	c 254	17	10.7	473	14	CA576019
c 198	17	10.7	363	9	AA083940	c 255	17	10.7	475	9	AL619574
c 199	17	10.7	369	12	BJ430127	c 256	17	10.7	476	12	BI324501
c 200	17	10.7	371	9	AA303096	c 257	17	10.7	477	9	AL552896
c 201	17	10.7	372	14	RJ1632	c 258	17	10.7	479	28	AQ959902
c 202	17	10.7	374	9	AV678271	c 259	17	10.7	480	9	AL597343
c 203	17	10.7	375	14	CB691517	c 260	17	10.7	482	28	AZ887273
c 204	17	10.7	378	12	BI245004	c 261	17	10.7	483	13	BY533608
c 205	17	10.7	378	13	BI343189	c 262	17	10.7	487	12	BM539027
c 206	17	10.7	378	29	CS597432	c 263	17	10.7	488	9	AV645834
c 207	17	10.7	381	28	BB517033	c 264	17	10.7	490	9	AA217066
c 208	17	10.7	383	12	BJ431652	c 265	17	10.7	491	12	BI314919
c 209	17	10.7	387	9	AL955613	c 266	17	10.7	491	28	CC092816
c 210	17	10.7	389	10	BB551454	c 267	17	10.7	492	10	BF548989
c 211	17	10.7	390	28	AQ326526	c 268	17	10.7	492	28	AZ813586
c 212	17	10.7	393	14	CB741819	c 269	17	10.7	493	28	AQ165956
c 213	17	10.7	396	10	BB644309	c 270	17	10.7	495	10	AAW90042
c 214	17	10.7	399	10	BE456611	c 271	17	10.7	501	29	CC968714
c 215	17	10.7	399	12	BI293288	c 272	17	10.7	503	28	AQ424830
c 216	17	10.7	404	10	BB544025	c 273	17	10.7	504	28	AZ909615
					BB200265						BY533913
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					AW227520						CE300363
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					BB117597						AL931574
					AZ589032						AA0813262
					BB139793						AZ818166
					BB313457						AQ338029
					BB790406						AQ275872
					BB208767						AL145286
					BG988238						BI244916
					BJ398636						AL550436
					BB131569						AZ061189
					BY602850						BJ388733
					AV732005						AZ389317
					AW022843						CA576019
					BJ343683						AL619574
					AW103146						BI324501
					BJ438375						AL552896
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					CIT-HSP-2						AL597343
					AA083940						AZ887273
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					BB545189						BF548989
					CS597432						AZ813586
					BI517033						AQ165956
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					AZ589032						AA0813262
					BB139793						AZ818166
					BB313457						AQ338029
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					BB208767						AL145286

c 274	17	10.7	507	28	A0970125	A0970125	RPCI-23-3	331	17	10.7	579	28	A2600236	A2600236	1M0416P22
c 275	17	10.7	508	12	B3340211	B3340211		332	17	10.7	582	28	A2247302	A2247302	RPCI-23-3
c 276	17	10.7	509	28	B2399132	A2993132	ZM0278J04	c 333	17	10.7	583	12	B3398578	B3398578	B3398578
c 277	17	10.7	511	28	A2300035	RPCI-23-1		334	17	10.7	584	29	BX498445	BX498445	PFSF7C806
c 278	17	10.7	512	10	BFO20110	uM14607.x		335	17	10.7	584	29	BK123596	BK123596	Danlo .rer
c 279	17	10.7	513	10	BFO04323	EST432821		336	17	10.7	587	12	BK340457	BK340457	Danlo .rer
c 280	17	10.7	515	14	CD392609	Gm.cK1180		337	17	10.7	587	12	BMO65413	BMO65413	KS07003C1
c 281	17	10.7	516	28	BH361522	CH230-95L		338	17	10.7	589	29	DR7N1.41	DR7N1.41	Danlo .rer
c 282	17	10.7	517	10	BM444057	AB160	Bae	c 339	17	10.7	590	28	CC447399	CC447399	B3340830
c 283	17	10.7	520	9	AU052886	AU052886		c 340	17	10.7	591	12	B3340830	B3340830	B3340830
c 284	17	10.7	524	13	BQ273054	aao15d08.		c 341	17	10.7	591	28	A2272675	A2272675	RPCI-23-1
c 285	17	10.7	524	28	AQ497881	HS.5080	B	c 342	17	10.7	593	28	AQ346274	AQ346274	RPCI11-101
c 286	17	10.7	525	28	AQ142625	HS.2223	B	c 343	17	10.7	594	9	AM089592	AM089592	x420904.x
c 287	17	10.7	526	10	AW943589	Ld11963.3		c 344	17	10.7	595	12	B3371858	B3371858	B3371858
c 288	17	10.7	526	28	AQ189934	AQ189934	HS.3211_B	c 345	17	10.7	595	12	BP131920	BP131920	BP131920
c 289	17	10.7	530	9	AV081862	AV081862		c 346	17	10.7	600	12	B1990635	B1990635	2084-47
c 290	17	10.7	530	12	B3346570	B3346570		c 347	17	10.7	600	12	B1990635	B1990635	4073-64
c 291	17	10.7	532	28	AQ124040	HS.3121_A		c 348	17	10.7	600	12	B3435709	B3435709	B3435709
c 292	17	10.7	533	12	B3343063	B3343063		c 349	17	10.7	601	12	B3343019	B3343019	B3430198
c 293	17	10.7	534	9	AM087860	AM087860	xB39B08.x	c 350	17	10.7	601	12	B3435004	B3435004	B3435004
c 294	17	10.7	536	9	AL598047	AL598047	DKEP2131	c 351	17	10.7	602	9	AV684250	AV684250	AV684250
c 295	17	10.7	536	28	AQ476570	AQ476570	CITB1-EL-	c 352	17	10.7	603	9	AU039898	AU039898	AU039898
c 296	17	10.7	537	12	B2429921	B2429921	B346570	c 353	17	10.7	603	12	B3346810	B3346810	B3346810
c 297	17	10.7	544	12	B1443222	B1443222	da656c12.	c 354	17	10.7	603	12	B3399560	B3399560	B3399560
c 298	17	10.7	545	9	AI637536	AI637536	CS45b09.x	c 355	17	10.7	603	13	BO622891	BO622891	ZOCR20-3
c 299	17	10.7	545	28	AQ733126	HS.5552	B	c 356	17	10.7	605	28	BZ131640	BZ131640	CH2P30-3101
c 300	17	10.7	546	12	B3346379	B3346379		c 357	17	10.7	605	29	DR191205	DR191205	
c 301	17	10.7	547	14	CD564772	CD564772	B0484605-	c 358	17	10.7	606	29	CC942283	CC942283	Danlo .rer
c 302	17	10.7	547	28	B2441802	B2441802	B0N02197R	c 359	17	10.7	607	29	CE647430	CE647430	LI9F-gs-
c 303	17	10.7	548	29	BK163366	BK163366	Danlo .rer	c 360	17	10.7	608	12	B3373734	B3373734	B3373734
c 304	17	10.7	551	29	CG828059	ZMMB031		c 361	17	10.7	610	12	B0068315	B0068315	B0068315
c 305	17	10.7	553	10	BE981103	BE981103	UI-M-CGO-	c 362	17	10.7	610	12	B3344375	B3344375	B3344375
c 306	17	10.7	553	29	BK130553	BK130553	Danlo .rer	c 363	17	10.7	610	13	BK498504	BK498504	DKEP2779R
c 307	17	10.7	554	28	AO625296	AO625296	CITB1-EL-	c 364	17	10.7	610	28	AQ917650	AQ917650	RPCI-23-2
c 308	17	10.7	554	28	BH741819	BH741819	g137411.g	c 365	17	10.7	611	29	CE470082	CE470082	LI9F-gs-
c 309	17	10.7	560	10	BE688107	BE688107	uM42208.x	c 366	17	10.7	612	12	B3341040	B3341040	B3341040
c 310	17	10.7	560	10	B3344657	B3344657		c 367	17	10.7	613	12	B3343623	B3343623	B3343623
c 311	17	10.7	560	29	CE033046	CE033046	LI9F-gs-	c 368	17	10.7	613	29	AG240856	AG240856	Lotus con
c 312	17	10.7	561	28	CC002275	CC002275	PUGHA667B	c 369	17	10.7	614	9	AV826583	AV826583	AV826583
c 313	17	10.7	562	12	BMO65383	K507003AO		c 370	17	10.7	614	14	CF788508	CF788508	860466.M
c 314	17	10.7	563	28	BH761564	BH761564	BMBAC323G	c 371	17	10.7	615	9	AU261531	AU261531	AU261531
c 315	17	10.7	563	29	CE113732	CE113732	LI9F-gs-	c 372	17	10.7	616	13	B3398425	B3398425	NI5C-m007
c 316	17	10.7	564	12	B3036761	B3036761		c 373	17	10.7	616	28	BHO59497	BHO59497	RPCI-24-2
c 317	17	10.7	564	28	B2450344	B2450344	BONAD397F	c 374	17	10.7	617	13	P0828076	P0828076	B0828076
c 318	17	10.7	565	9	AL711563	AL711563	DKEP6861	c 375	17	10.7	618	28	A2850932	A2850932	LM61n2174
c 319	17	10.7	565	12	B3343212	B3343212		c 376	17	10.7	618	28	CE090595	CE090595	CE090595
c 320	17	10.7	567	14	CD074022	MA3-0001U		c 377	17	10.7	619	29	CE090595	CE090595	LI9F-gs-
c 321	17	10.7	568	10	AM990299	uF63601.Y		c 378	17	10.7	621	28	BH492873	BH492873	BOHF4878R
c 322	17	10.7	570	14	CA577104	CA577104	K0704P07-	c 379	17	10.7	626	12	B3340860	B3340860	B3340860
c 323	17	10.7	570	28	A2872695	ZM0186F09		c 380	17	10.7	627	28	BH452613	BH452613	AV691602
c 324	17	10.7	571	29	CE229178	LI9F-gs-		c 381	17	10.7	628	9	AU263773	AU263773	AU263773
c 325	17	10.7	572	12	B3033838	B3033838		c 382	17	10.7	629	28	A2373483	A2373483	1M0127J19
c 326	17	10.7	575	9	AV528506	AV528506		c 383	17	10.7	632	12	B3342808	B3342808	B3342808
c 327	17	10.7	575	28	BH002153	BH002153	BMBAC02C1	c 384	17	10.7	633	12	B3342362	B3342362	B3342362
c 328	17	10.7	576	10	BF472334	UI-M-BH3-		c 385	17	10.7	633	14	CB473724	CB473724	8n74.H09
c 329	17	10.7	576	28	AO353859	RPCI-11-3		c 386	17	10.7	636	12	CE333181	CE333181	LI9F-gs-
c 330	17	10.7	579	12	B0428094	B0428094		c 387	17	10.7	636	12	B3341958	B3341958	B3341958

c 388	17	10.7	636	12	Bj429018	Bj429018	Bj429018	445	17	10.7	674	14	CB448101	702161 MA
c 389	17	10.7	637	29	CB441600	c1grt-999-	AG130526	c 446	17	10.7	674	29	AG130526	AG130526 Pan trogl
c 390	17	10.7	638	10	BF295849	029PB504	BB031133	c 447	17	10.7	675	10	BB031133	BB031133
c 391	17	10.7	638	13	BK846326	BK846326	Bj429473	c 448	17	10.7	675	12	Bj429473	Bj429473
c 392	17	10.7	639	10	BB657037	BB657037	AO288036	c 449	17	10.7	675	28	AO288036	AO288036 rnbh0030
c 393	17	10.7	639	28	A2507265	A2507265	BM348M17	c 450	17	10.7	676	28	BK131335	BK131335
c 394	17	10.7	640	12	BQ042168	BQ042168	UT-W-CO-	c 451	17	10.7	678	12	BP516683	Darlo for
c 395	17	10.7	641	28	A2590598	A2590598	1M0400114	c 452	17	10.7	678	12	BP516683	BP516683
c 396	17	10.7	642	10	BB652597	BB652597	BM250504	c 453	17	10.7	680	9	BM250504	BM250504
c 397	17	10.7	642	29	CC966741	CC966741	BO1F239TF	c 454	17	10.7	680	10	BB227725	BB227725
c 398	17	10.7	643	12	Bj372517	Bj372517	Bj372517	c 455	17	10.7	680	28	B2028531	B2028531
c 399	17	10.7	644	10	BB457204	BB457204	BM457204	c 456	17	10.7	681	14	CB556703	CB556703
c 400	17	10.7	644	12	BM939750	BM939750	UT-W-CG-	c 457	17	10.7	681	28	AO780105	AO780105
c 401	17	10.7	645	12	Bj399763	Bj399763	Bj399763	c 458	17	10.7	681	28	A2534508	A2534508
c 402	17	10.7	645	12	Bj401764	Bj401764	Bj401764	c 459	17	10.7	681	29	CG415709	CG415709
c 403	17	10.7	646	12	Bj342632	Bj342632	CF359600	c 460	17	10.7	682	12	Bj402996	Bj402996
c 404	17	10.7	646	14	CF359600	CF359600	820863 MA	c 461	17	10.7	683	12	BG506881	BG506881
c 405	17	10.7	647	12	Bj435157	Bj435157	Bj435157	c 462	17	10.7	683	12	Bj399165	Bj399165
c 406	17	10.7	649	13	BU775320	BU775320	STBBAH09	c 463	17	10.7	684	12	Bj345043	Bj345043
c 407	17	10.7	649	13	BM032128	BM032128	BM032128	c 464	17	10.7	685	12	Bj343473	Bj343473
c 408	17	10.7	650	9	AV711848	AV711848	AV711848	c 465	17	10.7	685	14	CF789112	CF789112
c 409	17	10.7	650	12	Bj344094	Bj344094	Bj344094	c 466	17	10.7	685	28	BH945560	BH945560
c 410	17	10.7	651	10	BB445269	BB445269	BM445269	c 467	17	10.7	687	29	AG099358	AG099358
c 411	17	10.7	652	28	B2499384	B2499384	B2499384	c 468	17	10.7	688	12	Bj433213	Bj433213
c 412	17	10.7	653	10	BB259184	BB259184	BB259184	c 469	17	10.7	688	12	Bj434452	Bj434452
c 413	17	10.7	654	14	CF911383	CF911383	AO614507-	c 470	17	10.7	688	28	BH601810	BH601810
c 414	17	10.7	655	12	Bj344261	Bj344261	Bj344261	c 471	17	10.7	689	12	Bj377870	Bj377870
c 415	17	10.7	656	12	Bj347001	Bj347001	Bj347001	c 472	17	10.7	689	12	Bj436364	Bj436364
c 416	17	10.7	656	14	Bj402905	Bj402905	Bj402905	c 473	17	10.7	690	10	BB185755	BB185755
c 417	17	10.7	656	14	CD245092	CD245092	AGENCOURT	c 474	17	10.7	690	12	Bj428865	Bj428865
c 418	17	10.7	657	10	BB246599	BB246599	BB246599	c 475	17	10.7	692	12	Bj347656	Bj347656
c 419	17	10.7	658	12	Bj344967	Bj344967	Bj344967	c 476	17	10.7	692	29	CG793345	CG793345
c 420	17	10.7	658	12	Bj432168	Bj432168	Bj432168	c 477	17	10.7	693	12	Bj339923	Bj339923
c 421	17	10.7	659	13	BM244120	BM244120	BM244120	c 478	17	10.7	693	12	Bj339954	Bj339954
c 422	17	10.7	659	12	Bj342501	Bj342501	Bj342501	c 479	17	10.7	693	12	Bj341541	Bj341541
c 423	17	10.7	660	9	AV990367	AV990367	AV990367	c 480	17	10.7	693	12	Bj434328	Bj434328
c 424	17	10.7	661	28	B2035204	B2035204	oe645605-	c 481	17	10.7	694	12	Bj343377	Bj343377
c 425	17	10.7	662	12	Bj345464	Bj345464	Bj345464	c 482	17	10.7	695	12	Bj344915	Bj344915
c 426	17	10.7	662	12	Bj435959	Bj435959	Bj435959	c 483	17	10.7	695	12	Bj346222	Bj346222
c 427	17	10.7	663	10	BB435790	BB435790	BB435790	c 484	17	10.7	695	12	Bj429041	Bj429041
c 428	17	10.7	663	13	BM077377	BM077377	BM077377	c 485	17	10.7	695	12	Bj433177	Bj433177
c 429	17	10.7	665	12	Bj398569	Bj398569	Bj398569	c 486	17	10.7	696	12	Bj345820	Bj345820
c 430	17	10.7	666	12	Bj344068	Bj344068	Bj344068	c 487	17	10.7	697	12	Bj377518	Bj377518
c 431	17	10.7	666	12	Bj345547	Bj345547	Bj345547	c 488	17	10.7	697	28	BH976156	od664d07.
c 432	17	10.7	666	12	Bj428278	Bj428278	Bj428278	c 489	17	10.7	698	12	Bj430133	Bj430133
c 433	17	10.7	667	12	Bj343483	Bj343483	Bj343483	c 490	17	10.7	699	28	BH466671	BOHPOT5FR
c 434	17	10.7	667	28	B2017640	B2017640	oe681d05-	c 491	17	10.7	700	13	BM082354	BM082354
c 435	17	10.7	668	14	CB456866	CB456866	714172 MA	c 492	17	10.7	702	12	Bj347315	Bj347315
c 436	17	10.7	670	12	Bj347463	Bj347463	CB94463	c 493	17	10.7	702	28	B2257069	B2257069
c 437	17	10.7	670	29	CG942657	CG942657	MBELCO6TF	c 494	17	10.7	705	28	B2450395	B2450395
c 438	17	10.7	671	12	Bj346734	Bj346734	Bj346734	c 495	17	10.7	707	28	BH958857	BH958857
c 439	17	10.7	671	28	AQ428230	AQ428230	CITBI-EI-	c 496	17	10.7	708	28	B2014478	B2014478
c 440	17	10.7	672	9	AU200398	AU200398	AU200398	c 497	17	10.7	708	29	CE796985	CE796985
c 441	17	10.7	673	9	AU270319	AU270319	AU270319	c 498	17	10.7	713	28	BH944504	BH944504
c 442	17	10.7	673	28	BH883813	hm47c06.g	BH883813	c 499	17	10.7	713	29	CE666940	CE666940
c 443	17	10.7	673	29	AG149990	Pan trogl	AG149990	c 500	17	10.7	714	12	Bj344935	Bj344935
c 444	17	10.7	674	14	CB265472	1008379 H	CB265472	c 501	17	10.7	716	9	AV877951	AV877951

502	17	10.7	716	28	BH944479	BH944479	cbu83508.	559	17	10.7	771	29	CC559013	CC559013	CH240_467
c 503	17	10.7	717	12	BJ346332	BJ346332		c 560	17	10.7	775	12	BJ345183	BJ345183	BJ345183
c 504	17	10.7	719	12	BJ341872	BJ341872		561	17	10.7	782	28	BH681474	BH681474	BH681474
c 505	17	10.7	720	12	BJ347039	BJ347039		c 562	17	10.7	785	29	CC925589	CC925589	CC925589
c 506	17	10.7	720	12	BJ399414	BJ399414		563	17	10.7	787	29	CC9862041	CC9862041	CC9862041
c 507	17	10.7	722	29	CE114816	CE114816	tlqr-gss-	564	17	10.7	788	12	B1560821	B1560821	ZMBB-027
c 508	17	10.7	723	12	BJ346049	BJ346049		c 565	17	10.7	789	28	B2439893	B2439893	B2439893
c 509	17	10.7	725	13	BJ341083	BJ341083		566	17	10.7	790	13	BH748838	BH748838	BH748838
c 510	17	10.7	725	13	BW048011	BW048011		c 567	17	10.7	792	28	B2462127	B2462127	BONIVA4TF
c 511	17	10.7	726	28	B2830052	B2830052	PUECL37TD	568	17	10.7	793	29	CC643807	CC643807	CC643807
c 512	17	10.7	727	29	CC475914	CC475914	CH240_301	569	17	10.7	800	28	BH552315	BH552315	BH552315
c 513	17	10.7	727	29	BK164609	BK164609	Darlo_rer	570	17	10.7	800	29	AG216474	AG216474	AG216474
c 514	17	10.7	728	28	A0482048	A0482048	RRC1-11-2	571	17	10.7	805	13	B0568042	B0568042	B0568042
c 515	17	10.7	729	12	BJ433480	BJ433480		572	17	10.7	806	14	CE444853	CE444853	CE444853
c 516	17	10.7	731	12	BJ402546	BJ402546		c 573	17	10.7	811	28	BH586401	BH586401	BH586401
c 517	17	10.7	731	28	BH673789	BH673789	BOFED0TF	c 574	17	10.7	811	28	BH586401	BH586401	BH586401
c 518	17	10.7	735	28	BH957419	BH957419	cd669408-	c 575	17	10.7	811	28	B2188329	B2188329	CH230-378
c 519	17	10.7	735	28	B2003100	B2003100	oab85608-	576	17	10.7	816	13	BU910378	BU910378	BU910378
c 520	17	10.7	736	13	BW048210	BW048210		c 577	17	10.7	817	29	CC505LHQ	CC505LHQ	CC505LHQ
c 521	17	10.7	737	12	BJ400601	BJ400601		c 578	17	10.7	820	11	CC508012	CC508012	CC508012
c 522	17	10.7	740	10	AW914299	AW914299	EST345603	c 579	17	10.7	821	14	CF207942	CF207942	CAB20002
c 523	17	10.7	740	12	BG245277	BG245277	602357394	580	17	10.7	821	29	CC916032	CC916032	CC916032
c 524	17	10.7	740	28	BH266860	BH266860	602795632	581	17	10.7	822	14	CA329159	CA329159	CA329159
c 525	17	10.7	740	29	CC649144	CC649144	CGM1239TV	582	17	10.7	822	29	CG119726	CG119726	CG119726
c 526	17	10.7	741	29	CC920401	CC920401	CGM1239TV	583	17	10.7	823	10	BF161090	BF161090	BF161090
c 527	17	10.7	744	28	BH505544	BH505544	BOH0196TR	584	17	10.7	823	29	CC500ADW	CC500ADW	CC500ADW
c 528	17	10.7	744	28	B2053006	B2053006	1kx42412-	c 585	17	10.7	824	28	BZ437619	BZ437619	BZ437619
c 529	17	10.7	745	12	BG862096	BG862096	602795632	c 586	17	10.7	824	28	CC005340	CC005340	CC005340
c 530	17	10.7	745	29	CC958540	CC958540	MHEEP7TF	587	17	10.7	826	29	CC846307	CC846307	CC846307
c 531	17	10.7	745	29	AG163909	AG163909	Pen_trocl	c 588	17	10.7	827	29	CC209453	CC209453	CC209453
c 532	17	10.7	746	12	BJ345981	BJ345981		c 589	17	10.7	828	29	CC868816	CC868816	CC868816
c 533	17	10.7	747	12	BJ342432	BJ342432		c 590	17	10.7	832	28	BH584551	BH584551	BH584551
c 534	17	10.7	749	13	BW131573	BW131573		c 591	17	10.7	833	28	BH584551	BH584551	BH584551
c 535	17	10.7	750	14	CD250829	CD250829	AGENCOURT	592	17	10.7	835	13	BU111622	BU111622	BU111622
c 536	17	10.7	750	28	B2559435	B2559435	1d73d12_b	593	17	10.7	835	13	BU537583	BU537583	BU537583
c 537	17	10.7	750	28	B2518021	B2518021	BOMQ277TR	c 594	17	10.7	836	28	BH704423	BH704423	BH704423
c 538	17	10.7	751	28	BH455324	BH455324	BOGNY50TR	595	17	10.7	837	13	BU10604	BU10604	BU10604
c 539	17	10.7	751	28	B2444039	B2444039	BONGE07TF	c 596	17	10.7	839	13	BU600088	BU600088	BU600088
c 540	17	10.7	753	12	BJ340949	BJ340949		c 597	17	10.7	840	29	CC324061	CC324061	CC324061
c 541	17	10.7	753	13	BW144797	BW144797		c 598	17	10.7	841	29	CC673686	CC673686	CC673686
c 542	17	10.7	755	14	CA195930	CA195930	SCE2AD108	c 599	17	10.7	843	11	CC508014	CC508014	CC508014
c 543	17	10.7	756	12	BJ347212	BJ347212		600	17	10.7	845	29	CC933666	CC933666	CC933666
c 544	17	10.7	756	13	BW038600	BW038600	DH01D02_H	601	17	10.7	846	14	CB204606	CB204606	CB204606
c 545	17	10.7	756	28	BH447128	BH447128	BOGPD8TF	602	17	10.7	846	29	BX246490	BX246490	BX246490
c 546	17	10.7	757	13	BW142553	BW142553		c 603	17	10.7	848	13	EU927730	EU927730	EU927730
c 547	17	10.7	757	14	CD675133	CD675133	fa19d08_Y	c 604	17	10.7	849	28	AZ669753	AZ669753	AZ669753
c 548	17	10.7	758	29	BK133682	BK133682	Darlo_rer	605	17	10.7	855	28	AZ674251	AZ674251	AZ674251
c 549	17	10.7	761	29	CE660294	CE660294	tlqr-gss-	c 606	17	10.7	860	28	BH688369	BH688369	BH688369
c 550	17	10.7	761	29	B2431152	B2431152		607	17	10.7	860	28	CC096281	CC096281	CC096281
c 551	17	10.7	766	28	BZ015134	BZ015134	oa106b09.	608	17	10.7	863	28	AZ667582	AZ667582	AZ667582
c 552	17	10.7	767	14	CD250754	CD250754		609	17	10.7	866	14	CF224086	CF224086	CF224086
c 553	17	10.7	767	14	CK129219	CK129219	AGENCOURT	c 610	17	10.7	867	28	AZ532968	AZ532968	AZ532968
c 554	17	10.7	767	28	AF010827	AF010827		c 611	17	10.7	873	28	CC102268	CC102268	CC102268
c 555	17	10.7	768	28	AQ745892	AQ745892	HS_2275_A	c 612	17	10.7	882	28	CC102169	CC102169	CC102169
c 556	17	10.7	768	28	BW061232	BW061232	1kf38605-	c 613	17	10.7	887	29	CC504836	CC504836	CC504836
c 557	17	10.7	770	13	BW097318	BW097318		c 614	17	10.7	896	28	AZ673635	AZ673635	AZ673635
c 558	17	10.7	771	28	BZ320729	BZ320729	hz12d12_g	c 615	17	10.7	913	10	BF694306	BF694306	BF694306

616	17	10.7	913	28	A074899	HS_5575_A	673	16	10.1	167	12	BI13490	BI13490 dan98c-09.
617	17	10.7	927	29	CC233141	CC233141 OGZADT17	674	16	10.1	168	9	A186547	A186547 wmb2b06.x
618	17	10.7	931	28	CC239758	CC239758 CH261-75E	675	16	10.1	178	10	BF31792	BF31792 OVI_9_E08
619	17	10.7	931	29	CG96620	MBENT25TF	676	16	10.1	178	28	BH901284	BH901284 SALX_0742
620	17	10.7	936	29	CG324071	CG324071 OGZAM63TV	677	16	10.1	184	13	CO1402	CO1402 HMG000838
621	17	10.7	939	29	CG339707	CG339707 OGZAM74TH	678	16	10.1	184	14	F28634	F28634 HSPD17902 H
622	17	10.7	941	29	CG312010	CG312010 OGZAM61TV	679	16	10.1	185	14	F34756	F34756 HSPD00057 H
623	17	10.7	941	29	CNS02626	AL195793 Tetradon	680	16	10.1	185	14	F34756	F34756 HSPD00057 H
624	17	10.7	948	28	A2541020	A2541020 ENTDM2TR	681	16	10.1	185	14	N74083	N74083 zA58h04.s1
625	17	10.7	963	11	BC040740	BC040740 Homo sapi	682	16	10.1	186	14	F27085	F27085 HSPD14842 H
626	17	10.7	964	13	BUI59269	BUI59269 AGENCOURT	683	16	10.1	188	29	CE050730	CE050730 t1gr-gs-g
627	17	10.7	986	29	CNS04MA8	AL297161 Tetradon	684	16	10.1	189	14	F36413	F36413 HSPD34024 H
628	17	10.7	990	29	CNS04MW1	AL297946 Tetradon	685	16	10.1	191	9	AV107802	AV107802 AV107802
629	17	10.7	996	13	BY711106	BY711106 BY711106	686	16	10.1	192	10	BE116158	BE116158 UI-R-B51-
630	17	10.7	996	29	CNS03DTH	AL238742 Tetradon	687	16	10.1	192	10	BF081768	BF081768 PM2-AN008
631	17	10.7	1001	28	CC283474	CC283474 CH261-138	688	16	10.1	194	9	AA771809	AA771809 a134f06.s
632	17	10.7	1020	12	BM472044	BM472044 AGENCOURT	689	16	10.1	194	13	BU889904	BU889904 P027004_P
633	17	10.7	1021	29	CNS05BNC	AL326145 Tetradon	690	16	10.1	194	29	CG817985	CG817985 SOYF007H
634	17	10.7	1051	29	CNS020HW	AL209309 Tetradon	691	16	10.1	199	12	BG35027	BG35027 91703 YAR
635	17	10.7	1058	28	CC245840	CC245840 CH261-148	692	16	10.1	205	10	BR065169	BR065169 BB065169
636	17	10.7	1063	28	CC215169	CC215169 CH261-77E	693	16	10.1	205	28	B2117988	B2117988 CH230-523
637	17	10.7	1076	28	CC208627	CC208627 CH261-126	694	16	10.1	208	10	AM576285	AM576285 UI-HF-BNO
638	17	10.7	1082	12	BM557847	BM557847 AGENCOURT	695	16	10.1	208	14	W38801	W38801 zB27f03.f1
639	17	10.7	1088	12	BM450763	BM450763 AGENCOURT	696	16	10.1	209	13	CO4293	CO4293 CO4293 Huma
640	17	10.7	1091	12	BM477620	BM477620 AGENCOURT	697	16	10.1	211	9	AA094524	AA094524 qp0620..se
641	17	10.7	1099	14	CDM98364	CDM98364 CDA33-B12	698	16	10.1	211	10	BB025218	BB025218 BB025218
642	17	10.7	1101	29	CNS00528	AL061987 Drcosphi11	699	16	10.1	212	9	AA093757	AA093757 zn51a02.f
643	17	10.7	1123	29	CG684199	CG684199 ZMWB6015	700	16	10.1	212	10	BE087679	BE087679 QVI-BT068
644	17	10.7	1124	28	B2219909	B2219909 CH230-518	701	16	10.1	212	12	BM898269	BM898269 Ph62412.Y
645	17	10.7	1125	28	CC294226	CC294226 CH261-63E	702	16	10.1	215	10	BE181363	BE181363 CMO-HT063
646	17	10.7	1137	29	CNS04LBB	AL295990 Tetradon	703	16	10.1	215	13	BQ310475	BQ310475 MRO-BT300
647	17	10.7	1155	28	CC252734	CC252734 CH261-19E	704	16	10.1	215	29	CE029001	CE029001 t1gr-gs-g
648	17	10.7	1198	29	AY411728	AY411728 Mus muscu	705	16	10.1	218	9	AL137647	AL137647 UI-R-CO-h
649	17	10.7	1201	9	AL523872	AL523872 AL523872	706	16	10.1	218	29	CE376323	CE376323 t1gr-gs-g
650	17	10.7	1458	28	B2574818	B2574818 msh2_3888	707	16	10.1	219	10	BB060670	BB060670 BB060670
651	17	10.7	1574	12	BM542661	BM542661 AGENCOURT	708	16	10.1	220	10	BE630035	BE630035 uis9a012.x
652	17	10.7	1799	11	AK011899	AK011899 Mus muscu	709	16	10.1	221	9	AY232898	AY232898 AY232898
653	17	10.7	1853	11	AK082940	AK082940 Mus muscu	710	16	10.1	222	14	F23378	F23378 HSPD12394 H
654	17	10.7	1915	11	AK039342	AK039342 Mus muscu	711	16	10.1	222	28	CC089474	CC089474 CSU-K33E.
655	17	10.7	2362	11	AK041400	AK041400 Mus muscu	712	16	10.1	226	9	AA107123	AA107123 EST7A_JL
656	17	10.7	2595	28	BH770927	BH770927 L1MGtag65	713	16	10.1	226	13	BU674857	BU674857 UI-CF-ID0
657	17	10.7	2735	11	AK016540	AK016540 Mus muscu	714	16	10.1	226	14	F30054	F30054 HSPD20306 H
658	17	10.7	2936	11	BC034963	BC034963 Homo sapi	715	16	10.1	228	9	AA093466	AA093466 KK4677.se
659	17	10.7	3019	11	AK030928	AK030928 Mus muscu	716	16	10.1	234	9	AA283274	AA283274 TH700 HTC
660	17	10.7	3114	11	AK051372	AK051372 Mus muscu	717	16	10.1	234	14	F29762	F29762 HSPD19832 H
661	17	10.7	3241	11	AK051462	AK051462 Mus muscu	718	16	10.1	235	9	AA585361	AA585361 ZTH663 HT
662	17	10.7	3659	11	AK053093	AK053093 Mus muscu	719	16	10.1	236	28	BH478281	BH478281 BORNK71TF
663	17	10.7	4301	11	AK030745	AK030745 Mus muscu	720	16	10.1	237	9	AA190233	AA190233 TH671 HTC
664	16	10.1	97	10	AM198775	AM198775 da06c07.x	721	16	10.1	238	10	BE691822	BE691822 hp1119..se
665	16	10.1	107	28	A2217492	A2217492 Sheared D	722	16	10.1	238	28	B2594262	B2594262 uTC0c03.x
666	16	10.1	116	12	BP510848	BP510848 BP510848	723	16	10.1	239	9	AA1802949	AA1802949 cJ58c11.x
667	16	10.1	125	14	CP645152	CP645152 Lab24a11.	724	16	10.1	239	9	AA190222	AA190222 TH53 HTC
668	16	10.1	125	14	CF330892	CF330892 NACL--06-	725	16	10.1	239	13	CO4671	CO4671 CO4671 Huma
669	16	10.1	139	14	CA340996	CA340996 haa76602.	726	16	10.1	240	9	AA224570	AA224570 zt17b09.s
670	16	10.1	145	14	F26021	F26021 HSPD13292 H	727	16	10.1	241	14	N92024	N92024 z42le11.f1
671	16	10.1	150	9	AA190211	AA190211 TH147 HTC	728	16	10.1	242	9	AI602370	AI602370 UI-R-AA0-
672	16	10.1	161	14	N85619	N85619 J4189F Huma	729	16	10.1	242	10	BE966179	BE966179 UI-M-B21-

730	16	10.1	243	F29289	HSPD19078	H	787	16	10.1	284	9	AU275389	AU275389	AU275389	
731	16	10.1	243	N87284	L3131F	Huma	788	16	10.1	284	10	BB479082	BB479082	BB479082	
732	16	10.1	244	AA190224	TH353	HTC	789	16	10.1	284	10	BB719469	BB719469	BB719469	
733	16	10.1	245	F22682	HSPD07552	H	790	16	10.1	284	10	BB116655	BB116655	BB116655	
734	16	10.1	246	AV408063	AV408063	H	791	16	10.1	285	9	A1872815	A1872815	W7-P-B31-	
735	16	10.1	246	AM316018	AM316018	13894	MAR	792	16	10.1	286	10	BB022414	BB022414	BB022414
736	16	10.1	250	AMB11071	MR2-ST013		793	16	10.1	286	14	MM8848	MM8848	W7-P-B31-	
737	16	10.1	251	AV259063	AU259063		794	16	10.1	287	9	AV014782	AV014782	AV014782	
738	16	10.1	251	BB452103	BB452103		795	16	10.1	287	10	BB380261	BB380261	BB380261	
739	16	10.1	251	BB222136	BB222136		796	16	10.1	287	14	H51387	H51387	W7-P-B31-	
740	16	10.1	252	AA725493	AA725493	a117h10.s	797	16	10.1	288	14	F26057	F26057	F26057	
741	16	10.1	252	AA125002	AA125002	qW95b11.x	798	16	10.1	288	14	F28844	F28844	HSPD18325	
742	16	10.1	252	F26301	F26301	HSPD13733	H	799	16	10.1	289	29	CC056018	CC056018	W7-P-B31-
743	16	10.1	252	BB222419	BB222419	CH230-260	800	16	10.1	291	10	BB351418	BB351418	W7-P-B31-	
744	16	10.1	253	AA035493	AA035493	AK27d05.s	801	16	10.1	291	14	F15665	F15665	W7-P-B31-	
745	16	10.1	253	AV114712	AV114712		802	16	10.1	292	9	A1476147	A1476147	W7-P-B31-	
746	16	10.1	254	BB253566	BB253566		803	16	10.1	292	9	AA572039	AA572039	AA572039	
747	16	10.1	255	N84748	J0759F	Huma	804	16	10.1	292	10	BB065938	BB065938	BB065938	
748	16	10.1	257	F35135	F35135	HSPD30866	H	805	16	10.1	293	10	BB050277	BB050277	BB050277
749	16	10.1	259	AA093732	AA093732	cl0720.s	806	16	10.1	293	10	BB934647	BB934647	BB934647	
750	16	10.1	259	AA168303	AA168303	tk77c07.x	807	16	10.1	293	14	F15746	F15746	W7-P-B31-	
751	16	10.1	259	AA249667	AA249667	KK2523.s	808	16	10.1	293	14	F25270	F25270	W7-P-B31-	
752	16	10.1	260	C03545	C03545	C03545	809	16	10.1	293	14	N48853	N48853	W774c11.f1	
753	16	10.1	262	AA1383627	AA1383627	cc46e09.x	810	16	10.1	294	29	CNS00NTE	CNS00NTE	AA081560	
754	16	10.1	264	A2820012	A2820012	2M0092A03	811	16	10.1	295	9	AA574500	AA574500	AA574500	
755	16	10.1	264	B2769137	B2769137	SAUK	1416	16	10.1	295	9	AU267573	AU267573	AU267573	
756	16	10.1	265	AA912311	AA912311	cl197c02.s	812	16	10.1	295	10	BB245931	BB245931	BB245931	
757	16	10.1	265	CD667588	CD667588	NC573c05	813	16	10.1	295	14	F33624	F33624	W7-P-B31-	
758	16	10.1	266	BB288358	BB288358		814	16	10.1	296	10	BB477900	BB477900	BB477900	

c 844	16	10.1	310	9	AA194302	AA194302 zq04e10.s	c 901	16	10.1	329	13	BY371962	BY371962 BY371962
c 845	16	10.1	310	10	BF092443	BF092443 MR0-TN010	c 902	16	10.1	329	29	CE719338	CE719338 t1gr-gsa-
c 846	16	10.1	311	9	A1077805	A1077805 oy35d02.s	c 903	16	10.1	329	29	CG382997	CG382997 CGCCE2TH
c 847	16	10.1	311	13	B0536548	B0536548 AGNCCURT	c 904	16	10.1	329	29	CG383005	CG383005 OGCGE2TV
c 848	16	10.1	312	9	A115590	A115590 ub87d11.r	c 905	16	10.1	330	9	AA1401457	AA1401457 t666g10.x
c 849	16	10.1	312	9	AA144499	AA144499 mf76e05.r	c 906	16	10.1	330	14	F26664	F26664 HSPD14223.H
c 850	16	10.1	312	9	A1645870	A1645870 mf76e05.y	c 907	16	10.1	331	9	A1264052	A1264052 q105f07.x
c 851	16	10.1	312	10	BB104144	BB104144 BB104144	c 908	16	10.1	331	9	AU276995	AU276995 UI-CF-FNO
c 852	16	10.1	312	12	B1043590	B1043590 PMO-OT021	c 909	16	10.1	331	14	CA314429	CA314429 UI-CF-FNO
c 853	16	10.1	312	13	BQ940185	BQ940185 AGNCCURT	c 910	16	10.1	333	14	HA61503	HA61503 yf60d02.r1
c 854	16	10.1	312	14	F19143	F19143 HSPD03741.H	c 911	16	10.1	334	9	AA129597	AA129597 t112b09.s
c 855	16	10.1	313	14	F27527	F27527 HSPD03741.H	c 912	16	10.1	334	14	T47249	T47249 yb64d01.r1
c 856	16	10.1	314	9	AU259559	AU259559 HSPD5500.H	c 913	16	10.1	335	12	BG958655	BG958655 PM4-CF080
c 857	16	10.1	314	13	CO3748	CO3748 CO3748.Huma	c 914	16	10.1	335	12	BG958655	BG958655 PM4-CF080
c 858	16	10.1	315	9	AA181377	AA181377 zp42d12.s	c 915	16	10.1	336	12	BG955665	BG955665 PM4-CF065
c 859	16	10.1	315	10	BB375776	BB375776 BB375776	c 916	16	10.1	337	9	AA004597	AA004597 z8t8a08.s
c 860	16	10.1	315	29	CE792824	CE792824 t1gr-gsa-	c 917	16	10.1	337	9	AA570098	AA570098 ne57a08.s
c 861	16	10.1	316	9	AA767883	AA767883 oa30h07.s	c 918	16	10.1	337	10	BB137033	BB137033 BB137033
c 862	16	10.1	316	10	BB257391	BB257391 BB257391	c 919	16	10.1	339	9	AA093917	AA093917 c11392.se
c 863	16	10.1	316	10	BB802674	BB802674 BB802674	c 920	16	10.1	339	10	BB085107	BB085107 BB085107
c 864	16	10.1	316	12	BP512976	BP512976 BP512976	c 921	16	10.1	339	10	BB251395	BB251395 BB251395
c 865	16	10.1	316	12	BP513021	BP513021 BP513021	c 922	16	10.1	339	28	AQ070375	AQ070375 HS.3035.B
c 866	16	10.1	316	12	BP513231	BP513231 BP513231	c 923	16	10.1	339	29	BX532507	BX532507 A-rb-dops
c 867	16	10.1	316	14	F19006	F19006 HSPD03603.H	c 924	16	10.1	340	9	AA859365	AA859365 UI-R-EO-c
c 868	16	10.1	316	14	R28472	R28472 yb50f12.r1	c 925	16	10.1	340	9	AA092298	AA092298 l16533.se
c 869	16	10.1	317	10	AAW820506	AAW820506 QV2-ST029	c 926	16	10.1	340	9	AA295766	AA295766 zr82f02.r
c 870	16	10.1	317	14	F37090	F37090 HSPD53132.H	c 927	16	10.1	340	10	BF360021	BF360021 PM2-MT010
c 871	16	10.1	318	9	A1056346	A1056346 oy48a06.x	c 928	16	10.1	340	10	BG055929	BG055929 n8t83d01.
c 872	16	10.1	318	9	AAW058311	AAW058311 km18g02.x	c 929	16	10.1	340	10	BE770937	BE770937 RCO-FT007
c 873	16	10.1	318	13	BQ091347	BQ091347 kul6c01.y	c 930	16	10.1	340	13	BY085504	BY085504 B1085504
c 874	16	10.1	318	14	F00187	F00187 HSB67H081.S	c 931	16	10.1	341	14	F21748	F21748 HSPD06337.H
c 875	16	10.1	318	28	BB366406	BB366406 tcs6g906.b	c 932	16	10.1	342	14	CA990245	CA990245 EST643753
c 876	16	10.1	319	10	BE770923	BE770923 RCO-FT007	c 933	16	10.1	342	28	AQ923423	AQ923423 RPCI-23-2
c 877	16	10.1	319	12	B1043561	B1043561 PMO-OT021	c 934	16	10.1	343	12	B1016052	B1016052 PMO-ET025
c 878	16	10.1	319	14	F28646	F28646 HSPD17919.H	c 935	16	10.1	344	10	BF871137	BF871137 CMO-ET012
c 879	16	10.1	320	13	BU717944	BU717944 SUM2B1A04	c 936	16	10.1	344	10	AA561866	AA561866 KJTB13524
c 880	16	10.1	320	14	F29030	F29030 HSPD18718.H	c 937	16	10.1	344	14	F31243	F31243 HSPD22246.H
c 881	16	10.1	321	9	AA211591	AA211591 zn556c04.s	c 938	16	10.1	346	10	BE714899	BE714899 I15-HT073
c 882	16	10.1	321	10	BB098654	BB098654 BB098654	c 939	16	10.1	347	9	AJ572947	AJ572947 PM2-MT010
c 883	16	10.1	321	14	F26467	F26467 HSPD13956.H	c 940	16	10.1	347	10	BF360027	BF360027 PM2-MT010
c 884	16	10.1	322	9	A1420607	A1420607 tf08d12.x	c 941	16	10.1	347	10	BE714925	BE714925 I15-HT073
c 885	16	10.1	322	9	AA176458	AA176458 xp33b06.s	c 942	16	10.1	348	9	AA213908	AA213908 zn57h09.s
c 886	16	10.1	322	10	AAW427027	AAW427027 62120.MAR	c 943	16	10.1	349	9	AA1742923	AA1742923 n339g03.r
c 887	16	10.1	324	9	AA1653369	AA1653369 AL653369	c 944	16	10.1	349	9	AA899344	AA899344 UI-R-EO-c
c 888	16	10.1	324	14	CE922451	CE922451 gmthmww24	c 945	16	10.1	350	10	AAW572437	AAW572437 AJ572437
c 889	16	10.1	324	14	DB0080	DB0080 HM084FI2A	c 946	16	10.1	350	14	AAW605883	AAW605883 MR0-HT024
c 890	16	10.1	325	10	AAW275645	AAW275645 xp39b08.x	c 947	16	10.1	350	10	CB844639	CB844639 M2PM-0187
c 891	16	10.1	325	10	BB101918	BB101918 BB101918	c 948	16	10.1	351	14	T29701	T29701 EST90491.Hu
c 892	16	10.1	325	14	F21882	F21882 HSPD06478.H	c 949	16	10.1	352	13	BQ668531	BQ668531 QG014E10.
c 893	16	10.1	325	14	F37981	F37981 HSPD07589.H	c 950	16	10.1	352	28	B2351429	B2351429 hm01a11.g
c 894	16	10.1	326	10	BB388324	BB388324 BB388324	c 951	16	10.1	353	13	BG810902	BG810902 dm32h11.
c 895	16	10.1	327	9	AA213517	AA213517 zt92a12.r	c 952	16	10.1	353	13	BY632966	BY632966 BY632966
c 896	16	10.1	328	9	AA183924	AA183924 qt66d05.x	c 953	16	10.1	354	14	F24165	F24165 HSPD10239.H
c 897	16	10.1	328	13	CO4265	CO4265 CO4265.Huma	c 954	16	10.1	354	9	AU039063	AU039063 AU039063
c 898	16	10.1	328	13	F35999	F35999 HSPD33256.H	c 955	16	10.1	355	9	AA437904	AA437904 vd22g07.s
c 899	16	10.1	329	9	AA413115	AA413115 w697d04.r	c 956	16	10.1	356	9	AJ572577	AJ572577 AJ572577
c 900	16	10.1	329	10	BB221788	BB221788 7o62f11.x	c 957	16	10.1	356	9	AA184300	AA184300 mt30d01.r

958	16	10.1	356	9	AV817582	AV817582
959	16	10.1	356	13	BY474878	BY474878
960	16	10.1	356	14	F22132	F22132 HSPD06815 H
961	16	10.1	356	14	F25805	F25805 HSPD13021 H
962	16	10.1	357	9	AA193172	AA193172 zp94q01.s
963	16	10.1	357	12	BM659243	BM659243 RMX602767
964	16	10.1	358	9	AI073804	AI073804 oy69c08.x
965	16	10.1	358	9	AI480855	AI480855 v061911.x
966	16	10.1	358	9	AA192104	AA192104 zq02f09.s
967	16	10.1	358	9	AA194326	AA194326 zq04e10.f
968	16	10.1	358	9	AV648037	AV648037 AV648037
969	16	10.1	359	9	AA501555	AA501555 ne68h02.s
970	16	10.1	359	14	F21208	F21208 HSPD05692 H
971	16	10.1	359	28	AA098517	AA098517 HS_3046.B
972	16	10.1	359	28	AA560854	AA560854 RPCI-23-2
973	16	10.1	360	9	AJ572851	AJ572851 AJ572851
974	16	10.1	361	9	AA482822	AA482822 n748b10.s
975	16	10.1	361	14	F33470	F33470 HSPD26923 H
976	16	10.1	361	14	F33845	F33845 HSPD28150 H
977	16	10.1	362	13	BQ410205	BQ410205 GA_E34002
978	16	10.1	362	14	F24271	F24271 HSPD10416 H
979	16	10.1	363	9	AU257485	AU257485 AU257485
980	16	10.1	363	10	AW379899	AW379899 RC4-HT025
981	16	10.1	363	10	AW658504	AW658504 94572 MAR
982	16	10.1	363	12	BM659309	BM659309 RMX602767
983	16	10.1	363	14	F21375	F21375 HSPD05894 H
984	16	10.1	364	10	BE668328	BE668328 137017 MA
985	16	10.1	364	10	BE770063	BE770063 CMI-FT005
986	16	10.1	364	12	BM273376	BM273376 PFEStoa4
987	16	10.1	364	12	BM659358	BM659358 RMX602767
988	16	10.1	365	9	AI675540	AI675540 wC01907.x
989	16	10.1	365	13	BQ539975	BQ539975 PTM0290
990	16	10.1	367	9	AA873455	AA873455 o169908.s
991	16	10.1	367	10	BF897149	BF897149 ILO-MT021
992	16	10.1	367	10	BF919308	BF919308 ILO-MT017
993	16	10.1	367	12	BM659313	BM659313 RMX602767
994	16	10.1	368	10	BF575892	BF575892 602132752
995	16	10.1	368	10	BF925591	BF925591 MR2-MT013
996	16	10.1	368	13	BQ334613	BQ334613 ILO-MT021
997	16	10.1	368	13	BQ344283	BQ344283 ILO-MT017
998	16	10.1	368	28	B2116067	B2116067 CH230-460
999	16	10.1	369	9	AJ572211	AJ572211 AJ572211
1000	16	10.1	369	10	BE770071	BE770071 CMI-FT005

Search completed: October 15, 2004, 06:28:09
Job time : 801.134 secs

OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 09:12:14 ; Search time 816.186 Seconds
(without alignments)
8443.595 Million cell updates/sec

Title: US-09-407-804A-8

Sequence: 1 atggttaaccagaagattttt.....ccgcatacgcgaattata 159

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_htg: +
3: gb_in: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_gta: +
12: gb_gy: +
13: gb_un: +
14: gb_vt: +
15: em_da: +
16: em_fun: +
17: em_hum: +
18: em_in: +
19: em_mu: +
20: em_om: +
21: em_or: +
22: em_ov: +
23: em_pat: +
24: em_ph: +
25: em_pl: +
26: em_ro: +
27: em_gta: +

28: em_un: +
29: em_vt: +
30: em_htg_hum: +
31: em_htg_inv: +
32: em_htg_other: +
33: em_htg_mus: +
34: em_htg_pin: +
35: em_htg_rtd: +
36: em_htg_mam: +
37: em_htg_vrt: +
38: em_gy: +
39: em_htgo_hum: +
40: em_htgo_mus: +
41: em_htgo_other: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	6	BD245279
2	159	100.0	159	6	AR368771
3	159	100.0	41708	6	BD245281
4	159	100.0	41708	6	AR368770
5	149.4	94.0	42942	7	AB045978
6	146.2	91.9	42722	7	AF424783
7	143	89.9	346527	1	AP003360
8	52.6	33.1	43081	7	AP001553
9	41.2	25.9	234864	5	BX004819
10	40	25.2	45636	7	AB044554
11	36.8	23.1	3824	6	BD243849
12	36.8	23.1	3824	6	AR435602
13	36.8	23.1	4620	6	AB037782
14	36.8	23.1	4972	6	AX405735
15	36.8	23.1	23943	3	CEC38C6
16	36.8	23.1	87790	9	AC090698
17	36.8	23.1	161198	2	AC015867
18	36.8	23.1	188346	2	AC010189
19	35.8	22.5	149109	2	AC023181
20	35.8	22.5	149252	9	AC066580
21	35.8	22.5	183120	2	AC109770
22	35.8	22.5	207606	9	AC024910
23	35.8	22.5	222542	9	AC022379
24	35.6	22.4	110352	8	AC006220
25	35.2	22.1	60645	2	AC105228
26	35.2	22.1	159874	2	AC113867
27	35.2	22.1	171206	9	AC090946
28	35.2	22.1	179723	9	AC087858
29	35.2	22.1	196519	2	AC133761
30	34.8	21.9	155290	2	AL359175
31	34.8	21.9	166065	2	AC013552
32	34.8	21.9	174646	5	AL929151
33	34.6	21.8	105842	9	AC107387

34 34.4 21.6 162413 9 AC091530
35 34.4 21.6 182069 10 AL662829
36 34.4 21.6 261322 2 AC095985
37 34.2 21.5 230603 2 AC120635
38 34.2 21.5 246778 2 AC097961
39 34 21.4 11622 6 AX345576
40 34 21.4 259474 2 AC095692
41 33.8 21.3 106100 2 AC138099
42 33.8 21.3 176201 2 AC095629
43 33.8 21.3 196140 10 AL672150
44 33.6 21.1 64799 5 AL732411
45 33.6 21.1 87235 2 AC022963

ALIGNMENTS

RESULT 1
BD245279 159 bp DNA linear PAT 17-JUL-2003
LOCUS BD245279
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245279.1 GI:33055049
VERSION JP 2002531107-A/14.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 159)
AUTHORS Polletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 14 24-SEP-2002;
PHARTECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/14
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/434252 PT JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N15/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FF Key
FT source 1..159
FT aureus bacteriophage 77',
FT

FEATURES
source Location/Qualifiers
1..159
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.8e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTACCAAGATTTTAAACCTAAGTGTTCAGATATGTAAGCTCAGAA 60
DB 1 ATGGTACCAAGATTTTAAACCTAAGTGTTCAGATATGTAAGCTCAGAA 60
QY 61 CTGATGATGAGGACAGGGGCGATGAATAGTTGTACACCTATTATCCAAA 120
DB 61 CTGATGATGAGGACAGGGGCGATGAATAGTTGTACACCTATTATCCAAA 120
QY 121 GCAGAACTCATACAGCCCGCTATGTCGAAATTTAA 159
DB 121 GCAGAACTCATACAGCCCGCTATGTCGAAATTTAA 159

RESULT 2
AR368771 159 bp DNA linear PAT 12-SEP-2003
LOCUS AR368771
DEFINITION Sequence 4 from patent US 6376652.
ACCESSION AR368771
VERSION AR368771.1 GI:34603078
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Polletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus
aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 4 23-Apr-2002;
FEATURES Location/Qualifiers
source 1..159
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 159; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.8e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTACCAAGATTTTAAACCTAAGTGTTCAGATATGTAAGCTCAGAA 60
DB 1 ATGGTACCAAGATTTTAAACCTAAGTGTTCAGATATGTAAGCTCAGAA 60
QY 61 CTGATGATGAGGACAGGGGCGATGAATAGTTGTACACCTATTATCCAAA 120
DB 61 CTGATGATGAGGACAGGGGCGATGAATAGTTGTACACCTATTATCCAAA 120
QY 121 GCAGAACTCATACAGCCCGCTATGTCGAAATTTAA 159
DB 121 GCAGAACTCATACAGCCCGCTATGTCGAAATTTAA 159
RESULT 3

BD245281 41708 bp DNA linear PAT 17-JUL-2003
LOCUS BD245281
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245281
VERSION BD245281.1 GI:33055031
KEYWORDS JP 200231107-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 200231107-A 16 24-SEP-2002;
PHARTECH INC
COMMENT OS Staphylococcus aureus bacteriophage 77
PN JP 200231107-A/16
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PT JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K45/00,A61P31/04,C07K14/005,
PC C12N1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Genome Sequence
FH Key Location/Qualifiers
FT source 1..41708
FT aureus bacteriophage 77' /organism='Staphylococcus
FEATURES
source Location/Qualifiers
1..41708
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
ORIGIN
Query Match 100.0%; Score 159; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 5e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAAGTTCAGATATGTAGCTCAGAAA 60
DB 34393 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAAGTTCAGATATGTAGCTCAGAAA 34452
QY 61 CTCATGATGAGGACAGGGCGATGAATAAGTTGTACGACCTATTATCAAAAAAATT 120
DB 34453 CTCATGATGAGGACAGGGCGATGAATAAGTTGTACGACCTATTATCAAAAAAATT 34512
QY 121 GCAGAACGTCTATACACGCCGCCCTATGTCGAAATATTA 159
DB 34513 GCAGAACGTCTATACACGCCGCCCTATGTCGAAATATTA 34551

RESULT 4
AR368770 41708 bp DNA linear PAT 12-SEP-2003
LOCUS AR368770
DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus
aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-Apr-2002;
FEATURES
source Location/Qualifiers
1..41708
/organism='unknown'
/mol_type='genomic DNA'
ORIGIN
Query Match 100.0%; Score 159; DB 6; Length 41708;
Best Local Similarity 100.0%; Pred. No. 5e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAAGTTCAGATATGTAGCTCAGAAA 60
DB 34393 ATGGTAAACCAAGAAATTTTAAAACTAACTTGAAGTTCAGATATGTAGCTCAGAAA 34452
QY 61 CTCATGATGAGGACAGGGCGATGAATAAGTTGTACGACCTATTATCAAAAAAATT 120
DB 34453 CTCATGATGAGGACAGGGCGATGAATAAGTTGTACGACCTATTATCAAAAAAATT 34512
QY 121 GCAGAACGTCTATACACGCCGCCCTATGTCGAAATATTA 159
DB 34513 GCAGAACGTCTATACACGCCGCCCTATGTCGAAATATTA 34551
RESULT 5
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS AB045978
DEFINITION Staphylococcus aureus temperate phage phIS1T genomic DNA, complete
sequence.
ACCESSION AB045978
VERSION AB045978.1 GI:12697822
KEYWORDS
SOURCE Staphylococcus aureus temperate phage phIS1T
ORGANISM Staphylococcus aureus temperate phage phIS1T
REFERENCE 1 (sites)
AUTHORS Naito,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J.
and Kamio,Y.
TITLE Phage conversion of Pantone-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phIS1T
JOURNAL Gene 266 (1-2), 195-206 (2001)
MEDLINE 21261956
PUBMED 11368915

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/db_xref="GI:12697832"
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/db_xref="GI:12697833"
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/transl_table=11
/product="pnl PVL ORF 38 homologue"
/protein_id="BAB21707.1"
/db_xref="GI:12697835"
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FYKEFYEE"
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/transl_table=11
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/db_xref="GI:12697836"
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/db_xref="GI:12697837"
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/db_xref="GI:12697838"
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EGASIVERSTYVRGE"
8083..8733
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8730..9173

Query Match 94.0%; Score 149.4; DB 7; Length 42942;
Best Local Similarity 96.2%; Pred. No. 4,66-35;
Matches 153; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGGTAACMAAGATTTTAAACGTAAGTTCAGATGATGACCTCAGAA 60
DB 11998 ATGGTAACMAAGATTTTGAATAATTAACGTGATGATGATGACCTCAGAA 11957
QY 61 CTGATAGTGAAGCAGGCGATGAATAAGTTGTACGACTATTATCCAAAATT 120
DB 11958 CTGATAGCAGGCGACAGGCGATGAATAAGTTATGACCTATTATCCAAAATT 12017
QY 121 GCAGAACTCATACAGCCCGCTATGTCGAAATATA 159
DB 12018 GCAGAACTCATACAGCCCGCTATGTCGAAATATA 12056

Search completed: October 14, 2004, 16:00:35
Job time : 819.186 secs

OM nucleic - nucleic search, using mw model

Run on: October 14, 2004, 07:30:59 ; Search time 106 Seconds
(without alignments)

6372.297 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159
Sequence: 1 atgttaacacaaagaattttt.....ccgcatacgtcgaaatttaa 159

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_29Jan04:*
2: geneseqn1980s:*
3: geneseqn1980s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	AAA68252	Aa68252 Bacterioph
2	159	100.0	159	AAC86107	Aa86107 Bacterioph
3	159	100.0	41708	AAA68247	Aa68247 Bacterioph
4	159	100.0	41708	AAC86106	Aa86106 Complete
5	144.6	90.9	1134	2 AAT83989	Aa83989 DNA encod
6	36.8	23.1	1401	5 ABA19641	Ab19641 Human ner
7	36.8	23.1	1401	5 ABA19640	Ab19640 Human ner

8	36.8	23.1	1401	5	ABA19639	Ab19639 Human ner
9	36.8	23.1	2023	3	AAC76979	Aa76979 Human ORF
10	36.8	23.1	3824	2	AA240489	Aa240489 Human SUL
11	36.8	23.1	4535	8	AA162250	AA162250 Human TAO
12	36.8	23.1	4536	8	AA162249	AA162249 Human TAO
13	36.8	23.1	4620	7	ACC50205	Acc50205 Breast ca
14	36.8	23.1	4620	8	AA162248	AA162248 Human TAO
15	36.8	23.1	4972	6	ABV59739	Abv59739 Novel hum
16	36.8	23.1	50000	9	ADC60735	Adc60735 Human e11
17	35.2	22.1	290	2	AA060638	AA060638 Human bra
18	34	21.4	11622	6	AB132674	Ab132674 Human imm
19	33.4	21.0	2782	3	AAC77695	Aa77695 Human can
20	33.4	21.0	2946	2	AAV34005	Aav34005 Human Rab
21	33.4	21.0	3389	4	AAH17587	Aah17587 Human c1N
22	33.4	21.0	3635	6	AB164076	Ab164076 Breast ca
23	33.4	21.0	4455	4	AAH99544	Aah99544 Human pro
24	33.4	21.0	4509	5	AA572171	Aa572171 DNA encod
25	33.4	21.0	7327	5	ABV21859	Abv21859 Human pro
26	33.4	21.0	7328	5	ABV27686	Abv27686 Human pro
27	33	20.8	110000	7	ABQ84281_1	Abq84281_1 of
28	32	20.1	110000	2	AAV21209_04	AAV21209_04 of
29	31.8	20.0	18888	6	ABQ75562	Abq75562 Human rel
30	31.6	19.9	1835	3	AA63914	Aa63914 Cucumbe
31	31.4	19.7	19937	9	ADC35071	Adc35071 Mouse gen
32	31.2	19.6	21580	8	ABT44140	Abt44140 Human nuc
33	30.6	19.2	948	7	ACF68708	Acf68708 Phototrab
34	30.6	19.2	110000	7	ACF67367_14	ACF67367_14 of
35	30.6	19.2	249878	7	ACF65381_1	ACF65381_1 Phototrab
36	30.4	19.1	3150	2	AAV74654	Aav74654 Stephyloc
37	30.4	19.1	3730	7	ADN89879	Adn89879 Stephyloc
38	30.2	19.0	3570	9	ADC35141	Adc35141 Human bre
39	30.2	19.0	3872	2	AAK39630	Aak39630 Breast ca
40	30.2	19.0	4089	9	ADD14759	Add14759 Human src
41	30.2	19.0	4214	5	ABV24766	Abv24766 Human pro
42	30	18.9	110000	6	ABA90521_16	ABA90521_16 of
43	30	18.9	110000	6	ABR90521_17	ABR90521_17 of
44	29.8	18.7	8603	6	AB132534	Ab132534 Human imm
45	29.6	18.6	390	5	ABV01144	Abv01144 Human pro

ALIGNMENTS

RESULT 1

AAA68252 standard; DNA; 159 BP.

XX	AC	AAA68252;	
XX	AC	AAA68252;	
DT	DT	15-SEP-2003 (revised)	
DT	DT	06-AUG-2003 (revised)	
DT	DT	27-OCT-2000 (first entry)	
XX	DE	Bacteriophage 77 770RF104 nucleotide sequence.	
XX	KW	Bacteriophage; antimicrobial; genome; identification; antibacterial;	
KW	KW	Bacterial growth inhibition; bacterial infection; ds.	

XX Staphylococcus aureus; bacteriophage 77.
 OS WO200032825-A2.
 PN 08-JUN-2000.
 PD
 XX
 XX 03-DEC-1999; 99WO-1B002040.
 PF
 XX 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1999; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 XX Polletier J, Gros P, Dubow M;
 PI WPI; 2000-412361/35.
 DR P-PSDB; AAB16527.
 DR
 XX
 XX Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 XX
 PS Disclosure; Page 162; 456pp; English.
 XX
 XX The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an
 CC uncharacterized bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAB68243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC (Updated on 13-SEP-2003 to standardise OS field)
 CC
 XX Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;
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 Query Match 100.0%; Score 159; DB 3; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.2e-41;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGTAACCAAGAAATTTTAAACTAACTGAGTGTCAATATGAGCTCAGAA 60
 DB 1 ATGGTAACCAAGAAATTTTAAACTAACTGAGTGTCAATATGAGCTCAGAA 60
 QY 61 CTCATATGATGAGGCACAGGCGCATGAAATAGGTGTACAGACTATTATTCAAAAA 120
 DB 61 CTCATATGATGAGGCACAGGCGCATGAAATAGGTGTACAGACTATTATTCAAAAA 120
 QY 121 GCAGAACTCATACAGCCCGCGCTATGTCGAATATTAA 159
 DB 121 GCAGAACTCATACAGCCCGCGCTATGTCGAATATTAA 159

DB 121 GCAGAACTCATACAGCCCGCGCTATGTCGAATATTAA 159
 RESULT 2
 AAC86107
 ID AAC86107 standard; cDNA; 159 BP.
 XX
 AC AAC86107;
 XX
 DT 06-AUG-2003 (rev1sed)
 DT 29-AUG-2001 (first entry)
 XX
 DE Bacteriophage 77 ORF 104.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 XX
 OS Bacteriophage.
 XX
 PN WO200146383-A2.
 PD 28-JUN-2001.
 PF 21-DEC-2000; 2000WO-US035180.
 PR 22-DEC-1999; 99US-00470512.
 PR 12-OCT-2000; 2000US-00689952.
 XX
 PA (PHAG-) PHAGETECH INC.
 PA (WILL) WILLIAMS K M.
 XX
 PI Polletier J, Gros P, Dubow M;
 DR WPI; 2001-418052/44.
 DR P-PSDB; AAB47318.
 XX
 PT Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by Staphylococcus
 PT aureus.
 XX
 PS Example 1; Fig 4; 107pp; English.
 XX
 CC This sequence represents open reading frame (ORF) 104 of Bacteriophage
 CC 77. The growth inhibitory gene product of ORF 104 interacts with DnaI
 CC derived from S. aureus, to form the basis of a screening assay. DnaI
 CC polypeptides and polynucleotides are useful for treating microbial,
 CC preferably bacterial, especially Staphylococcal, infections. DnaI
 CC polypeptides and polynucleotides are useful for biological, diagnostic,
 CC prophylactic, clinical and therapeutic use, and as components in
 CC databases useful for search analyses as well as in sequence analysis
 CC algorithms. (Updated on 06-AUG-2003 to correct OS field.)
 CC
 XX Sequence 159 BP; 58 A; 31 C; 30 G; 40 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 159; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.2e-41;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTACCAAGAAATTTTAAAACTAACTGATGTGATATGTACCTCAGAA 60
D6 1 ATGGTACCAAGAAATTTTAAAACTAACTGATGTGATATGTACCTCAGAA 60
QY 61 CTGATGATGAGGACAGGGCGATGAAATAGGTTGTAGACCTATTATCCAAAATT 120
D6 61 CTGATGATGAGGACAGGGCGATGAAATAGGTTGTAGACCTATTATCCAAAATT 120
QY 121 GCAGAACGTCTATACAGCCGCCCTATCGTCGAATATTAA 159
D6 121 GCAGAACGTCTATACAGCCGCCCTATCGTCGAATATTAA 159
RESULT 3
AAA68247
ID AAA68247 standard; DNA; 41708 BP.
XX
AC AAA68247;
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
DE Bacteriophage 77 complete genome sequence.
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
OS StephiLococcus aureus; bacteriophage 77.
XX
PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WO-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGETECH INC.
XX
PI Pelletier J, Gros P, Dubow M;
XX
DR WPI; 2000-412361/35.
XX
PT Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
PS Example 3; Page 141-151; 456pp; English.
CC The present invention describes a method for identifying a bacteriophage

CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAA69442 and AB16523 to AB16594 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
Query Match 100.0%; Score 159; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 6, 6e-41;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTACCAAGAAATTTTAAAACTAACTGATGTGATATGTACCTCAGAA 60
D6 34393 ATGGTACCAAGAAATTTTAAAACTAACTGATGTGATATGTACCTCAGAA 34452
QY 61 CTGATGATGAGGACAGGGCGATGAAATAGGTTGTAGACCTATTATCCAAAATT 120
D6 34453 CTGATGATGAGGACAGGGCGATGAAATAGGTTGTAGACCTATTATCCAAAATT 34512
QY 121 GCAGAACGTCTATACAGCCGCCCTATCGTCGAATATTAA 159
D6 34513 GCAGAACGTCTATACAGCCGCCCTATCGTCGAATATTAA 34551
RESULT 4
AAC86106
ID AAC86106 standard; cDNA; 41708 BP.
XX
AC AAC86106;
XX
DT 06-AUG-2003 (revised)
DT 29-AUG-2001 (first entry)
XX
DE Complete genome of bacteriophage 77.
XX
KW Draft S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW screening assay; ss.
XX
OS Bacteriophage.
XX
OS
XX
PN WO200146383-A2.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-US035180.
PF 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-00689952.
XX
PA (PHAG-) PHAGETECH INC.
PA (WILLI) WILLIAMS K M.

XX Polletier J, Gros P, Dubow M;
 XX WPI; 2001-418052/44.
 XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by *Staphylococcus*
 PT aureus.
 XX Disclosure; Fig 2; 107pp; English.
 XX This sequence represents the genome of *Bacteriophage* 77. The growth
 CC inhibitory gene product of ORF 104 interacts with DnaI derived from *S.*
 CC aureus, to form the basis of a screening assay. DnaI polypeptides and
 CC polynucleotides are useful for treating microbial, preferably bacterial,
 CC especially *Staphylococcus*, infections. DnaI polypeptides and
 CC polynucleotides are useful for biological, diagnostic, prophylactic,
 CC clinical and therapeutic use, and as components in databases useful for
 CC search analyses as well as in sequence analysis algorithms. (Updated on
 CC 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 4; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 6, 6e-41;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ATGGTAACCAAGATTTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 60
 DB 34393 ATGGTAACCAAGATTTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 34452
 OY 61 CTCATGATGAGGCGACATGAAATAGTGTGACACCTATTATCCAAAACCT 120
 DB 34453 CTCATGATGAGGCGACATGAAATAGTGTGACACCTATTATCCAAAACCT 34512
 OY 121 GCAGAAAGTCATACAGCCCGCTATGTCGAATATTAA 159
 DB 34513 GCAGAAAGTCATACAGCCCGCTATGTCGAATATTAA 34551

RESULT 5
 AAT83989
 ID AAT83989 standard; DNA; 1134 BP.
 AC AAT83989;
 DT 27-AUG-1998 (first entry)
 XX DNA encoding a *Staphylococcus aureus* protein of unknown function.
 DE
 XX
 KW *Staphylococcus aureus* protein; ribozyme; antisense sequence; control;
 KW *Staphylococcus* gene; regulatory element; bacterial gene expression;
 KW vaccine; *Staphylococcus* infection; food poisoning; scaled skin syndrome;
 KW toxic shock syndrome; ss.
 XX
 OS *Staphylococcus aureus*.
 XX

EH Key Location/Qualifiers
 FT CDS 593..946
 FT /*tag= a
 XX
 XX WO9730070-A1.
 XX
 XX 21-AUG-1997.
 XX
 XX 19-FEB-1997; 97WO-US002318.
 XX
 XX 20-FEB-1996; 96US-001188BP.
 XX
 XX (SMK) SMITHKLINE BEECHAM CORP.
 XX
 XX Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
 PI Pratt JM, Reichard RW, Rosenberg M, Ward JW;
 XX WPI; 1997-424969/39.
 DR P-PSDB; AAM28036.
 XX
 PT Novel polypeptide(s) from *Staphylococcus aureus* strain WCUH29 - used to
 PT isolate antimicrobial compounds, and in vaccines against *S. aureus*
 PT infection.
 XX
 PS Claim 9; Page 797; 989pp; English.
 XX
 CC The present sequence encodes a *Staphylococcus aureus* protein of unknown
 CC function. The present sequence was isolated from a library of clones of
 CC *S. aureus* WCUH 29 in *Escherichia coli*. The DNA sequence can be used in
 CC the construction of ribozymes and antisense sequences to control the
 CC expression of *Staphylococcus* genes. The DNA sequence is also useful as a
 CC source of regulatory elements for the control of bacterial gene
 CC expression. The encoded protein may be used to produce vaccines to enable
 CC a host to produce specific antibodies with antibacterial action. These
 CC vaccines and antibodies would protect a host against invasion by *S.*
 CC aureus, and conditions relating to *Staphylococcus* infection, e.g.
 CC *Staphylococcus* food poisoning, scaled skin syndrome, and toxic shock
 CC syndrome
 XX
 SQ Sequence 1134 BP; 407 A; 179 C; 247 G; 290 T; 0 U; 11 Other;
 Query Match 90.9%; Score 144.6; DB 2; Length 1134;
 Best Local Similarity 94.3%; Pred. No. 1e-36; 9; Indels 0; Gaps 0;
 Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 1 ATGGTAACCAAGATTTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 60
 DB 5 ATGGTAACCAAGATTTTAACTAACTGAGTGTGAGATATGTAGCTCAGAA 64
 OY 61 CTCATGATGAGGCGACATGAAATAGTGTGACACCTATTATCCAAAACCT 120
 DB 65 CTCATGATGAGGCGACATGAAATAGTGTGACACCTATTATCCAAAACCT 124
 OY 121 GCAGAAAGTCATACAGCCCGCTATGTCGAATATTAA 159
 DB 125 GCAGAAAGTCATACAGCCCGCTATGTCGAATATTAA 163

Search completed: October 14, 2004, 12:48:19
Job time : 108 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 742.638 Seconds
(without alignments)
6393.544 Million cell updates/sec

Title: US-09-407-804A-B

Perfect score: 139
Sequence: 1 atggtaccacaaagaatttt.....ccgcatacgcgaataataa 139

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hnc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hnc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estcom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rtd:*
- 26: em_gss_png:*
- 27: em_gss_vpl:*

28: gp_ges1:*

29: gp_ges2:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	38	23.9	913	29	CG112425	CG112425 PUPV31TD
c 2	36.8	23.1	398	9	AA812069	AA812069 ob75b07.s
c 3	36.8	23.1	399	9	AA426563	AA426563 zw02404.s
c 4	36.8	23.1	545	13	BUS32303	BUS32303 AGENCOURT
c 5	36.8	23.1	628	12	BG938678	BG938678 cn27f10.x
c 6	36.8	23.1	974	10	BF794164	BF794164 602255543
c 7	35.6	22.4	704	12	BG169535	BG169535 602321355
c 8	35.2	22.1	290	14	M86125	M86125 EST02651 Fe
c 9	35.2	22.1	564	28	AQ372904	AQ372904 RPEC11-15
c 10	35.2	22.1	708	11	AY067269	AY067269 Schmidtea
c 11	35.2	22.1	716	14	CB172558	CB172558 UMJ603014
c 12	35	22.0	418	13	BQ457264	BQ457264 ke37a01.Y
c 13	34.4	21.6	937	11	AK039507	AK039507 Mus muscu
c 14	34.4	21.6	979	28	CC190084	CC190084 CH261-958
c 15	34.4	21.6	1051	28	CC243328	CC243328 CH261-120
c 16	34.2	21.5	277	9	AA684791	AA684791 EST105419
c 17	33.8	21.3	1128	9	AL514043	AL514043 AL514043
c 18	33.6	21.1	535	28	BZ187708	BZ187708 CH230-435
c 19	33.6	21.1	792	28	BH980133	BH980133 ocd45a04.
c 20	33.4	21.0	328	10	AW903175	AW903175 CM4-NN102
c 21	33.4	21.0	346	10	BE812146	BE812146 RCO-AM004
c 22	33.4	21.0	352	29	CE699981	CE699981 t1gr-9s-
c 23	33.4	21.0	364	9	AJ430442	AJ430442 AJ430442
c 24	33.4	21.0	510	9	AI940791	AI940791 CM0-ST005
c 25	33.4	21.0	572	9	AI940804	AI940804 CM0-ST005
c 26	33.4	21.0	659	9	AU137533	AU137533 AU137533
c 27	33.4	21.0	684	12	BM015272	BM015272 603641411
c 28	33.4	21.0	869	13	BUI54160	BUI54160 AGENCOURT
c 29	33.4	21.0	881	28	BZ068209	BZ068209 1kh85d09.
c 30	33.4	21.0	969	28	CC239125	CC239125 CH261-66f
c 31	33.4	21.0	1038	28	CC215035	CC215035 CH261-189
c 32	33.4	21.0	1090	28	CC218385	CC218385 CH261-371
c 33	33.4	21.0	1094	12	BM465386	BM465386 AGENCOURT
c 34	33.4	21.0	2868	29	AY412813	AY412813 Pan trogl
c 35	33.4	21.0	2928	29	AY412812	AY412812 Homo sapi
c 36	33.2	20.9	856	29	CNS02PPI	AL208287 Tetracton
c 37	33.2	20.9	989	28	CC392353	CC392353 PUNRKS6TB
c 38	32.8	20.6	602	14	CH105217	CH105217 1077P94.5
c 39	32.8	20.6	633	28	BH081489	BH081489 RPEC-24-3
c 40	32.8	20.6	661	10	BB626448	BB626448 BB626448
c 41	32.8	20.6	686	10	BB189020	BB189020 BB189020
c 42	32.8	20.6	711	28	BZ686533	BZ686533 PUBCA42TD
c 43	32.8	20.6	853	28	CC378784	CC378784 PUNDB82TD
c 44	32.8	20.6	2976	11	AK079101	AK079101 Mus muscu
c 45	32.6	20.5	518	28	AQ251087	AQ251087 F18F12-SP

Search completed: October 14, 2004, 18:55:20
Job time : 746.638 secs

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 19:00:14 / Search time 1524.71 Seconds

(without alignments)
8442.862 Million cell updates/sec

Title: US-09-407-804A-9

Perfect score: 297

Sequence: 1 atgttcacatataaacgaaa.....acttgatcatgaatgtag 297

Scoring table: OLIGO_NUC

Gapop 60.0 / Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: GenBank:
1: gb_ba:.*
2: gb_hg:.*
3: gb_in:.*
4: gb_ov:.*
5: gb_ov:.*
6: gb_ov:.*
7: gb_ov:.*
8: gb_ov:.*
9: gb_ov:.*
10: gb_ov:.*
11: gb_ov:.*
12: gb_ov:.*
13: gb_ov:.*
14: gb_ov:.*
15: gb_ov:.*
16: gb_ov:.*
17: gb_ov:.*
18: gb_ov:.*
19: gb_ov:.*
20: gb_ov:.*
21: gb_ov:.*
22: gb_ov:.*
23: gb_ov:.*
24: gb_ov:.*
25: gb_ov:.*
26: gb_ov:.*
27: gb_ov:.*

28: em_un:.*
29: em_vl:.*
30: em_htg_hum:.*
31: em_htg_inv:.*
32: em_htg_other:.*
33: em_htg_mus:.*
34: em_htg_pln:.*
35: em_htg_rod:.*
36: em_htg_mam:.*
37: em_htg_vrt:.*
38: em_sy:.*
39: em_htgo_hum:.*
40: em_htgo_mus:.*
41: em_htgo_other:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	6	BD245280
2	297	100.0	41708	6	BD245281
3	297	100.0	41708	6	AR368770
4	261	87.9	261	6	BD245277
5	183	61.6	45636	7	AB044554
6	181	60.9	348527	1	AP003360
7	172	57.9	41401	7	AB009866
8	161	54.2	42942	7	AB045978
9	133	44.8	43081	7	AP001553
10	39	13.1	291150	1	AP003135
11	29	9.8	267	6	AX618246
12	29	9.8	42722	7	AF424783
13	29	9.8	272850	1	AP004828
14	28	9.4	580	6	AR355085
15	28	9.4	43594	6	BD245634
16	28	9.4	43604	7	AF424781
17	27	9.1	348650	1	AP003364
18	25	8.4	258	6	AX618548
19	21	7.1	190220	5	AL935305
20	20	6.7	163899	2	AC073060
21	20	6.7	168459	5	AL772289
22	20	6.7	177517	2	AC140389
23	20	6.7	241347	2	AC096352
24	20	6.7	241679	2	AC020861
25	20	6.7	257471	2	AC139675
26	20	6.7	267943	2	AC136702
27	19	6.4	237	6	AR383649
28	19	6.4	480	8	RID428847
29	19	6.4	991	6	A26050
30	19	6.4	991	6	166499
31	19	6.4	7037	6	AX346653
32	19	6.4	10408	6	166486
33	19	6.4	10408	6	166487

34	19	6.4	17309	9	AC130709	AC130709 Homo sapi	c	91	18	6.1	836	11	BV051957	BV051957 S212P6049
35	19	6.4	46024	2	AC100659	AC100659 Mus muscu	c	92	18	6.1	1880	5	BC052972	BC052972 Dantio rer
36	19	6.4	64167	9	HSBA89B2	AL080245 Human DNA	c	93	18	6.1	2000	6	AX510142	AX510142 Sequence
37	19	6.4	82700	2	AC015635	AL015635 Homo sapi	c	94	18	6.1	2000	6	AX596276	AX596276 Sequence
38	19	6.4	93476	2	AC112352_3	Continuation (4 of	c	95	18	6.1	2000	6	AX829574	AX829574 Sequence
39	19	6.4	93476	2	AC112352_3	Continuation (4 of	c	96	18	6.1	2000	6	AX831604	AX831604 Sequence
40	19	6.4	106253	8	AP003815	AP003815 Oryza sat	c	97	18	6.1	3486	8	AX121411	AX121411 Oryza sat
41	19	6.4	110000	2	AC096457_1	Continuation (2 of	c	98	18	6.1	3542	8	SCYD1149W	SCYD1149W Sequence
42	19	6.4	134308	9	AC011488	AC011488 Homo sapi	c	99	18	6.1	4307	9	HSTYL	HSTYL Sequence
43	19	6.4	136377	9	HSBJ76N10	AL121959 Human DNA	c	100	18	6.1	5958	6	AX779908	AX779908 Sequence
44	19	6.4	139629	2	AP003809	AP003809 Oryza sat	c	101	18	6.1	7699	9	AL603626	AL603626 Sequence
45	19	6.4	139648	2	AP004335	AP004335 Oryza sat	c	102	18	6.1	11859	4	AC144695	AC144695 Sequence
46	19	6.4	145476	2	AC044911	AC044911 Homo sapi	c	103	18	6.1	23096	8	SC1V23	SC1V23 Sequence
47	19	6.4	147638	8	AP003303	AP003303 Oryza sat	c	104	18	6.1	29885	9	AC093679	AC093679 Sequence
48	19	6.4	152046	2	AC101763	AC101763 Mus muscu	c	105	18	6.1	33099	6	AX059508	AX059508 Sequence
49	19	6.4	157244	9	AP005204	AP005204 Homo sapi	c	106	18	6.1	37991	9	AP000565	AP000565 Sequence
50	19	6.4	158432	2	AC105438	AC105438 Sus scrofa	c	107	18	6.1	44583	6	AX059545	AX059545 Sequence
51	19	6.4	158577	9	AP001485	AP001485 Homo sapi	c	108	18	6.1	58608	2	AC100499	AC100499 Sequence
52	19	6.4	159774	2	AC113867	AC113867 Rattus no	c	109	18	6.1	64426	2	AC014778	AC014778 Sequence
53	19	6.4	165761	2	AC145750	AC145750 Homo sapi	c	110	18	6.1	70626	9	AL356274	AL356274 Human DNA
54	19	6.4	167280	2	AC102825	AC102825 Mus muscu	c	111	18	6.1	72590	5	AL603744	AL603744 Zebrafish
55	19	6.4	169116	5	BX324202	BX324202 Zebrafish	c	112	18	6.1	74589	8	AB010068	AB010068 Arabidops
56	19	6.4	169682	9	AC010854	AC010854 Homo sapi	c	113	18	6.1	82596	8	FGH8	FGH8 Sequence
57	19	6.4	170123	9	AC018371	AC018371 Homo sapi	c	114	18	6.1	83594	8	AB008268	AB008268 Arabidops
58	19	6.4	172113	2	AP001176	AP001176 Homo sapi	c	115	18	6.1	86004	9	HS11023	HS11023 Sequence
59	19	6.4	173802	10	AL805929	AL805929 Mouse DNA	c	116	18	6.1	87726	2	AC014337	AC014337 Drosophill
60	19	6.4	177379	10	AC140212	AC140212 Mus muscu	c	117	18	6.1	90425	2	AC138337	AC138337 Homo sapi
61	19	6.4	178239	2	AC011968	AC011968 Homo sapi	c	118	18	6.1	93276	9	AL139124	AL139124 Human DNA
62	19	6.4	178469	2	BX248504	BX248504 Dantio rer	c	119	18	6.1	103920	2	AC014955	AC014955 Drosophill
63	19	6.4	179494	2	BX664752	BX664752 Dantio rer	c	120	18	6.1	109491	9	AC022224	AC022224 Homo sapi
64	19	6.4	181170	2	AC109244	AC109244 Mus muscu	c	121	18	6.1	110000	2	AC098244_1	AC098244_1 Continuation (2 of
65	19	6.4	186394	2	BX330068	BX330068 Dantio rer	c	122	18	6.1	110000	2	AL359032	AL359032 Homo sapi
66	19	6.4	194504	2	AC007832	AC007832 Homo sapi	c	123	18	6.1	110000	2	AL360016_2	AL360016_2 Continuation (3 of
67	19	6.4	194604	2	AP001275	AP001275 Homo sapi	c	124	18	6.1	110000	2	AL928982_1	AL928982_1 Continuation (2 of
68	19	6.4	201182	9	AC069540	AC069540 Homo sapi	c	125	18	6.1	111692	9	AL161783	AL161783 Human DNA
69	19	6.4	202205	2	AC068895	AC068895 Homo sapi	c	126	18	6.1	112886	9	AL599726	AL599726 Human DNA
70	19	6.4	206675	2	AC133827	AC133827 Rattus no	c	127	18	6.1	118473	10	AL671969	AL671969 Mouse DNA
71	19	6.4	208363	10	AL691416	AL691416 Mouse DNA	c	128	18	6.1	123576	9	AC015969	AC015969 Homo sapi
72	19	6.4	209335	2	BX346476	BX346476 Dantio rer	c	129	18	6.1	125502	8	ATT41420	ATT41420 Sequence
73	19	6.4	210617	2	AC034201	AC034201 Homo sapi	c	130	18	6.1	126807	9	HS391022	HS391022 Arabidops
74	19	6.4	212643	2	BX511103	BX511103 Dantio rer	c	131	18	6.1	128765	3	AC010053	AC010053 Human DNA
75	19	6.4	223808	2	AC114139	AC114139 Rattus no	c	132	18	6.1	128722	9	HS15005	HS15005 Drosophill
76	19	6.4	226147	9	AP002478	AP002478 Homo sapi	c	133	18	6.1	133263	2	AC126235	AC126235 Human DNA
77	19	6.4	231946	2	AC115544	AC115544 Rattus no	c	134	18	6.1	137043	9	AC068794	AC068794 Canis fam
78	19	6.4	244739	2	AC112042	AC112042 Rattus no	c	135	18	6.1	138350	2	AC010801	AC010801 Homo sapi
79	19	6.4	245090	2	BX890597	BX890597 Dantio rer	c	136	18	6.1	140212	2	AC016730	AC016730 Homo sapi
80	19	6.4	278299	2	AC129681	AC129681 Rattus no	c	137	18	6.1	140987	9	AC099061	AC099061 Homo sapi
81	19	6.4	288339	14	AF198100	AF198100 Fowlpox v	c	138	18	6.1	141742	9	AC099621	AC099621 Homo sapi
82	19	6.4	288888	9	HSN310932	HSN310932 Homo sapi	c	139	18	6.1	141915	2	AC099636	AC099636 Homo sapi
83	19	6.4	324399	2	AC098418	AC098418 Rattus no	c	140	18	6.1	143220	9	AL389887	AL389887 Mus muscu
84	19	6.4	329181	2	AC094238	AC094238 Rattus no	c	141	18	6.1	145763	2	AC064809	AC064809 Human DNA
85	19	6.1	249	11	G21301	G21301 human STR W	c	142	18	6.1	146248	2	AC013677	AC013677 Homo sapi
86	18	6.1	480	6	AR388675	AR388675 Sequence	c	143	18	6.1	146843	9	AC0096761	AC0096761 Homo sapi
87	18	6.1	520	6	AR424133	AR424133 Sequence	c	144	18	6.1	146921	9	AC007992	AC007992 Homo sapi
88	18	6.1	520	6	BD119686	BD119686 EST and e	c	145	18	6.1	147114	9	AP001939	AP001939 Homo sapi
89	18	6.1	520	6	BD119686	BD119686 EST and e	c	146	18	6.1	147419	9	HS738P11	HS738P11 Human DNA
90	18	6.1	597	6	AR388671	AR388671 Sequence	c	146	18	6.1	147419	9	HS738P11	HS738P11 Human DNA

167	18	6.1 148282	9	AC024649	AC024649 Homo sapi	204	18	6.1 181725	2	AC102430	AC102430 Mus muscu
168	18	6.1 149907	4	AC091436	AC091436 fells cat	205	18	6.1 181864	9	AL353743	AL353743 Human DNA
169	18	6.1 150242	9	AC006195	AC006195 Homo sapi	206	18	6.1 182240	2	AC074201	AC074201 Homo sapi
150	18	6.1 152022	9	AC094081	AC094081 Homo sapi	207	18	6.1 182504	2	AC146660	AC146660 Ootolemur
151	18	6.1 152324	2	AC136938	AC136938 Homo sapi	208	18	6.1 182925	2	AC128749	AC128749 Rattus no
152	18	6.1 153099	9	CNS0507CE	AL355095 Human chr	209	18	6.1 183462	5	BX571976	BX571976 Zebrafish
153	18	6.1 153439	8	AP003113	AP003113 Oryza sat	210	18	6.1 183706	2	BK470078	BK470078 Danio rer
154	18	6.1 153448	2	AC105263	AC105263 Drosophill	211	18	6.1 183925	2	AC078870	AC078870 Homo sapi
155	18	6.1 155028	2	BX347940	BX347940 Danio rer	212	18	6.1 184317	10	AL606494	AL606494 Mouse DNA
156	18	6.1 155039	2	AC012548	AC012548 Homo sapi	213	18	6.1 184433	9	AC108479	AC108479 Homo sapi
157	18	6.1 155475	5	BX321885	BX321885 Zebrafish	214	18	6.1 184600	2	AC117347	AC117347 Rattus no
158	18	6.1 156873	9	AC015998	AC015998 Homo sapi	215	18	6.1 184706	9	AC004782	AC004782 Rattus no
159	18	6.1 157088	5	AL353500	AL353500 Zebrafish	216	18	6.1 186117	9	AC072046	AC072046 Homo sapi
160	18	6.1 157494	10	AL606512	AL606512 Mouse DNA	217	18	6.1 186322	2	BX294389	BX294389 Danio rer
161	18	6.1 159231	2	AC116499	AC116499 Mus muscu	218	18	6.1 187684	2	AC016008	AC016008 Homo sapi
162	18	6.1 159670	2	AC027626	AC027626 Homo sapi	219	18	6.1 189386	2	AP001456	AP001456 Homo sapi
163	18	6.1 159806	2	AC024340	AC024340 Homo sapi	220	18	6.1 189579	9	AL354733	AL354733 Human DNA
164	18	6.1 161001	9	AC068775	AC068775 Homo sapi	221	18	6.1 190506	2	AC096890	AC096890 Homo sapi
165	18	6.1 161104	9	AL732499	AL732499 Zebrafish	222	18	6.1 190520	2	AC138271	AC138271 Homo sapi
166	18	6.1 161402	9	AP003113	AP003113 Homo sapi	223	18	6.1 192332	10	AL606745	AL606745 Mouse DNA
167	18	6.1 161660	2	AC115920	AC115920 Mus muscu	224	18	6.1 192437	5	BX322665	BX322665 Zebrafish
168	18	6.1 162386	9	AC113397	AC113397 Homo sapi	225	18	6.1 192673	2	AC018870	AC018870 Homo sapi
169	18	6.1 162428	2	BX005112	BX005112 Danio rer	226	18	6.1 193147	2	AC097960	AC097960 Rattus no
170	18	6.1 163209	2	AC007949	AC007949 Homo sapi	227	18	6.1 193553	9	AC097634	AC097634 Homo sapi
171	18	6.1 163353	10	AL627076	AL627076 Mouse DNA	228	18	6.1 194091	9	AP003534	AP003534 Homo sapi
172	18	6.1 163551	2	AC015777	AC015777 Homo sapi	229	18	6.1 194813	2	AC100723	AC100723 Mus muscu
173	18	6.1 163741	3	AC007821	AC007821 Drosophill	230	18	6.1 195031	9	AC141325	AC141325 Pan trogl
174	18	6.1 163942	9	AC034207	AC034207 Homo sapi	231	18	6.1 195323	2	AP003549	AP003549 Homo sapi
175	18	6.1 163966	5	AL954708	AL954708 Zebrafish	232	18	6.1 195592	8	AC090982	AC090982 Homo sapi
176	18	6.1 164763	2	BX470262	BX470262 Danio rer	233	18	6.1 195921	8	ATCRH181	ATCRH181 Homo sapi
177	18	6.1 164806	10	AC138715	AC138715 Mus muscu	234	18	6.1 196044	2	AC102296	AC102296 Mus muscu
178	18	6.1 165006	8	AP003791	AP003791 Oryza sat	235	18	6.1 196602	2	AC114248	AC114248 Rattus no
179	18	6.1 165617	9	AF165926	AF165926 Homo sapi	236	18	6.1 196766	8	ATCRH1V16	ATCRH1V16 Homo sapi
180	18	6.1 167015	9	BX649387	BX649387 Mus muscu	237	18	6.1 197159	3	AC009340	AC009340 Homo sapi
181	18	6.1 167237	9	AC007938	AC007938 Homo sapi	238	18	6.1 198281	10	AC122254	AC122254 Mus muscu
182	18	6.1 168124	2	AC021971	AC021971 Homo sapi	239	18	6.1 198734	3	AC007820	AC007820 Homo sapi
183	18	6.1 168344	2	AC024334	AC024334 Homo sapi	240	18	6.1 198911	2	AC111975	AC111975 Rattus no
184	18	6.1 168866	8	OSJN00023	AL606588 Oryza sat	241	18	6.1 199036	9	AC025449	AC025449 Homo sapi
185	18	6.1 169162	9	AL138926	AL138926 Human DNA	242	18	6.1 199569	2	AC103676	AC103676 Homo sapi
186	18	6.1 170116	9	AC087257	AC087257 Homo sapi	243	18	6.1 200689	2	AC067865	AC067865 Homo sapi
187	18	6.1 170247	2	AC110896	AC110896 Mus muscu	244	18	6.1 200841	10	AC108830	AC108830 Mus muscu
188	18	6.1 172036	9	AC046181	AC046181 Homo sapi	245	18	6.1 202843	9	CNS01891	AL135961 Human chr
189	18	6.1 172494	2	BX572089	BX572089 Danio rer	246	18	6.1 203178	2	AC114678	AC114678 Mus muscu
190	18	6.1 173226	10	AC132120	AC132120 Mus muscu	247	18	6.1 203317	2	AC021062	AC021062 Mus muscu
191	18	6.1 174074	2	BX842671	BX842671 Mus muscu	248	18	6.1 205475	2	AC130033	AC130033 Rattus no
192	18	6.1 174138	5	AC008871	AC008871 Homo sapi	249	18	6.1 206093	2	BX571844	BX571844 Danio rer
193	18	6.1 174646	5	AL929151	AL929151 Zebrafish	250	18	6.1 206222	2	AC108891	AC108891 Bos tauru
194	18	6.1 177020	2	AC091326	AC091326 Homo sapi	251	18	6.1 206291	10	AL672091	AL672091 Mouse DNA
195	18	6.1 177087	2	AC093687	AC093687 Homo sapi	252	18	6.1 207365	2	AC093653	AC093653 Homo sapi
196	18	6.1 177734	9	AC073569	AC073569 Homo sapi	253	18	6.1 207695	2	AC097190	AC097190 Rattus no
197	18	6.1 178455	2	AC137969	AC137969 Mus muscu	254	18	6.1 210057	10	AC124501	AC124501 Mus muscu
198	18	6.1 179497	2	BX663521	BX663521 Danio rer	255	18	6.1 210892	2	AC132420	AC132420 Mus muscu
199	18	6.1 180486	2	AC118051	AC118051 Mus muscu	256	18	6.1 214146	2	AC096822	AC096822 Rattus no
200	18	6.1 180555	9	AC079384	AC079384 Homo sapi	257	18	6.1 221070	10	AC026949	AC026949 Mus muscu
201	18	6.1 180962	2	AC068917	AC068917 Homo sapi	258	18	6.1 223465	2	AC098603	AC098603 Rattus no
202	18	6.1 181315	2	AC147271	AC147271 Pan trogl	259	18	6.1 223678	2	AC130000	AC130000 Rattus no
203	18	6.1 181460	9	AC090877	AC090877 Homo sapi	260	18	6.1 225379	2	AC121485	AC121485 Rattus no

c 261	18	6.1 225538	2	AC109577	AC109577 Rattus no	c 318	17	5.7 1146	10	MRC0DA	X12801 Murline mRNA
c 262	18	6.1 226637	2	AC124613	AC124613 Mus muscu	c 319	17	5.7 1284	5	XEHAND	Z95080 X.laevis mR
c 263	18	6.1 227182	2	AC099283	AC099283 Rattus no	c 320	17	5.7 1515	8	AF227978	AF227978 Brassica
c 264	18	6.1 227411	10	AC130821	AC130821 Mus muscu	c 321	17	5.7 1593	8	AK070418	AK070418 Oryza sat
c 265	18	6.1 228893	2	AC111848	AC111848 Rattus no	c 322	17	5.7 1597	5	BC049424	BC049424 Dantio rer
c 266	18	6.1 229082	2	AC111600	AC111600 Rattus no	c 323	17	5.7 1597	5	BC053150	BC053150 Dantio rer
c 267	18	6.1 229606	2	AC105519	AC105519 Rattus no	c 324	17	5.7 1781	9	HSN805147	HSN805147 Homo sapi
c 268	18	6.1 230155	2	AC114073	AC114073 Rattus no	c 325	17	5.7 1837	5	AF22388253	AF22388253 Homo sapi
c 269	18	6.1 230444	2	AC117368	AC117368 Rattus no	c 326	17	5.7 1838	5	AF22381953	AF22381953 Oncorhyn
c 270	18	6.1 230449	2	AC105504	AC105504 Rattus no	c 327	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 271	18	6.1 230940	10	AC123043	AC123043 Mus muscu	c 328	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 272	18	6.1 231746	9	AC011389	AC011389 Homo sapi	c 329	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 273	18	6.1 232190	2	AC123645	AC123645 Mus muscu	c 330	17	5.7 1838	5	AF22382553	AF22382553 Oncorhyn
c 274	18	6.1 232223	2	AC132692	AC132692 Rattus no	c 331	17	5.7 1838	5	AF22383153	AF22383153 Oncorhyn
c 275	18	6.1 232251	2	AC093690	AC093690 Rattus no	c 332	17	5.7 1838	5	AF22383453	AF22383453 Oncorhyn
c 276	18	6.1 232610	2	AC123157	AC123157 Rattus no	c 333	17	5.7 1838	5	AF22383753	AF22383753 Oncorhyn
c 277	18	6.1 233274	2	AC098636	AC098636 Rattus no	c 334	17	5.7 1838	5	AF22384053	AF22384053 Oncorhyn
c 278	18	6.1 236096	3	AE003775	AE003775 Drosophill	c 335	17	5.7 1838	5	AF22384653	AF22384653 Oncorhyn
c 279	18	6.1 237067	2	AC118339	AC118339 Rattus no	c 336	17	5.7 1838	5	AF22384653	AF22384653 Oncorhyn
c 280	18	6.1 237712	9	AC012634	AC012634 Homo sapi	c 337	17	5.7 1838	5	AF22384953	AF22384953 Oncorhyn
c 281	18	6.1 239623	2	AC121220	AC121220 Rattus no	c 338	17	5.7 1838	5	AF22385253	AF22385253 Oncorhyn
c 282	18	6.1 240253	2	BX537326	BX537326 Dantio rer	c 339	17	5.7 1838	5	AF22385553	AF22385553 Oncorhyn
c 283	18	6.1 242384	2	AC105847	AC105847 Rattus no	c 340	17	5.7 1838	5	AF22385853	AF22385853 Oncorhyn
c 284	18	6.1 242743	2	AC137367	AC137367 Rattus no	c 341	17	5.7 1838	5	AF22386453	AF22386453 Oncorhyn
c 285	18	6.1 242907	2	AC106660	AC106660 Rattus no	c 342	17	5.7 1838	5	AF22386453	AF22386453 Oncorhyn
c 286	18	6.1 243768	2	AC125725	AC125725 Rattus no	c 343	17	5.7 1838	5	AF22386753	AF22386753 Oncorhyn
c 287	18	6.1 244974	2	AC111249	AC111249 Rattus no	c 344	17	5.7 1838	5	AF22387053	AF22387053 Oncorhyn
c 288	18	6.1 250087	2	AC096931	AC096931 Rattus no	c 345	17	5.7 1838	5	AF22387353	AF22387353 Oncorhyn
c 289	18	6.1 250937	2	AC098144	AC098144 Rattus no	c 346	17	5.7 1838	5	AF22387653	AF22387653 Oncorhyn
c 290	18	6.1 251852	2	AC114625	AC114625 Mus muscu	c 347	17	5.7 1838	5	AF22387953	AF22387953 Oncorhyn
c 291	18	6.1 252129	2	AC133975	AC133975 Rattus no	c 348	17	5.7 1838	5	AF22388553	AF22388553 Oncorhyn
c 292	18	6.1 261775	3	AE003639	AE003639 Drosophill	c 349	17	5.7 1838	5	AF22388853	AF22388853 Oncorhyn
c 293	18	6.1 261938	2	AC103691	AC103691 Rattus no	c 350	17	5.7 1838	5	AF22388853	AF22388853 Oncorhyn
c 294	18	6.1 263855	2	AC127197	AC127197 Rattus no	c 351	17	5.7 1947	6	AR321206	AR321206 Sequence
c 295	18	6.1 265977	2	AC134623	AC134623 Mus muscu	c 352	17	5.7 2002	8	AX099582	AX099582 Sequence
c 296	18	6.1 266574	2	AC087129	AC087129 Mus muscu	c 353	17	5.7 2109	8	BT003163	BT003163 Arabidops
c 297	18	6.1 267326	2	AC109722	AC109722 Rattus no	c 354	17	5.7 2159	9	HSU26396	HSU26396 Human fetal
c 298	18	6.1 269296	2	AC107602	AC107602 Rattus no	c 355	17	5.7 2247	3	DMU66460	DMU66460 Human fetal
c 299	18	6.1 271788	2	AC110973	AC110973 Rattus no	c 356	17	5.7 2318	5	ONHP60L	ONHP60L Human fetal
c 300	18	6.1 276372	2	AC123569	AC123569 Rattus no	c 357	17	5.7 2534	1	ECRCB	ECRCB Human fetal
c 301	18	6.1 278227	2	AC128099	AC128099 Rattus no	c 358	17	5.7 2551	8	SCRCB	SCRCB Human fetal
c 302	18	6.1 279666	2	AC130931	AC130931 Rattus no	c 359	17	5.7 2552	2	AC020498	AC020498 Drosophill
c 303	18	6.1 280394	3	AE003544	AE003544 Drosophill	c 360	17	5.7 2625	8	AK070975	AK070975 Oryza sat
c 304	18	6.1 333192	2	AC113779	AC113779 Rattus no	c 361	17	5.7 2671	5	D106363	D106363 Oncorhyn
c 305	18	6.1 340000	9	AP001718	AP001718 Homo sapi	c 362	17	5.7 2760	9	HUMALPFD	HUMALPFD Human alpha
c 306	18	6.1 349505	2	AC130443	AC130443 Rattus no	c 363	17	5.7 2760	9	HUMEDRINA	HUMEDRINA Human alpha
c 307	18	6.1 349505	2	AC130443	AC130443 Rattus no	c 364	17	5.7 2875	8	AY383719	AY383719 Human alpha
c 308	17	5.7 232	6	AR251699	AR251699 Sequence	c 365	17	5.7 3024	10	BC057064	BC057064 Brassaica
c 309	17	5.7 401	6	AX521179	AX521179 Sequence	c 366	17	5.7 3105	6	AX794253	AX794253 Sequence
c 310	17	5.7 441	6	AX570166	AX570166 Sequence	c 367	17	5.7 3452	3	AT128432	AT128432 Drosophill
c 311	17	5.7 607	11	BY040243	BY040243 S208P6811	c 368	17	5.7 3476	3	BT009955	BT009955 Drosophill
c 312	17	5.7 647	8	AJ600965	AJ600965 Arabidops	c 369	17	5.7 3577	3	DMROSA	DMROSA Arabidops
c 313	17	5.7 785	6	BD019395	BD019395 Novel gen	c 370	17	5.7 3618	8	HUMTYP	HUMTYP Homo sapien
c 314	17	5.7 785	6	BD099533	BD099533 Novel gen	c 371	17	5.7 3935	8	SCYK127W	SCYK127W Homo sapien
c 315	17	5.7 785	6	BD186809	BD186809 Nucleic a	c 372	17	5.7 4077	10	BC064438	BC064438 Rattus no
c 316	17	5.7 786	11	BY038169	BY038169 S212P6629	c 373	17	5.7 4513	10	BC027791	BC027791 Mus muscu
c 317	17	5.7 1021	8	GAN251559	AJ251559 Genetum gn	c 374	17	5.7 4734	9	HSN800826	HSN800826 Homo sapi

c 375	17	5.7	5355	6	E30079	E30079 Novel prote	c 432	17	5.7	45014	2	AC147003	AC147003 Homo sapi
c 376	17	5.7	5355	6	E30080	E30080 Novel prote	c 433	17	5.7	45472	3	CEY59A8A	AL132895 Caenorhab
c 377	17	5.7	5355	9	AB011422	AB011422 Homo sapi	c 434	17	5.7	46826	3	AC084155	AC084155 Caenorhab
c 378	17	5.7	5777	8	AT133743	AT133743 Arabidops	c 435	17	5.7	51648	2	AC015434	AC015434 Drosophill
c 379	17	5.7	5830	9	HSMB07900	BX647754 Homo sapi	c 436	17	5.7	51860	10	ALB080109	ALB080109 Mouse DNA
c 380	17	5.7	6177	6	AX281402	AX281402 Sequence	c 437	17	5.7	52417	9	AC114777	AC114777 Homo sapi
c 381	17	5.7	6177	6	AX319151	AX319151 Sequence	c 438	17	5.7	53411	2	AC087287	AC087287 Homo sapi
c 382	17	5.7	6207	6	AX251536	AX251536 Sequence	c 439	17	5.7	55343	9	AL139152	AL139152 Human DNA
c 383	17	5.7	6497	8	AF159061	AF159061 Oryza sat	c 440	17	5.7	55687	9	AC079464	AC079464 Homo sapi
c 384	17	5.7	6514	9	AF148808	AF148808 Homo sapi	c 441	17	5.7	57198	2	AL590046	AL590046 Continuation (4 of
c 385	17	5.7	7172	6	AR218888	AR218888 Sequence	c 442	17	5.7	58190	9	HS498124	AL031057 Human DNA
c 386	17	5.7	7172	6	BD003800	BD003800 Polynucle	c 443	17	5.7	58449	10	AL929218	AL929218 Mouse DNA
c 387	17	5.7	7499	1	EC85DMR	X13145 Escherichia	c 444	17	5.7	59219	2	AC090585	AC090585 Homo sapi
c 388	17	5.7	7672	6	AR274887	AR274887 Sequence	c 445	17	5.7	59303	8	AP004955	AP004955 Lotus cor
c 389	17	5.7	7672	6	AX780070	AX780070 Sequence	c 446	17	5.7	61150	2	AC100284	AC100284 Mus muscu
c 390	17	5.7	7672	6	HS083667	HS083667 Human alpha	c 447	17	5.7	61267	3	AC004336	AC004336 Drosophill
c 391	17	5.7	7787	6	AX334524	AX334524 Sequence	c 448	17	5.7	61725	2	AC100105	AC100105 Mus muscu
c 392	17	5.7	7787	9	HUMASPX	J05243 Human noner	c 449	17	5.7	62219	2	AC120844	AC120844 Mus muscu
c 393	17	5.7	7827	9	BC053521	BC053521 Homo sapi	c 450	17	5.7	63268	2	AC103683	AC103683 Homo sapi
c 394	17	5.7	8303	6	AX345324	AX345324 Sequence	c 451	17	5.7	63268	2	AC103683	AC103683 Homo sapi
c 395	17	5.7	10029	1	AE007457	AE007457 Streptococ	c 452	17	5.7	64139	9	AL929000	AL929000 Human DNA
c 396	17	5.7	10189	1	AE005549	AE005549 Escherich	c 453	17	5.7	64208	2	AC069064	AC069064 Homo sapi
c 397	17	5.7	10189	1	AE015336	AE015336 Shigella	c 454	17	5.7	64786	2	AC017805	AC017805 Homo sapi
c 398	17	5.7	10382	1	AE008517	AE008517 Streptococ	c 455	17	5.7	64849	2	AC113037	AC113037 Mus muscu
c 399	17	5.7	10710	6	AX344589	AX344589 Sequence	c 456	17	5.7	65014	2	AC100176	AC100176 Mus muscu
c 400	17	5.7	10846	1	AE013594	AE013594 Methanosa	c 457	17	5.7	66137	2	AC101526	AC101526 Mus muscu
c 401	17	5.7	11857	2	AC018299	AC018299 Drosophill	c 458	17	5.7	66310	2	AC135728	AC135728 Homo sapi
c 402	17	5.7	13460	8	SPBC685	AE000400 Escherich	c 459	17	5.7	66668	2	AC134694	AC134694 Homo sapi
c 403	17	5.7	14295	1	AE000400	AE000400 Escherich	c 460	17	5.7	69514	9	AY129465	Continuation (5 of
c 404	17	5.7	14764	10	AL974311	AL974311 Mouse DNA	c 461	17	5.7	71380	9	AC092605	AC092605 Homo sapi
c 405	17	5.7	16697	9	AL591687	AL591687 Human DNA	c 462	17	5.7	72591	2	AC080137	AC080137 Homo sapi
c 406	17	5.7	18556	2	AC017481	AC017481 Drosophill	c 463	17	5.7	73184	2	AC090864	AC090864 Homo sapi
c 407	17	5.7	19814	6	AX349041	AX349041 Sequence	c 464	17	5.7	78054	3	AC004296	AC004296 Drosophill
c 408	17	5.7	21011	8	AB025627	AB025627 Arabidops	c 465	17	5.7	78643	3	AC004352	AC004352 Drosophill
c 409	17	5.7	24139	10	AF463765	AF463765 Mus muscu	c 466	17	5.7	81147	9	AL606504	AL606504 Human DNA
c 410	17	5.7	24667	9	AF001295	AF001295 Homo sapi	c 467	17	5.7	81476	10	EX004788	EX004788 Mouse DNA
c 411	17	5.7	25464	6	A91686	A91686 Sequence 4	c 468	17	5.7	82064	2	AC006937	AC006937 Drosophill
c 412	17	5.7	25464	6	AR307527	AR307527 Sequence	c 469	17	5.7	83490	8	AP004039	AP004039 Oryza sat
c 413	17	5.7	25464	6	BD023435	BD023435 Nucleotid	c 470	17	5.7	83511	8	AB013389	AB013389 Arabidops
c 414	17	5.7	26514	2	AC005649	AC005649 Drosophill	c 471	17	5.7	83557	9	AL138735	AL138735 Human DNA
c 415	17	5.7	27503	9	AL160404	AL160404 Human DNA	c 472	17	5.7	84551	3	AC004295	AC004295 Drosophill
c 416	17	5.7	28716	10	AL928795	AL928795 Mouse DNA	c 473	17	5.7	85785	8	ATF21P8	ATF21P8 Homo sapi
c 417	17	5.7	30985	8	SPAC961	Z98763 S.pombe chr	c 474	17	5.7	87256	9	AC091865	AC091865 Homo sapi
c 418	17	5.7	31151	2	AC107201_8	Continuation (9 of	c 475	17	5.7	90463	5	AP003810	AP003810 Oryza sat
c 419	17	5.7	31557	3	AC004267	AC004267 Drosophill	c 476	17	5.7	90875	5	AL672192	AL672192 Zebrafish
c 420	17	5.7	31737	3	U50072	U50072 Caenorhabdi	c 477	17	5.7	91025	9	AL359270	AL359270 Homo sapi
c 421	17	5.7	32479	2	AC090240	AC090240 Homo sapi	c 478	17	5.7	91059	9	AP003463	AP003463 Homo sapi
c 422	17	5.7	32703	3	CEP14D1	Z92967 Caenorhabdi	c 479	17	5.7	93217	2	AC023171	AC023171 Homo sapi
c 423	17	5.7	33156	3	CET25612	Z82053 Caenorhabdi	c 480	17	5.7	93586	2	SPNE01913	SPNE01913 Homo sapi
c 424	17	5.7	37386	8	LMFL8806	LMFL8806 Sequence	c 481	17	5.7	94802	2	AL590487	AL590487 Human DNA
c 425	17	5.7	38475	8	SPCC350	SPCC350 Sequence	c 482	17	5.7	94924	9	AL355997	AL355997 Streptococ
c 426	17	5.7	38692	3	AC116919	AC116919 Dictyoste	c 483	17	5.7	99878	2	AC087108	AC087108 Homo sapi
c 427	17	5.7	39013	1	AF088896	AF088896 Zymomonas	c 484	17	5.7	101029	9	AC026954	AC026954 Homo sapi
c 428	17	5.7	39328	9	AL590456	AL590456 Human DNA	c 485	17	5.7	101333	8	AP004030	AP004030 Oryza sat
c 429	17	5.7	40699	8	SPBC119	AL022117 S.pombe c	c 486	17	5.7	101882	9	AC021089	AC021089 Homo sapi
c 430	17	5.7	40753	8	SPBC119	Y18367 Branchiosto	c 487	17	5.7	101923	10	AC138172	AC138172 Mus muscu
c 431	17	5.7	44326	2	AC025719	AC025719 Caenorhab	c 488	17	5.7	102282	9	AL158033	AL158033 Human DNA

c 489	17	5.7 102965	2	AC146727	Oryzomur
c 490	17	5.7 103390	9	AL358533	Human DNA
c 491	17	5.7 103479	9	AC140059	Homo sapi
c 492	17	5.7 103523	9	AL390408	Human DNA
c 493	17	5.7 105070	8	AP006352	Lectus cor
c 494	17	5.7 105247	9	AL356266	Human DNA
c 495	17	5.7 105600	8	AP005173	Oryza sat
c 496	17	5.7 105695	2	BX571758	Danio rer
c 497	17	5.7 106961	2	AC119411	Medicago
c 498	17	5.7 106975	8	OSJN00045	Oryza sat
c 499	17	5.7 107025	3	AL139235	Continuation (4 of
c 500	17	5.7 109685	9	AC024578	Homo sapi
c 501	17	5.7 110000	1	EC0067_1	Continuation (2 of
c 502	17	5.7 110000	2	AC101676	Continuation (3 of
c 503	17	5.7 110000	2	AC107201	Continuation (8 of
c 504	17	5.7 110000	2	AC112133	Homo sapi
c 505	17	5.7 110000	2	AC113868	Continuation (3 of
c 506	17	5.7 110000	2	AC116279	Rattus no
c 507	17	5.7 110000	2	AC118411	Rattus no
c 508	17	5.7 110000	2	AC120762	Continuation (3 of
c 509	17	5.7 110000	2	AC123241	Continuation (2 of
c 510	17	5.7 110000	2	AC132794	Continuation (3 of
c 511	17	5.7 110000	2	AC141403	Continuation (2 of
c 512	17	5.7 110000	2	AL139235	Continuation (3 of
c 513	17	5.7 110000	2	BX294176	Continuation (3 of
c 514	17	5.7 110000	2	BX23020	Continuation (3 of
c 515	17	5.7 110000	2	PRM13_01	Continuation (2 of
c 516	17	5.7 110901	9	AL359675	Human DNA
c 517	17	5.7 110999	9	AC091983	Homo sapi
c 518	17	5.7 113862	9	AC104774	Homo sapi
c 519	17	5.7 114026	5	AL165501	Human DNA
c 520	17	5.7 114626	4	AC138157	Carollia
c 521	17	5.7 115040	8	AC124954	Medicago
c 522	17	5.7 115424	2	AC146806	Medicago
c 523	17	5.7 117217	9	AP002076	Homo sapi
c 524	17	5.7 117911	9	HS117P19	Human DNA
c 525	17	5.7 118755	9	AC090152	Homo sapi
c 526	17	5.7 118869	9	AC004903	Homo sapi
c 527	17	5.7 119491	9	AC098860	Homo sapi
c 528	17	5.7 119875	8	AC108051	Homo sapi
c 529	17	5.7 120562	8	AY268139	Hordeum v
c 530	17	5.7 120625	2	AC017563	Human DNA
c 531	17	5.7 121141	10	AC125314	Drosophila
c 532	17	5.7 122681	9	AC006062	Homo sapi
c 533	17	5.7 123386	8	F12F1	AC002131 Arabidops
c 534	17	5.7 124214	9	AL807246	Human DNA
c 535	17	5.7 125439	9	AC138990	Homo sapi
c 536	17	5.7 125527	9	AL353133	Human DNA
c 537	17	5.7 125760	2	AC080122	Human DNA
c 538	17	5.7 125785	9	AC107393	Homo sapi
c 539	17	5.7 125973	2	AC010353	Homo sapi
c 540	17	5.7 127178	9	AC005160	Homo sapi
c 541	17	5.7 127472	2	AC124962	Medicago
c 542	17	5.7 127506	8	OSJN00096	Oryza sat
c 543	17	5.7 128016	2	AC138131	Medicago
c 544	17	5.7 128218	2	AC121096	Mus muscu
c 545	17	5.7 128751	5	BX649386	Zebrafish
c 546	17	5.7 128965	9	AL357562	Human DNA
c 547	17	5.7 129083	2	AC096853	Sus scrofa
c 548	17	5.7 129984	9	AC115620	Homo sapi
c 549	17	5.7 130361	10	AL929546	Mouse DNA
c 550	17	5.7 130586	2	AC073238	Homo sapi
c 551	17	5.7 130632	9	AC004547	Homo sapi
c 552	17	5.7 131704	2	AP004313	Oryza sat
c 553	17	5.7 132200	2	AL161619	Homo sapi
c 554	17	5.7 132782	8	AC120983	Oryza sat
c 555	17	5.7 132927	8	AC078890	Oryza sat
c 556	17	5.7 133157	9	AC109351	Homo sapi
c 557	17	5.7 133330	10	AL928871	Mouse DNA
c 558	17	5.7 135513	3	BS000023	Pen trogl
c 559	17	5.7 136164	3	AC099006	Medicago
c 560	17	5.7 136551	9	AC123786	Homo sapi
c 561	17	5.7 136901	9	AC073626	Homo sapi
c 562	17	5.7 136906	2	RN86120	Rattus no
c 563	17	5.7 137289	9	AC022828	Homo sapi
c 564	17	5.7 137441	5	AL928712	Zebrafish
c 565	17	5.7 137445	2	AP004780	Oryza sat
c 566	17	5.7 137985	2	AP005634	Oryza sat
c 567	17	5.7 138419	9	AL137793	Human DNA
c 568	17	5.7 138769	2	BX571896	Danio rer
c 569	17	5.7 139033	8	HS0180804	Human DNA
c 570	17	5.7 139330	2	AC119415	Medicago
c 571	17	5.7 140606	2	AC135761	Homo sapi
c 572	17	5.7 140680	2	BX510917	Danio rer
c 573	17	5.7 141889	2	AC032006	Homo sapi
c 574	17	5.7 142021	10	AL645843	Mouse DNA
c 575	17	5.7 142123	2	AC068890	Homo sapi
c 576	17	5.7 142353	2	AC073286	Homo sapi
c 577	17	5.7 142911	2	BX835398	Danio rer
c 578	17	5.7 142959	2	AC025453	Homo sapi
c 579	17	5.7 143146	9	AC079855	Homo sapi
c 580	17	5.7 143687	9	AC016572	Homo sapi
c 581	17	5.7 144062	5	AL954190	Zebrafish
c 582	17	5.7 144631	9	AC069027	Homo sapi
c 583	17	5.7 144649	2	AC145841	Macropus
c 584	17	5.7 144979	2	AC138597	Homo sapi
c 585	17	5.7 145085	2	AC090261	Homo sapi
c 586	17	5.7 145173	9	AC005599	Homo sapi
c 587	17	5.7 145629	2	BX322794	Danio rer
c 588	17	5.7 145829	2	BX571953	Danio rer
c 589	17	5.7 145913	2	AP005821	Danio rer
c 590	17	5.7 145947	9	AL353588	Human DNA
c 591	17	5.7 146170	2	AC079224	Human DNA
c 592	17	5.7 146275	2	AC080119	Homo sapi
c 593	17	5.7 146396	10	AL929449	Mouse DNA
c 594	17	5.7 146468	2	AC118126	Rattus no
c 595	17	5.7 146690	2	AC102254	Mus muscu
c 596	17	5.7 146810	9	AC084706	Homo sapi
c 597	17	5.7 146952	9	AC068522	Homo sapi
c 598	17	5.7 147008	2	AC138980	Homo sapi
c 599	17	5.7 147177	2	AC138981	Homo sapi
c 600	17	5.7 148003	2	BX537320	Danio rer
c 601	17	5.7 149085	2	AC123364	Rattus no
c 602	17	5.7 149143	2	AC092974	Homo sapi

c 603	17	5.7	148428	2	ACO10264	ACO10264 Homo sapi	660	17	5.7	159735	10	AL672101	AL672101 Mouse DNA
604	17	5.7	148559	9	AL139327	AL139327 Human DNA	661	17	5.7	160002	5	BX000446	BX000446 Zebrafish
605	17	5.7	149901	2	ACO22243	ACO22243 Homo sapi	662	17	5.7	160069	2	ACO64867	ACO64867 Homo sapi
c 606	17	5.7	150026	2	AL589868	AL589868 Homo sapi	663	17	5.7	160197	2	AC115700	AC115700 Mus muscu
607	17	5.7	150096	2	AC117562	AC117562 Mus muscu	c 664	17	5.7	160302	9	ACO10685	ACO10685 Homo sapi
c 608	17	5.7	150162	9	ACO26722	ACO26722 Homo sapi	c 665	17	5.7	160624	2	AC144418	AC144418 Rattus no
c 609	17	5.7	150350	9	CNS01DMW	AL138539 Human chr	666	17	5.7	161054	2	AC123744	AC123744 Mus muscu
c 610	17	5.7	150355	9	HS3364H10	AL078603 Human DNA	c 667	17	5.7	161364	2	ACO68637	ACO68637 Homo sapi
c 611	17	5.7	150399	9	ACO93680	ACO93680 Homo sapi	668	17	5.7	161638	9	AC107934	AC107934 Homo sapi
c 612	17	5.7	150400	10	AC122911	AC122911 Mus muscu	669	17	5.7	161672	2	AC136667	AC136667 Rattus no
c 613	17	5.7	150887	2	ACO18580	ACO18580 Homo sapi	670	17	5.7	162046	2	AC127375	AC127375 Mus muscu
c 614	17	5.7	151203	8	CNS09S4W	BX55875 Oryza sat	c 671	17	5.7	162075	9	HS127D3	AL021026 Human DNA
c 615	17	5.7	151319	9	AC108036	AC108036 Homo sapi	c 672	17	5.7	162151	9	AL138753	AL138753 Human DNA
616	17	5.7	151540	2	AL772252	AL772252 Homo sapi	c 673	17	5.7	162411	2	AC147061	AC147061 Pan trogl
617	17	5.7	151696	2	AP001768	AP001768 Homo sapi	c 674	17	5.7	162492	3	ACO95039	ACO95039 Drosophi1
618	17	5.7	151761	9	HS493D19	AL096868 Human DNA	c 675	17	5.7	162880	2	AC120363	AC120363 Mus muscu
619	17	5.7	151822	9	ACO04478	ACO04478 Homo sapi	676	17	5.7	162922	2	ACO11281	ACO11281 Homo sapi
620	17	5.7	152081	9	ACO07381	ACO07381 Homo sapi	c 677	17	5.7	162995	10	AL663032	AL663032 Mouse DNA
c 621	17	5.7	152246	9	ACO23473	ACO23473 Homo sapi	678	17	5.7	163066	2	AC116506	AC116506 Mus muscu
622	17	5.7	152454	2	ACO67909	ACO67909 Homo sapi	c 679	17	5.7	163110	2	ACO68705	ACO68705 Homo sapi
623	17	5.7	153064	8	CNS08CAL	AL831808 Oryza sat	c 680	17	5.7	163231	9	AL162575	AL162575 Human DNA
c 624	17	5.7	153155	2	ACO60783	ACO60783 Homo sapi	c 681	17	5.7	163357	2	ACO23276	ACO23276 Homo sapi
625	17	5.7	153319	2	AC136027	AC136027 Mus muscu	682	17	5.7	163404	2	AC118883	AC118883 Rattus no
626	17	5.7	153402	9	HS247E2	AL773569 Homo sapi	683	17	5.7	163443	5	AL773542	AL773542 Zebrafish
c 627	17	5.7	153553	2	AC124338	AC124338 Mus muscu	684	17	5.7	163706	2	AL354927	AL354927 Homo sapi
628	17	5.7	153716	9	AL590631	AL590631 Human DNA	c 685	17	5.7	163712	9	ACO04065	ACO04065 Homo sapi
629	17	5.7	154016	2	ACO91311	ACO91311 Mus muscu	c 686	17	5.7	164007	2	ACO69218	ACO69218 Homo sapi
c 630	17	5.7	154323	2	ACO91311	ACO91311 Homo sapi	687	17	5.7	164118	2	ACO21384	ACO21384 Homo sapi
c 631	17	5.7	154417	2	AC102530	AC102530 Mus muscu	688	17	5.7	164278	2	ACO73126	ACO73126 Homo sapi
c 632	17	5.7	154455	2	ACO21844	ACO21844 Homo sapi	689	17	5.7	164799	2	BX511121	BX511121 Dario rer
633	17	5.7	154604	5	AL954739	AL954739 Zebrafish	c 690	17	5.7	165011	9	AL445255	AL445255 Human DNA
c 634	17	5.7	154753	2	ACO20605	ACO20605 Homo sapi	691	17	5.7	165089	9	ACO21646	ACO21646 Homo sapi
635	17	5.7	154758	9	AC112491	AC112491 Homo sapi	c 692	17	5.7	165768	2	ACO23517	ACO23517 Homo sapi
c 636	17	5.7	155326	9	CNS07E2	AL512311 Human chr	693	17	5.7	165798	2	AC117794	AC117794 Mus muscu
637	17	5.7	155394	2	ACO92328	ACO92328 Homo sapi	694	17	5.7	166007	9	CNS01DRC	AL553093 Human DNA
c 638	17	5.7	156008	9	AL353093	AL353093 Homo sapi	695	17	5.7	166071	2	ACO22336	ACO22336 Homo sapi
c 639	17	5.7	156142	3	ACO91228	ACO91228 Homo sapi	c 696	17	5.7	166168	2	AC115193	AC115193 Rattus no
c 640	17	5.7	156190	2	ACO97651	ACO97651 Homo sapi	697	17	5.7	166174	2	ACO09633	ACO09633 Homo sapi
c 641	17	5.7	156232	8	AC108884	AC108884 Oryza sat	698	17	5.7	166231	9	AL773537	AL773537 Human DNA
c 642	17	5.7	156332	10	AC116581	AC116581 Mus muscu	c 699	17	5.7	166252	9	ACO22413	ACO22413 Homo sapi
c 643	17	5.7	156392	2	ACO26341	ACO26341 Homo sapi	700	17	5.7	166551	2	BX890591	BX890591 Dario rer
644	17	5.7	157067	2	AC137265	AC137265 Rattus no	c 701	17	5.7	166651	4	ACO87160	ACO87160 Sus scrofa
c 645	17	5.7	157393	2	ACO36212	ACO36212 Homo sapi	702	17	5.7	166716	9	AC108482	AC108482 Homo sapi
c 646	17	5.7	157591	2	BX323068	BX323068 Dario rer	c 703	17	5.7	167162	2	AC139872	AC139872 Rattus no
c 647	17	5.7	157747	2	ACO67915	ACO67915 Homo sapi	c 704	17	5.7	167214	2	ACO96202	ACO96202 Homo sapi
c 648	17	5.7	157816	9	ACO93666	ACO93666 Homo sapi	705	17	5.7	167853	2	AP001798	AP001798 Homo sapi
649	17	5.7	157949	9	AL355578	AL355578 Human DNA	706	17	5.7	167974	9	AL591073	AL591073 Human DNA
c 650	17	5.7	158549	9	HS796CA	297200 Human DNA	707	17	5.7	168043	2	ACO11935	ACO11935 Homo sapi
651	17	5.7	158600	2	BX296541	BX296541 Dario rer	c 708	17	5.7	168108	9	AL445687	AL445687 Human DNA
652	17	5.7	158684	2	ACO79493	ACO79493 Mus muscu	c 709	17	5.7	168197	9	ACO23307	ACO23307 Homo sapi
653	17	5.7	158830	10	AC131740	AC131740 Mus muscu	710	17	5.7	168306	3	ACO08135	ACO08135 Drosophi1
c 654	17	5.7	159013	2	BX323995	BX323995 Dario rer	711	17	5.7	168431	2	BX470138	BX470138 Dario rer
c 655	17	5.7	159024	2	ACO25495	ACO25495 Homo sapi	c 712	17	5.7	168843	2	ACO91711	ACO91711 Rattus no
656	17	5.7	159188	2	ACO37432	ACO37432 Homo sapi	713	17	5.7	168996	2	ACO15785	ACO15785 Homo sapi
c 657	17	5.7	159242	2	ACO78800	ACO78800 Homo sapi	c 714	17	5.7	169083	2	AL355346	AL355346 Homo sapi
c 658	17	5.7	159300	9	HS279E22	AL662879 Homo sapi	c 715	17	5.7	169479	2	BX890540	BX890540 Dario rer
c 659	17	5.7	159331	9	AL589741	AL589741 Human DNA	716	17	5.7	169557	9	ACO24706	ACO24706 Homo sapi

717	17	5.7 169570	5	AL928989	AL928989 Zebrafish	774	17	5.7 177083	3	AC068285	AC068285 Drosophila
718	17	5.7 169628	5	BK322567	BK322567 Zebrafish	775	17	5.7 177112	9	AC002452	AC002452 Homo sapi
719	17	5.7 170001	9	HS4921	AL021917 Human DNA	776	17	5.7 177121	2	AC010955	AC010955 Homo sapi
720	17	5.7 170311	9	AC021701	AC021701 Homo sapi	777	17	5.7 177145	2	AC113156	AC113156 Homo sapi
721	17	5.7 170625	2	AC144620	AC144620 Mus muscu	778	17	5.7 177202	2	AC118703	AC118703 Mus muscu
722	17	5.7 170682	2	AC021245	AC021245 Homo sapi	779	17	5.7 177528	2	AC093444	AC093444 Pan trogl
723	17	5.7 170793	9	AC044907	AC044907 Homo sapi	780	17	5.7 177599	2	AC097630	AC097630 Homo sapi
724	17	5.7 170817	9	AL131366	AL131366 Human DNA	781	17	5.7 177797	2	AC140039	AC140039 Sus scrofa
725	17	5.7 170849	2	AC109803	AC109803 Homo sapi	782	17	5.7 177812	2	AC133226	AC133226 Mus muscu
726	17	5.7 170923	2	AC110042	AC110042 Mus muscu	783	17	5.7 178311	9	AC104795	AC104795 Homo sapi
727	17	5.7 171206	2	AC026573	AC026573 Homo sapi	784	17	5.7 178742	2	AC134807	AC134807 Rattus nor
728	17	5.7 171375	3	AC007082	AC007082 Drosophila	785	17	5.7 179269	9	AC093627	AC093627 Homo sapi
729	17	5.7 171686	9	AC142284	AC142284 Pan trogl	786	17	5.7 179270	9	AC104580	AC104580 Homo sapi
730	17	5.7 171721	9	AC022821	AC022821 Homo sapi	787	17	5.7 179437	5	AL928892	AL928892 Zebrafish
731	17	5.7 171742	2	BK97662	BK97662 Dantio rer	788	17	5.7 179767	2	AC114584	AC114584 Mus muscu
732	17	5.7 171887	2	AL356355	AL356355 Homo sapi	789	17	5.7 180000	2	AC004578	AC004578 Homo sapi
733	17	5.7 171930	2	AC118687	AC118687 Mus muscu	790	17	5.7 180104	9	DJ526N18	DJ526N18 Homo sapi
734	17	5.7 172018	2	AC107672	AC107672 Mus muscu	791	17	5.7 180166	2	AC011898	AC011898 Homo sapi
735	17	5.7 172475	9	AL358972	AL358972 Homo sapi	792	17	5.7 180179	2	AC018881	AC018881 Homo sapi
736	17	5.7 172606	9	AL358972	AL358972 Human DNA	793	17	5.7 180273	2	AP002894	AP002894 Homo sapi
737	17	5.7 173031	9	AL359953	AL359953 Human DNA	794	17	5.7 180359	2	AC022064	AC022064 Homo sapi
738	17	5.7 173045	2	AC120413	AC120413 Mus muscu	795	17	5.7 180534	2	CNS08CB7	CNS08CB7 Homo sapi
739	17	5.7 173177	2	AC102661	AC102661 Mus muscu	796	17	5.7 180658	2	AC023956	AC023956 Homo sapi
740	17	5.7 173316	9	AL353754	AL353754 Human DNA	797	17	5.7 180766	2	AC090691	AC090691 Homo sapi
741	17	5.7 173415	9	CNS01DVS	AL136018 Human chr	798	17	5.7 180947	2	AC128079	AC128079 Rattus nor
742	17	5.7 173564	5	BK470230	BK470230 Zebrafish	799	17	5.7 180995	9	AC117500	AC117500 Homo sapi
743	17	5.7 173756	2	AC134948	AC134948 Rattus nor	800	17	5.7 181033	10	AL731663	AL731663 Homo sapi
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745	17	5.7 173911	9	AL354992	AL354992 Human DNA	802	17	5.7 181124	2	AP002390	AP002390 Homo sapi
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 ORGANISM
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 Staphylococcus aureus subsp. aureus Mu50
 Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE
 AUTHORS
 Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
 Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Iino, J., Ito, T., Kanamori, H.,
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 Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,
 Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.
 Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus
 Lancet 357 (9264), 1225-1240 (2001)
 JOURNAL
 MEDLINE
 21311952
 PUBMED
 11418146
 REFERENCE
 2 (bases 1 to 348527)
 AUTHORS
 Ohta, T.
 TITLE
 Direct Submission
 Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
 of Medical Technology and Nursing, Department of Medical
 Technology; 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan
 (E-mail: tohta@tsukuba.ac.jp, Tel: 81-298-53-3454,
 Fax: 81-298-53-3454)
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 On May 29, 2001 this sequence version replaced gi:13874937.
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VIDYLNKSTFEFSFKYGNVIKEYHDKLAFLKVEKODENSELELQKIAFNETKT
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Query Match 60.9%; Score 181; DB 1; Length 34857;
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Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 58 ATCATAGCGAAATATTCATGTTAAGCATTTAAGCATATTCATTTAAAGGT 117
DB 230695 ATCATAGCGAAATATTCATGTTAAGCATTTAAGCATATTCATTTAAAGGT
230754

OY 118 CATATGGGATATCAATACAGTTAAAGATGAACAGTACCAATTAACATGCTTAT 177
DB 230755 CATATGGGATATCAATACAGTTAAAGATGAACAGTACCAATTAACATGCTTAT
230814
OY 178 GTGGTAGTAGAATGACTAGATATGGCATGACTATTTACCAAGCATAGTAA 237
DB 230815 GTGGTAGTAGAATGACTAGATATGGCATGACTATTTACCAAGCATAGTAA
230874
OY 238 TGGATTGAAGGAAACAGACAGACAGACTAATTAAGTACATGA 289
DB 230875 TGGATTGAAGGAAACAGACAGACAGACTAATTAAGTACATGA 230926
RESULT 7
LOCUS AB009866 41401 bp DNA linear PHG 23-MAY-2000
DEFINITION Bacteriophage phi PVL proviral DNA, complete sequence.
ACCESSION AB009866
VERSION AB009866.2 GI:8051688
KEYWORDS dUTPase; ssDNA binding protein; anti repressor; repressor;
integrase; LukF-PV; LukS-PV; holin; amidase (peptidoglycan
hydrolase); capsid protein; portal protein.
SOURCE Staphylococcus aureus bacteriophage PVL
ORGANISM Staphylococcus aureus bacteriophage PVL
1 (strains)
REFERENCE Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
AUTHORS Pantone-valentine leukocidin genes in a phage-like particle isolated
TITLE from mltomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 98067870
PUBMED 9404084
REFERENCE 2 (strains)
AUTHORS Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE Complete nucleotide sequence and molecular characterization of the
JOURNAL complete staphylococcal bacteriophage phiPVL carrying
Gene 215 (1), 57-67 (1998)
MEDLINE 98332719
PUBMED 9666077
REFERENCE 3 (bases 1 to 41401)
AUTHORS Kaneko,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1997) Jun Kaneko, Tohoku University, Dept. Appl.
Biol. Chem., Faculty of Agriculture, 1-1 Tsutsumi-dori
Aramiyamachi, Aoba-ku, Sendai, Miyagi 981, Japan
(E-mail: j.kaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-717-8780)
COMMENT On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
FEATURES
source location/Qualifiers
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QYMEPVEKEKRTIKRYEYTSVNTDEQVTVADATKQISATTEPSCQKVTYATBQR
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Query Match 57.9%; Score 172; DB 7; Length 41401;
Best Local Similarity 99.3%; Pred. No. 3.5e-83;
Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 30540 GGAGGAAGTCAAGATGTATTACGAATAAGCGAATTCATACGCAAAAATATTCATGTTAA 30599
|||||
QY 84 CGGATTCGATTTTAAGCTATTCATTTTAAAGTCATATGGGCATTCATACAACTTAA 143
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DB 30600 CGGATTCGATTTTAAGCTATTCATTTTAAAGTCATATGGGCATTCATACAACTTAA 30659
QY 144 AGATATGAACAAGTACCAATTTAAACATCCTTATGCTAGATGAGATGACTAGATAT 203
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DB 30660 AGATATGAACAAGTACCAATTTAAACATCCTTATGCTAGATGAGATGACTAGATAT 30719
QY 204 GGATTCACACTTATTACCAAGCATATGATGAATGGATTGAAGAGAACACAGCAACA 263
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DB 30720 GGATTCACACTTATTACCAAGCATATGATGAATGGATTGAAGAGAACACAGCAACA 30779
QY 264 GGACAGACTAATTAAGTACATGAAATGGTAG 297
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DB 30780 GGACAGACTAATTAAGTACATGAAATGGTAG 30813

RESULT 8
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS
DEFINITION Staphylococcus aureus temperate phage phiSLT genomic DNA, complete
sequence.
ACCESSION
AB045978
AB045978.1 GI:12697822
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL
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Staphylococcus aureus temperate phage phiSLT
Staphylococcus aureus temperate phage phiSLT
Virus; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (sites)
Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J.
and Kamio,Y.
Phage conversion of Pantone-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phiSLT
Gene 266 (1-2), 193-206 (2001)
21261956
11368915
2 (bases 1 to 42942)
Kaneko,J., Narita,S. and Kamio,Y.
Direct Submission
Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural Sciences, 1-1 Tsutsunimadori Amamiyamachi,
Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-747-8780)
Location/Qualifiers
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DB 7294 ATCTACGGAAAAATTCATGTTAAGCATTCATTTTAAGCATTCATTTAAAGGT 733
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QY 118 CATATGGCATTCATATACAGTTAAAGATATGAACAGTACCATTTAAACATGCTAT 177
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DB 7354 CATATGGCATTCATATACAGTTAAAGATATGAACAGTACCATTTAAACATGCTTAT 7413
QY 178 GTGTATGATGAGTACTAGATATGCGATCATCTTAT 218
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RESULT 9
AP001553 43081 bp DNA circular PHG 14-MAR-2001
LOCUS
DEFINITION Bacteriophage phi ETA DNA, complete genome.
ACCESSION AP001553
VERSION AP001553.1 GI:8918415
KEYWORDS
SOURCE Bacteriophage phi ETA
ORGANISM Bacteriophage phi ETA
Virus; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
1 (ates)
REFERENCE
AUTHORS Yamaguchi,T., Hayashi,T., Takami,H., Nakasone,K., Ohnishi,M.,
Nakayama,K., Yamada,S., Komatsuzawa,H. and Sugai,M.
TITLE Phage conversion of exfoliative toxin A production in
Staphylococcus aureus
JOURNAL Mol. Microbiol. 38 (4), 694-705 (2000)
MEDLINE 20566787
PUBMED 1115106
REFERENCE
AUTHORS 2 (bases 1 to 43081)
TITLES Sugai,M., Yamaguchi,T., Hayashi,T., Nakasone,K. and Takami,H.
JOURNAL Direct Submission
SUBMITTED (28-MAR-2000) Motoyuki Sugai, Hiroshima University
Faculty of Dentistry, Microbiology; Kasumi 1-2-3, Hiroshima,
Hiroshima 734-8553, Japan (E-mail:sugai@hiroshima-u.ac.jp,
Tel:81-82-257-5637, Fax:81-82-257-5639)
FEATURES
source
location/Qualifiers
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CDS

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TITLE	Staphylococcus aureus proteins and nucleic acids
JOURNAL	Patent: WO 02094866-A 1209 28-NOV-2002;
Chiron Spa (IT)	
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	/organism="Staphylococcus aureus"
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RESULT 12	
LOCUS	AF424783 42722 bp DNA linear PHG 10-JUN-2002
DEFINITION	Staphylococcus aureus phage phi 13, complete genome.
ACCESSION	AF424783
VERSION	AF424783.1 GI:18920591
KEYWORDS	
SOURCE	Staphylococcus aureus phage phi 13
ORGANISM	Staphylococcus aureus phage phi 13
REFERENCE	1 (bases 1 to 42722)
AUTHORS	Iandolo,J.J., Worrell,V., Groicher,K.H., Qian,Y., Tlan,R.,
	Kenton,S., Dorman,A., Ji,H., Lin,S., Loh,P., Qi,S., Zhu,H. and
	Roe,B.A.
TITLE	Comparative analysis of the genomes of the temperate bacteriophages
JOURNAL	phi11, phi12 and phi13 of Staphylococcus aureus 8325
MEDLINE	Genes 289 (1-2), 109-118 (2002)
PMID	22032962
REFERENCE	2 (bases 1 to 42722)
AUTHORS	Iandolo,J.J., Worrell,V., Roe,B., Qian,Y., Dorman,A., Tlan,R.,
	Lin,S. and Ji,H.
TITLE	Direct Submission
JOURNAL	Submitted (26-SEP-2001) Microbiology and Immunology, Univ. of
	Oklahoma Health Sciences Center, 940 S.L. Young Bvd, Oklahoma City,
	OK 73190, USA
FEATURES	
source	Location/Qualifiers
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
233 ATGAATGATTTGAAGACACAGACGAA 261
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DB 7035 ATGAATGATTTGAAGACACAGACGAA 7063
RESULT 13
AP004828/c
LOCUS
DEFINITION
Staphylococcus aureus subsp. aureus MW2 DNA, complete genome,
strain:MW2, section 7/10.
AP004828 BA000033
AP004828.1 GI:21204850
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus subsp. aureus MW2
Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
AUTHORS
1
Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
Nagai,Y., Iwama,N., Asano,K., Naito,T., Kuroda,H., Cui,L.,
Yamanoto,K. and Hiramatsu,K.
Genome and virulence determinants of high virulence
community-acquired MRSA
Lancet 359 (9320), 1815-1827 (2002)
22040717
PUBMED
12044378
REFERENCE
2 (bases 1 to 272850)
Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
Direct Submission
Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center, 2Chome 49-10 Nishihara, Shiba-ku, Tokyo 151-0066, Japan
(E-mail:bioelite.go.jp, URL:http://www.bio.elite.go.jp/
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.00013;
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DB 256595 ATGAATGATTGAAGACACACAGCAA 256567
RESULT 14
AR355085 580 bp DNA linear PAT 17-AUG-2003
LOCUS AR355085
DEFINITION Sequence 1203 from patent US 6593114.
ACCESSION AR355085
VERSION AR355085.1 GI:33761169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 580)
AUTHORS Kunach,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
Rosen,C.A.

TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 1203 15-JUL-2003;
FEATURES
source Location/Qualifiers
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ORIGIN
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OY 270 ACTAATTAAGTCTAGTCATGAATGCTAG 297
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DB 437 ACTAATTAAGTCTAGTCATGAATGCTAG 464
RESULT 15
BD245634 43594 bp DNA linear PAT 17-JUL-2003
LOCUS BD245634
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245634
VERSION BD245634.1 GI:33055404
KEYWORDS JP 2002531107-A/369.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 43594)
AUTHORS Pelletier,J., Gros,P., and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 369 24-SEP-2002;
COMMENT PHARGETECH INC
OS Staphylococcus aureus bacteriophage 96
PN JP 2002531107-A/369
PD 24-SEP-2002
PE 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER,PHILIPPE GROS,MICHAEL DUBOW
PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
PC C12M1/00,
PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
C12N15/00,
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/db_xref="taxon:32644"
ORIGIN

Query Match 9.48; Score 28; DB 6; Length 43594;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 ACTAATTACTAGTCATGAATGGTAG 297
|||||
DB 5253 ACTAATTACTAGTCATGAATGGTAG 5280

Search completed: October 15, 2004, 03:33:13
Job time : 154.87 secs

GenCore version 5.1.6
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OK nucleic - nucleic search, using SW model

Run on: October 14, 2004, 18:55:29 ; Search time 198.132 Seconds
(without alignments)
6368.040 Million cell updates/sec

Title: US-09-407-804A-9

Perfect score: 297
Sequence: 1 atgttcataataaacgaaa.....acttgcatgaatgtag 297

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 212409041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_29jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2010s:*
5: geneseqn2010s:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	297	100.0	297	3	AAA68253 Bacterioph
2	297	100.0	41708	3	AAA68247 Bacterioph
3	297	100.0	41708	4	AAC86106 Complete
4	261	87.9	261	3	AAA68250 Bacterioph
5	29	9.8	267	7	ACF72925 Staphyloc
6	28	9.4	380	2	AAV75314 Staphyloc
7	28	9.4	43576	3	AAA68609 Bacterioph

8	25	8.4	258	7	ACF73076	AcF73076	Staphyloc	c	65	17	5.7	6177	6	ABL34513	Ab134513	Human met
9	19	6.4	988	2	AAO40104	AAO40104	FPV p2 pr	c	66	17	5.7	6177	6	AA63323	AA63323	Chemical1
c	10	19	6.4	7037	6	AB133751	Human imm	c	67	17	5.7	6177	6	AA56777	AA56777	Tumour au
c	11	18	6.4	266145	9	ADB87477	Fowlpox v	c	68	17	5.7	6177	4	AB109908	AB109908	Drosophil
c	12	18	6.1	1045	6	AB407010	Oligonuc1	c	69	17	5.7	7320	2	AAV52253	AAV52253	Strepococ
c	13	18	6.1	1045	6	AB407011	Oligonuc1	c	70	17	5.7	7672	9	ADB31308	ADB31308	Testoster
c	14	18	6.1	1049	6	ABQ29061	Oligonuc1	c	71	17	5.7	7787	6	ABL66696	ABL66696	Human imm
c	15	18	6.1	1049	6	ABQ29060	Oligonuc1	c	72	17	5.7	8303	6	ABL32422	ABL32422	Human che
c	16	18	6.1	1298	6	ABO13225	Oligonuc1	c	73	17	5.7	10710	6	ABN79997	ABN79997	Human che
c	17	18	6.1	1298	6	ABO13224	Oligonuc1	c	74	17	5.7	10925	4	ABL19664	ABL19664	Drosophil
c	18	18	6.1	2000	7	ABE217032	Arabi1dops	c	75	17	5.7	14899	4	ABL20584	ABL20584	Drosophil
c	19	18	6.1	2000	7	ABE217032	Arabi1dops	c	76	17	5.7	14899	4	ABL20584	ABL20584	Drosophil
c	20	18	6.1	2352	5	ABV22257	Gene sequ	c	77	17	5.7	19814	6	AB170609	AB170609	Human fla
c	21	18	6.1	2352	5	ABV28094	Human pro	c	78	17	5.7	25464	2	AAU57274	AAU57274	Human fla
c	22	18	6.1	3754	4	AAK51990	Human pol	c	79	17	5.7	27062	4	AAU71622	AAU71622	Human fla
c	23	18	6.1	82588	3	AAE22301	Human pol	c	80	17	5.7	27062	4	ABL05346	ABL05346	Human rep
c	24	18	6.1	110000	3	AAE22305	BAC conta	c	81	17	5.7	27062	4	ABL198215	ABL198215	Human tes
c	25	18	6.1	129722	6	ABQ898117	Continuati	c	82	17	5.7	110000	6	ABQ69245	ABQ69245	Continuati
c	26	18	6.1	147419	6	ABR898117	Continuati	c	83	17	5.7	110000	6	ABQ69245	ABQ69245	Continuati
c	27	17	5.7	100	7	ACD69949	Human ost	c	84	17	5.7	110000	7	ABQ67197	ABQ67197	Continuati
c	28	17	5.7	100	7	ACD69949	Human ost	c	85	17	5.7	110000	8	ABQ67197	ABQ67197	Continuati
c	29	17	5.7	232	7	ABX88598	E. coli K	c	86	17	5.7	269223	4	AAI33411	AAI33411	Continuati
c	30	17	5.7	313	5	ABY16310	Corn ear-	c	87	17	5.7	269223	4	AAI28354	AAI28354	Continuati
c	31	17	5.7	401	6	AA561653	Human pro	c	88	16	5.4	158	3	AAI11835	AAI11835	Genomic f
c	32	17	5.7	441	7	ABX07400	Lung smel	c	89	16	5.4	158	3	AAI11926	AAI11926	Genomic f
c	33	17	5.7	494	5	ABV46108	S. pneumo	c	90	16	5.4	159	7	ACEF73137	ACEF73137	Human sec
c	34	17	5.7	585	5	ABV48133	Human pro	c	91	16	5.4	240	7	ABZ54034	ABZ54034	Staphyloc
c	35	17	5.7	623	6	ABQ31645	Human pro	c	92	16	5.4	306	2	AAE71132	AAE71132	Aspergill
c	36	17	5.7	624	6	ABQ31644	Oligonuc1	c	93	16	5.4	320	7	ABE217653	ABE217653	Human gen
c	37	17	5.7	624	6	ABQ43382	Oligonuc1	c	94	16	5.4	327	2	AAV66788	AAV66788	EST clone
c	38	17	5.7	624	6	ABQ43383	Oligonuc1	c	95	16	5.4	337	3	AAZ34801	AAZ34801	Soybean m
c	39	17	5.7	637	5	ABV18347	Human pro	c	96	16	5.4	367	4	AAI61632	AAI61632	Human sec
c	40	17	5.7	703	6	ABO17127	Oligonuc1	c	97	16	5.4	375	7	ABX932197	ABX932197	Human pol
c	41	17	5.7	703	6	ABO17126	Oligonuc1	c	98	16	5.4	399	6	ABL40795	ABL40795	Human ova
c	42	17	5.7	768	6	ABQ17133	Oligonuc1	c	99	16	5.4	413	6	ABN75590	ABN75590	Human pro
c	43	17	5.7	768	6	ABO17132	Oligonuc1	c	100	16	5.4	414	4	AAK63511	AAK63511	Human ORF
c	44	17	5.7	785	4	AAI95756	Human neu	c	101	16	5.4	414	4	AAK64652	AAK64652	Human ORF
c	45	17	5.7	785	7	ABT42880	Human neu	c	102	16	5.4	414	4	AAK64652	AAK64652	Human ORF
c	46	17	5.7	801	7	ACA38940	Human neu	c	103	16	5.4	420	8	ADA32128	ADA32128	Human pro
c	47	17	5.7	805	6	ABQ48243	Prokaryot	c	104	16	5.4	434	6	ADAA32128	ADAA32128	DNA encod
c	48	17	5.7	805	6	ABQ48242	Oligonuc1	c	105	16	5.4	437	6	ABL40785	ABL40785	Human pro
c	49	17	5.7	868	2	AAV65217	DNA encod	c	106	16	5.4	437	6	ABL40780	ABL40780	Human pro
c	50	17	5.7	1005	6	ABQ46572	Oligonuc1	c	107	16	5.4	440	6	ABL61734	ABL61734	Human pro
c	51	17	5.7	1005	6	ABQ46573	Oligonuc1	c	108	16	5.4	440	6	ABL40786	ABL40786	Human pro
c	52	17	5.7	1947	8	AD32469	DNA encod	c	109	16	5.4	440	6	ABL40788	ABL40788	Human pro
c	53	17	5.7	2000	6	ABE15696	Arabi1dops	c	110	16	5.4	441	6	ABL40782	ABL40782	Human pro
c	54	17	5.7	3105	7	ACC57779	Restri1ct	c	111	16	5.4	441	6	ABL40789	ABL40789	Human pro
c	55	17	5.7	3509	9	ADBE6038	Medaka Rk	c	112	16	5.4	446	6	ABL40787	ABL40787	Human pro
c	56	17	5.7	3566	4	AB127603	Drosophil	c	113	16	5.4	446	6	ABL40784	ABL40784	Human pro
c	57	17	5.7	3678	9	ADD47480	Human gen	c	114	16	5.4	439	6	ABL40793	ABL40793	Human pro
c	58	17	5.7	3678	9	ADD47480	Human gen	c	115	16	5.4	460	8	ACH34973	ACH34973	Human pro
c	59	17	5.7	4731	4	AB147484	Human gen	c	116	16	5.4	468	6	ABL40782	ABL40782	Human end
c	60	17	5.7	5355	2	AAH89221	Seq ID No	c	117	16	5.4	472	6	ABL40780	ABL40780	Human pro
c	61	17	5.7	5355	2	AAH89220	Seq ID No	c	118	16	5.4	482	9	ADB57006	ADB57006	Toxicity-
c	62	17	5.7	5355	3	AAZ39405	Human tra	c	119	16	5.4	481	6	ABL40780	ABL40780	Human pro
c	63	17	5.7	5355	3	AAZ39404	Human tra	c	120	16	5.4	503	6	ABQ36162	ABQ36162	Oligonuc1
c	64	17	5.7	5814	5	AA5823231	DNA encod	c	121	16	5.4	503	6	ABQ36163	ABQ36163	Oligonuc1

c 122	16	5.4	505	6	ABQ19232	Abq19232 Oligonuc1	179	16	5.4	843	8	ADK32002	Adk32002 DNA encod
c 123	16	5.4	505	6	ABQ19233	Abq19233 Oligonuc1	c 180	16	5.4	868	6	ABQ21406	Abq21406 Oligonuc1
c 124	16	5.4	520	6	ABQ44923	Abq44923 Oligonuc1	181	16	5.4	868	6	ABQ21407	Abq21407 Oligonuc1
c 125	16	5.4	520	6	ABQ44922	Abq44922 Oligonuc1	c 182	16	5.4	871	4	AAH04183	Aah04183 Human c1N
c 126	16	5.4	525	7	ABX07672	Abx07672 S. pneumo	c 183	16	5.4	921	2	AAZ96435	Aaz96435 S. pneumo
c 127	16	5.4	527	6	ABQ44121	Abq44121 Oligonuc1	c 184	16	5.4	962	4	AAI11883	Aai11883 Probe #18
c 128	16	5.4	527	6	ABQ44120	Abq44120 Oligonuc1	c 185	16	5.4	962	4	ABK53584	Abk53584 Human foe
c 129	16	5.4	529	6	ABQ36883	Abq36883 Oligonuc1	c 186	16	5.4	962	4	AAI33210	Aai33210 Probe #18
c 130	16	5.4	529	6	ABQ36882	Abq36882 Oligonuc1	c 187	16	5.4	962	4	ABK43165	Abk43165 Human bre
c 131	16	5.4	529	9	ADBI7704	Adbi7704 DNA (Seqi	c 188	16	5.4	962	4	AAK23339	Aak23339 Probe #18
c 132	16	5.4	533	6	ABL40778	Abi40778 Human pro	c 189	16	5.4	962	4	AAK27309	Aak27309 Human bon
c 133	16	5.4	540	4	AAH11653	Aah11653 Human c1N	c 190	16	5.4	962	4	AAK01850	Aak01850 Human bra
c 134	16	5.4	570	4	AAI21091	Aai21091 Probe #11	c 191	16	5.4	962	4	AAK26883	Aak26883 Human liv
c 135	16	5.4	570	4	ABA66169	Ab66169 Human foe	c 192	16	5.4	962	5	AAI01821	Aai01821 Probe #18
c 136	16	5.4	570	4	ABA46353	Ab46353 Probe #15	c 193	16	5.4	962	6	ABK01829	Abk01829 Human gen
c 137	16	5.4	570	4	ABA48285	Ab48285 Human bre	c 194	16	5.4	993	6	ABL40772	Abi40772 Human gen
c 138	16	5.4	570	4	ABA33236	Ab33236 Probe #11	c 195	16	5.4	1005	6	ABQ32651	Abq32651 Oligonuc1
c 139	16	5.4	570	4	AAK40334	Aak40334 Human bon	c 196	16	5.4	1005	6	ABQ32650	Abq32650 Oligonuc1
c 140	16	5.4	570	4	AAK14588	Aak14588 Human bra	c 197	16	5.4	1115	6	ABQ16977	Abq16977 Oligonuc1
c 141	16	5.4	570	4	ABS39904	Ab339904 Human liv	c 198	16	5.4	1115	6	ABQ16976	Abq16976 Oligonuc1
c 142	16	5.4	570	5	AAI06811	Aai06811 Probe #68	c 199	16	5.4	1120	3	AAK46000	Aak46000 Arabidops
c 143	16	5.4	570	6	ABK14351	Abk14351 Human gen	c 200	16	5.4	1162	3	AAK74355	Aak74355 Human sec
c 144	16	5.4	582	6	ABQ22933	Abq22933 Oligonuc1	c 201	16	5.4	1254	7	ABX07332	Abx07332 S. pneumo
c 145	16	5.4	582	6	ABQ22932	Abq22932 Oligonuc1	c 202	16	5.4	1254	7	ABX06512	Abx06512 S. pneumo
c 146	16	5.4	586	6	ABQ23826	Abq23826 Oligonuc1	c 203	16	5.4	1260	2	AAK43925	Aak43925 Sequence
c 147	16	5.4	586	6	ABQ23827	Abq23827 Oligonuc1	c 204	16	5.4	1260	2	AAK72049	Aak72049 Sequence
c 148	16	5.4	599	6	ABQ49931	Abq49931 Oligonuc1	c 205	16	5.4	1269	6	ABQ07670	Abq07670 S. pneumo
c 149	16	5.4	599	6	ABQ49930	Abq49930 Oligonuc1	c 206	16	5.4	1324	7	ACK44808	Ack44808 Prokaryot
c 150	16	5.4	601	6	ABQ16468	Abq16468 Oligonuc1	c 207	16	5.4	1488	7	ADK31956	Adk31956 Human pro
c 151	16	5.4	601	6	ABQ16469	Abq16469 Oligonuc1	c 208	16	5.4	1532	6	ABL40773	Abi40773 Human pro
c 152	16	5.4	602	6	ABQ28649	Abq28649 Oligonuc1	c 209	16	5.4	1532	6	ABL40775	Abi40775 Human pro
c 153	16	5.4	602	6	ABQ28648	Abq28648 Oligonuc1	c 210	16	5.4	1532	6	ADK31956	Adk31956 Human nov
c 154	16	5.4	607	6	ABQ13791	Abq13791 Oligonuc1	c 211	16	5.4	1572	9	ABK63579	Abk63579 Rat seque
c 155	16	5.4	607	6	ABQ13790	Abq13790 Oligonuc1	c 212	16	5.4	1592	6	ADK63579	Adk63579 Rat seque
c 156	16	5.4	610	6	ABQ17906	Abq17906 Oligonuc1	c 213	16	5.4	1592	9	ADK63579	Adk63579 Rat seque
c 157	16	5.4	610	6	ABQ17907	Abq17907 Oligonuc1	c 214	16	5.4	1592	9	ADK63579	Adk63579 Rat seque
c 158	16	5.4	617	5	ABY58971	Ab58971 Human pro	c 215	16	5.4	1716	4	AAH14069	Aah14069 Human c1N
c 159	16	5.4	621	7	ABZ42307	Abz42307 Streptoco	c 216	16	5.4	1735	4	AAK51789	Aak51789 Strephylot
c 160	16	5.4	648	6	ABQ48108	Abq48108 Oligonuc1	c 217	16	5.4	1755	7	ABT14961	Abt14961 Pathogen
c 161	16	5.4	648	6	ABQ48109	Abq48109 Oligonuc1	c 218	16	5.4	1755	7	ACF74079	Acf74079 Staphyloc
c 162	16	5.4	665	4	AAK78214	Aak78214 Human imm	c 219	16	5.4	1758	4	AAK54885	Aak54885 Staphyloc
c 163	16	5.4	665	4	AAK78215	Aak78215 Human imm	c 220	16	5.4	1758	7	ACK20340	Ack20340 Prokaryot
c 164	16	5.4	675	6	ABQ25447	Abq25447 Oligonuc1	c 221	16	5.4	1778	6	ABQ45202	Abq45202 Oligonuc1
c 165	16	5.4	675	6	ABQ25446	Abq25446 Oligonuc1	c 222	16	5.4	1778	6	ABQ45203	Abq45203 Oligonuc1
c 166	16	5.4	700	4	AAH93105	Aah93105 Human inf	c 223	16	5.4	1785	2	AAV65219	Aav65219 DNA encod
c 167	16	5.4	700	4	AAH93104	Aah93104 Human inf	c 224	16	5.4	1785	2	AAV65219	Aav65219 DNA encod
c 168	16	5.4	716	4	AAH94861	Aah94861 Human neu	c 225	16	5.4	1803	7	ADK68440	Adk68440 Arabidops
c 170	16	5.4	726	6	ABQ47367	Abq47367 Oligonuc1	c 226	16	5.4	1803	7	ADK68440	Adk68440 Arabidops
c 171	16	5.4	726	6	ABQ47366	Abq47366 Oligonuc1	c 227	16	5.4	1932	7	ACK30294	Ack30294 Prokaryot
c 172	16	5.4	727	6	ABQ22702	Abq22702 Oligonuc1	c 228	16	5.4	1964	4	AAH15484	Aah15484 Human c1N
c 173	16	5.4	727	6	ABQ22703	Abq22703 Oligonuc1	c 229	16	5.4	2000	6	ABZ17385	Abz17385 Arabidops
c 174	16	5.4	739	6	ABL40776	Abi40776 Human pro	c 230	16	5.4	2025	7	AAZ76335	Aaz76335 L. cuprifin
c 175	16	5.4	775	6	ABL40777	Abi40777 Human pro	c 231	16	5.4	2157	5	AAK583775	Aak583775 DNA encod
c 176	16	5.4	792	6	ABQ13798	Abq13798 Oligonuc1	c 232	16	5.4	2181	7	ADK53781	Adk53781 Human cod
c 177	16	5.4	792	6	ABQ13799	Abq13799 Oligonuc1	c 233	16	5.4	2257	5	AAK583773	Aak583773 DNA encod
c 178	16	5.4	815	6	ABQ29894	Abq29894 Oligonuc1	c 234	16	5.4	2307	5	AAK79636	Aak79636 Eucel1yphu
							c 235	16	5.4	2315	2	AAV52327	Aav52327 Streptoco

c 236	16	5.4	2545	4	AAH14381	AbH14381 Human cDN	c 293	16	5.4	7312	6	AA561350	AA561350 Human gen
c 237	16	5.4	2665	4	AA660317	AA660317 Human ISO	c 294	16	5.4	7517	4	AAK89061	AAK89061 Human dtg
c 238	16	5.4	2918	2	AA400074	AA400074 Colon can	c 295	16	5.4	7643	9	ADC30027	ADC30027 Human nov
c 239	16	5.4	3047	4	AAH17851	AAH17851 Human cDN	c 296	16	5.4	8265	4	ADJ08192	ADJ08192 Drosophill
c 240	16	5.4	3112	7	ABX71034	ABX71034 Novel hum	c 297	16	5.4	8298	6	AEN80191	AEN80191 Human che
c 241	16	5.4	3141	7	ADA53313	ADA53313 Human cod	c 298	16	5.4	8748	5	AEN15607	AEN15607 Human nec
c 242	16	5.4	3201	7	AB280500	AB280500 Human aph	c 299	16	5.4	10002	7	AB276333	AB276333 Human che
c 243	16	5.4	3212	4	ABH12047	ABH12047 Drosophill	c 300	16	5.4	10341	7	AB276340	AB276340 L. cuprin
c 244	16	5.4	3226	4	AA513803	AA513803 Human cDN	c 301	16	5.4	10433	6	AAV74331	AAV74331 Human imm
c 245	16	5.4	3370	9	ADB62184	ADB62184 Human cDN	c 302	16	5.4	10470	2	AAV74331	AAV74331 Human imm
c 246	16	5.4	3483	4	ABL25574	ABL25574 Drosophill	c 303	16	5.4	11394	6	ABK28222	ABK28222 DNA trans
c 247	16	5.4	3534	4	ABL25564	ABL25564 Drosophill	c 304	16	5.4	11812	4	AA545501	AA545501 Chemical
c 248	16	5.4	3604	4	AA162638	AA162638 Human bre	c 305	16	5.4	11812	4	AA546741	AA546741 Tumour su
c 249	16	5.4	3604	4	AA106732	AA106732 Human rep	c 306	16	5.4	11812	6	ABL34118	ABL34118 Human imm
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c 251	16	5.4	3637	9	AA058500	AA058500 Human RSK	c 308	16	5.4	12711	6	ABL34524	ABL34524 Human met
c 252	16	5.4	3819	7	ACA37440	ACA37440 Prokaryot	c 309	16	5.4	12711	6	ABL70249	ABL70249 Chemical
c 253	16	5.4	3879	4	ABH13243	ABH13243 Drosophill	c 310	16	5.4	13133	6	ABK31231	ABK31231 Signal tr
c 254	16	5.4	3907	6	ABK34640	ABK34640 Human cDN	c 311	16	5.4	13440	2	AAV52261	AAV52261 Streptoco
c 255	16	5.4	4042	5	AA583774	AA583774 DNA encod	c 312	16	5.4	13714	6	ABL33173	ABL33173 Human imm
c 256	16	5.4	4226	5	ABK21324	ABK21324 Human ner	c 313	16	5.4	15714	6	ABQ67058	ABQ67058 Human ang
c 257	16	5.4	4507	4	AA073732	AA073732 Human rep	c 314	16	5.4	17141	6	AA264686	AA264686 Bovine ga
c 258	16	5.4	4507	4	ABAO7915	ABAO7915 Human ova	c 315	16	5.4	17417	8	ADA12195	ADA12195 Actinocoba
c 259	16	5.4	4651	5	AA569311	AA569311 DNA encod	c 316	16	5.4	17417	9	AA259831	AA259831 Human sec
c 260	16	5.4	4672	5	ABV25301	ABV25301 Human pro	c 317	16	5.4	17646	7	ABT17023	ABT17023 Human sec
c 261	16	5.4	5060	10	ADE77064	ADE77064 Human cDN	c 318	16	5.4	17646	7	AB268163	AB268163 Human sec
c 262	16	5.4	5275	6	ABH32285	ABH32285 Human imm	c 319	16	5.4	17646	7	AB274645	AB274645 Secreted
c 263	16	5.4	5337	6	ABH32438	ABH32438 Human imm	c 320	16	5.4	17646	7	ADA98997	ADA98997 Human sec
c 264	16	5.4	5377	6	ABK28380	ABK28380 DNA trans	c 321	16	5.4	17946	4	AA536812	AA536812 Human car
c 265	16	5.4	5448	4	ABH14644	ABH14644 Drosophill	c 322	16	5.4	17946	5	ABH15608	ABH15608 Human ner
c 266	16	5.4	5464	4	AA563343	AA563343 Chemical	c 323	16	5.4	17946	9	ABE47506	ABE47506 Human car
c 267	16	5.4	5572	4	ABH02646	ABH02646 Drosophill	c 324	16	5.4	18679	6	AEN80300	AEN80300 Human che
c 268	16	5.4	5841	6	ABN92872	ABN92872 Soybean d	c 325	16	5.4	19718	2	AAV52232	AAV52232 Streptoco
c 269	16	5.4	5882	4	ABD12046	ABD12046 Human src	c 326	16	5.4	19814	6	ABL70610	ABL70610 Chemical
c 270	16	5.4	6034	9	ADD14806	ADD14806 Human imm	c 327	16	5.4	21521	4	AAK76175	AAK76175 Human imm
c 271	16	5.4	6061	6	ABH32140	ABH32140 Human imm	c 328	16	5.4	21521	5	ABA21357	ABA21357 Human ner
c 272	16	5.4	6092	6	ABH33020	ABH33020 Human imm	c 329	16	5.4	22507	6	AB278866	AB278866 E. coli C
c 273	16	5.4	6124	6	ABH32965	ABH32965 Human imm	c 330	16	5.4	25656	4	ABH13242	ABH13242 Drosophill
c 274	16	5.4	6124	6	ABH34517	ABH34517 Human met	c 331	16	5.4	28136	4	AAK69755	AAK69755 Human imm
c 275	16	5.4	6124	6	ABH70242	ABH70242 Chemical	c 332	16	5.4	31749	4	AAK72959	AAK72959 Human imm
c 276	16	5.4	6160	6	ABH33533	ABH33533 Human imm	c 333	16	5.4	32236	4	AAK91250	AAK91250 Human dtg
c 277	16	5.4	6161	6	ABK31299	ABK31299 Signal tr	c 334	16	5.4	35425	9	ADC87616	ADC87616 Human GPC
c 278	16	5.4	6161	6	ABH70278	ABH70278 Chemical	c 335	16	5.4	36651	6	AA228072	AA228072 Human kin
c 279	16	5.4	6161	6	AA561201	AA561201 Human gen	c 336	16	5.4	36998	6	AA235961	AA235961 Human tra
c 280	16	5.4	6176	6	AA221847	AA221847 Zee maye	c 337	16	5.4	62909	4	AA28545	AA28545 Genomic f
c 281	16	5.4	6233	7	ABK63371	ABK63371 Human cDN	c 338	16	5.4	63327	6	AB555821	AB555821 Human tra
c 282	16	5.4	6283	6	ABK31434	ABK31434 Signal tr	c 339	16	5.4	72332	8	ADA02552	ADA02552 Human WNT
c 283	16	5.4	6283	6	ABH70403	ABH70403 Chemical	c 340	16	5.4	72332	9	ADB72290	ADB72290 Human WNT
c 284	16	5.4	6283	6	AA561351	AA561351 Human gen	c 341	16	5.4	78925	3	AA089888	AA089888 Human FN
c 285	16	5.4	6345	6	ABH33771	ABH33771 Human imm	c 342	16	5.4	96389	8	ADA02675	ADA02675 Mouse Top
c 286	16	5.4	6345	6	ABH70392	ABH70392 Chemical	c 343	16	5.4	96389	9	AAK95240	AAK95240 Mouse Top
c 287	16	5.4	6426	5	ABK20567	ABK20567 Human ner	c 344	16	5.4	110000	4	AAK96733	AAK96733 Continuation (12 o
c 288	16	5.4	6459	6	AB555225	AB555225 Human myo	c 345	16	5.4	110000	4	AAK96733	AAK96733 Continuation (12 o
c 289	16	5.4	6459	7	ABH14112	ABH14112 DNA encod	c 346	16	5.4	110000	6	ABT00010	ABT00010 Continuation (12 o
c 290	16	5.4	7201	6	ABH32337	ABH32337 Human imm	c 347	16	5.4	110000	6	ABK08336	ABK08336 Human pho
c 291	16	5.4	7312	6	ABH33815	ABH33815 Human imm	c 348	16	5.4	110000	6	ABK92787	ABK92787 Buchnera
c 292	16	5.4	7312	6	ABH70402	ABH70402 Chemical	c 349	16	5.4	110000	6	ABT01503	ABT01503 Continuation (12 o

c 350	16	5.4	110000	6	ABA03041_08	Continuation (9 of	c 407	15	5.1	231	4	AA548447	AA548447 Enterococ
c 351	16	5.4	110000	7	AB556454_06	Continuation (7 of	c 408	15	5.1	231	7	ACA13136	ACA13136 Prokaryot
c 352	16	5.4	110000	7	AB556454_13	Continuation (14 o	c 409	15	5.1	234	3	AA020084	AA020084 Human sec
c 353	16	5.4	110000	7	AB556454_16	Continuation (17 o	c 410	15	5.1	235	4	AAK77774	AAK77774 Human tmm
c 354	16	5.4	110000	7	AB556454_20	Continuation (21 o	c 411	15	5.1	235	4	AAK77773	AAK77773 Human tmm
c 355	16	5.4	110000	8	ACR03408_0	ACR03408 Genomic D	c 412	15	5.1	242	6	ABL63616	ABL63616 Human tmm
c 356	16	5.4	111282	6	AA144261	AA144261 Human pho	c 413	15	5.1	244	3	AAAI0119	AAI0119 Human tmm
c 357	16	5.4	111282	6	AB555190	AB555190 Genomic D	c 414	15	5.1	244	3	AAAI0119	AAI0119 Rat liver
c 358	16	5.4	139032	6	AB079105	AB079105 Human for	c 415	15	5.1	244	6	AAI42143	AAI42143 Rat targe
c 359	16	5.4	139257	9	ADC89520	ADC89520 Human COR	c 416	15	5.1	247	4	AAH78908	AAH78908 Human ORF
c 360	16	5.4	139904	6	ABK83362	ABK83362 Human cDN	c 417	15	5.1	247	4	AAH71289	AAH71289 Human ORF
c 361	16	5.4	265118	5	AAH41227	AAH41227 Pyrococcu	c 418	15	5.1	247	4	AAI51531	AAI51531 Probe #20
c 362	16	5.4	349901	9	ADC86940	ADC86940 Human GPC	c 419	15	5.1	247	4	AAK45594	AAK45594 Human bon
c 363	16	5.4	349901	9	ADC86940	ADC86940 Human GPC	c 420	15	5.1	247	4	AAK19591	AAK19591 Human bon
c 364	16	5.4	349938	9	ADC87621	ADC87621 Human GPC	c 421	15	5.1	247	4	AB545284	AB545284 Human bra
c 365	15	5.1	25	25	ACF03399	ACF03399 M. gallis	c 422	15	5.1	268	5	AAI51866	AAI51866 Human liv
c 366	15	5.1	33	33	AA212528	AA212528 PCR prime	c 423	15	5.1	268	6	AAI66381	AAI66381 Human lun
c 367	15	5.1	33	33	AB225162	AB225162 Cu/Zn SOD	c 424	15	5.1	268	6	AAK38292	AAK38292 cDNA onco
c 368	15	5.1	47	3	AA267197	AA267197 Human map	c 425	15	5.1	268	7	ACA10621	ACA10621 Human lun
c 369	15	5.1	56	2	AAV76389	AAV76389 Stephyloc	c 426	15	5.1	268	10	ABK95712	ABK95712 Lung canc
c 370	15	5.1	91	4	AA547846	AA547846 Enterococ	c 427	15	5.1	286	10	AAE72335	AAE72335 Human lun
c 371	15	5.1	91	7	ACA12573	ACA12573 Prokaryot	c 428	15	5.1	286	7	ACA12295	ACA12295 Prokaryot
c 372	15	5.1	117	7	ACA19997	ACA19997 Prokaryot	c 429	15	5.1	287	7	ABK87507	ABK87507 Corn ear-
c 373	15	5.1	150	2	AAH86832	AAH86832 Human sin	c 430	15	5.1	294	5	ABV58694	ABV58694 Human pro
c 374	15	5.1	152	3	AA022270	AA022270 Human sec	c 431	15	5.1	297	6	AB517999	AB517999 Human gen
c 375	15	5.1	165	4	ABK74657	ABK74657 Human foe	c 432	15	5.1	324	6	ABQ68225	ABQ68225 Listeria
c 376	15	5.1	165	4	AA155150	AA155150 Probe #23	c 433	15	5.1	325	4	AA518836	AA518836 Novel hum
c 377	15	5.1	165	4	AA49303	AA49303 Human bon	c 434	15	5.1	332	6	AAH18909	AAH18909 Human ORF
c 378	15	5.1	165	4	AAK23130	AAK23130 Human bra	c 435	15	5.1	334	4	AA547653	AA547653 Prokaryot
c 379	15	5.1	165	4	AB548942	AB548942 Human liv	c 436	15	5.1	334	7	ACA12352	ACA12352 Prokaryot
c 380	15	5.1	165	6	AB522824	AB522824 Human gen	c 437	15	5.1	337	4	AA188498	AA188498 Human pol
c 381	15	5.1	167	6	AB178996	AB178996 Human ova	c 438	15	5.1	339	6	ABK78592	ABK78592 Bacillus
c 382	15	5.1	176	4	AA547723	AA547723 Enterococ	c 439	15	5.1	350	7	AB256662	AB256662 Aspergill
c 383	15	5.1	176	7	ACA12419	ACA12419 Prokaryot	c 440	15	5.1	351	2	AAQ60794	AAQ60794 Human bra
c 384	15	5.1	178	6	AB208290	AB208290 Human leu	c 441	15	5.1	353	2	AAQ60794	AAQ60794 Human bra
c 385	15	5.1	191	4	AA547538	AA547538 Enterococ	c 442	15	5.1	357	3	AA059515	AA059515 Human sec
c 386	15	5.1	191	4	AA547582	AA547582 Enterococ	c 443	15	5.1	370	5	AAV17434	AAV17434 Human pro
c 387	15	5.1	191	4	AA547542	AA547542 Enterococ	c 444	15	5.1	370	7	ABK45244	ABK45244 Bovine ES
c 388	15	5.1	191	4	AA547557	AA547557 Enterococ	c 445	15	5.1	375	4	AAI14275	AAI14275 Human bre
c 389	15	5.1	191	7	ACA12277	ACA12277 Prokaryot	c 446	15	5.1	384	4	AAI13791	AAI13791 Probe #37
c 390	15	5.1	191	7	ACA12236	ACA12236 Prokaryot	c 447	15	5.1	384	4	AB555501	AB555501 Human foe
c 391	15	5.1	191	7	ACA12237	ACA12237 Prokaryot	c 448	15	5.1	384	4	AA135151	AA135151 Probe #38
c 392	15	5.1	191	7	ACA12249	ACA12249 Prokaryot	c 449	15	5.1	384	4	ABK45029	ABK45029 Human bre
c 393	15	5.1	195	3	AA014255	AA014255 Human sec	c 450	15	5.1	384	4	ABK25217	ABK25217 Probe #36
c 394	15	5.1	198	6	AB184328	AB184328 Human ova	c 451	15	5.1	384	4	AAK29199	AAK29199 Human bon
c 395	15	5.1	230	4	AA548353	AA548353 Enterococ	c 452	15	5.1	384	4	AAK03735	AAK03735 Human bra
c 396	15	5.1	230	4	AA548429	AA548429 Enterococ	c 453	15	5.1	384	4	AB528816	AB528816 Human liv
c 397	15	5.1	230	4	AA548284	AA548284 Enterococ	c 454	15	5.1	384	5	AAI03667	AAI03667 Probe #36
c 398	15	5.1	230	4	AA548388	AA548388 Enterococ	c 455	15	5.1	384	6	AB503751	AB503751 Human gen
c 399	15	5.1	230	4	AA548332	AA548332 Enterococ	c 456	15	5.1	386	2	AAV15598	AAV15598 Papilloma
c 400	15	5.1	230	4	AA548462	AA548462 Enterococ	c 457	15	5.1	386	2	AAV15599	AAV15599 Papilloma
c 401	15	5.1	230	7	ACA13142	ACA13142 Prokaryot	c 458	15	5.1	393	4	AAH00774	AAH00774 Clotridi
c 402	15	5.1	230	7	ACA13033	ACA13033 Prokaryot	c 459	15	5.1	398	4	AAI92814	AAI92814 Human pol
c 403	15	5.1	230	7	ACA13046	ACA13046 Prokaryot	c 460	15	5.1	403	2	AA062791	AA062791 Humanised
c 404	15	5.1	230	7	ACA13056	ACA13056 Prokaryot	c 461	15	5.1	407	7	ABK36649	ABK36649 Bovine ES
c 405	15	5.1	230	7	ACA13145	ACA13145 Prokaryot	c 462	15	5.1	407	7	ABK62547	ABK62547 Arabidops
c 406	15	5.1	230	7	ACA13008	ACA13008 Prokaryot	c 463	15	5.1	414	8	ADA31018	ADA31018 DNA encod

c 464	15	5.1	423	6	ABN19543	Abn19543 Human ORF	c 521	15	5.1	529	4	AA547497	AA547497 Enterococ
c 465	15	5.1	426	5	ABV47228	ABv47228 Human pro	c 522	15	5.1	529	4	AA547502	AA547502 Enterococ
c 466	15	5.1	426	3	ABx44832	ABx44832 Bovine ES	c 523	15	5.1	529	5	ABV47427	ABv47427 Human pro
c 467	15	5.1	428	7	AAc57698	AAc57698 Atechidon	c 524	15	5.1	529	7	AC112204	ACa12204 Prokaryot
c 468	15	5.1	430	5	ABV00400	ABv00400 Human pro	c 525	15	5.1	531	6	ABQ45171	ABq45171 Oligonuc1
c 469	15	5.1	432	6	ABK76313	ABk76313 Bacillus	c 526	15	5.1	531	6	ABQ45170	ABq45170 Oligonuc1
c 470	15	5.1	433	5	ABV48231	ABv48231 Human pro	c 527	15	5.1	532	6	ABQ47632	ABq47632 Oligonuc1
c 471	15	5.1	435	5	ABV52504	ABv52504 Human pro	c 528	15	5.1	532	6	ABQ47633	ABq47633 Oligonuc1
c 472	15	5.1	437	5	ABAI6674	ABa16674 Human ner	c 529	15	5.1	532	7	AC112192	ACa12192 Prokaryot
c 473	15	5.1	438	4	AA549430	AAa49430 Stephyloc	c 530	15	5.1	541	6	ABQ39476	ABq39476 Oligonuc1
c 474	15	5.1	438	7	ACAI6657	ACa16657 Prokaryot	c 531	15	5.1	541	6	ABQ39477	ABq39477 Oligonuc1
c 475	15	5.1	447	8	ADA48769	AdA48769 Barana ge	c 532	15	5.1	541	9	ADD33178	AdD33178 Human mit
c 476	15	5.1	456	6	ABV95163	ABv95163 Human pan	c 533	15	5.1	543	6	ABQ37914	ABq37914 Oligonuc1
c 477	15	5.1	457	8	ACH26876	ACH26876 Human adu	c 534	15	5.1	543	6	ABQ37915	ABq37915 Oligonuc1
c 478	15	5.1	458	5	ABV09569	ABv09569 Human pro	c 535	15	5.1	550	6	ABQ22438	ABq22438 Oligonuc1
c 479	15	5.1	459	5	ABV39713	ABv39713 Human pro	c 536	15	5.1	550	6	ABQ22439	ABq22439 Oligonuc1
c 480	15	5.1	459	5	ABV30745	ABv30745 Human pro	c 537	15	5.1	551	7	ABX57175	ABx57175 Atebldops
c 481	15	5.1	460	8	ACH25839	ACH25839 Human adu	c 538	15	5.1	554	6	ABQ32977	ABq32977 Oligonuc1
c 482	15	5.1	468	4	ABA58555	ABa58555 Human foe	c 539	15	5.1	554	6	ABQ32976	ABq32976 Oligonuc1
c 483	15	5.1	468	4	AA138216	AA138216 Probe #69	c 540	15	5.1	558	6	ABQ18099	ABq18099 Oligonuc1
c 484	15	5.1	468	4	AAK32370	AAK32370 Human bon	c 541	15	5.1	558	6	ABQ18098	ABq18098 Oligonuc1
c 485	15	5.1	468	4	AAK06674	AAK06674 Human bra	c 542	15	5.1	559	6	ABQ53806	ABq53806 Oligonuc1
c 486	15	5.1	468	4	ABS32078	ABs32078 Human liv	c 543	15	5.1	559	6	ABQ53807	ABq53807 Oligonuc1
c 487	15	5.1	468	6	ABS07153	ABs07153 Human gen	c 544	15	5.1	566	6	ABQ22523	ABq22523 Oligonuc1
c 488	15	5.1	478	6	ABS05296	ABs05296 Human gen	c 545	15	5.1	566	6	ABQ22522	ABq22522 Oligonuc1
c 489	15	5.1	480	4	AAK79680	AAK79680 Human imm	c 546	15	5.1	567	2	AAK27703	AAk27703 T7 RNA po
c 490	15	5.1	483	5	AAK78335	AAK78335 DNA encod	c 547	15	5.1	567	4	AAK92622	AAK92622 Human cDN
c 491	15	5.1	485	8	AC114945	AC114945 Human adu	c 548	15	5.1	567	8	ADA31675	ADa31675 DNA encod
c 492	15	5.1	488	5	ABAI6716	ABa16716 Human ner	c 549	15	5.1	569	2	AAK27765	AAk27765 Sequence
c 493	15	5.1	488	5	ABAI6715	ABa16715 Human ner	c 550	15	5.1	570	4	ABL13333	ABl13333 Prokaryot
c 494	15	5.1	488	5	ABAI6713	ABa16713 Human ner	c 551	15	5.1	570	4	ABX59707	ABx59707 Human foe
c 495	15	5.1	491	6	ABV99050	ABv99050 Human pan	c 552	15	5.1	570	4	AA139572	AA139572 Human liv
c 496	15	5.1	492	5	ABV59181	ABv59181 Human col	c 553	15	5.1	570	4	AA139573	AA139573 Human liv
c 497	15	5.1	492	6	ABJ36418	ABj36418 Human col	c 554	15	5.1	572	2	AAQ44852	AAQ44852 Bacillus
c 498	15	5.1	493	7	ACC60444	ACC60444 Rice leaf	c 555	15	5.1	576	6	ABQ45688	ABq45688 Oligonuc1
c 499	15	5.1	498	3	AAK7857	AAK7857 Human col	c 556	15	5.1	576	6	ABQ45689	ABq45689 Oligonuc1
c 500	15	5.1	498	4	AAK7857	AAK7857 Human col	c 557	15	5.1	576	6	ABQ45689	ABq45689 Oligonuc1
c 501	15	5.1	499	6	ABQ57276	ABq57276 Human col	c 558	15	5.1	579	6	ABQ25431	ABq25431 Oligonuc1
c 502	15	5.1	500	6	ABK53395	ABk53395 Human eos	c 559	15	5.1	581	6	ABQ38266	ABq38266 Oligonuc1
c 503	15	5.1	502	6	ABQ28401	ABq28401 Oligonuc1	c 560	15	5.1	581	6	ABQ38267	ABq38267 Oligonuc1
c 504	15	5.1	502	6	ABQ28400	ABq28400 Oligonuc1	c 561	15	5.1	581	7	AC110275	ACa10275 Rice leaf
c 505	15	5.1	506	6	ABJ99505	ABj99505 Target ca	c 562	15	5.1	582	7	ACF73303	ACf73303 Stephyloc
c 506	15	5.1	508	6	ABQ49691	ABq49691 Oligonuc1	c 563	15	5.1	586	6	ABQ39378	ABq39378 Oligonuc1
c 507	15	5.1	508	6	ABQ49690	ABq49690 Oligonuc1	c 564	15	5.1	586	6	ABQ39379	ABq39379 Oligonuc1
c 508	15	5.1	510	6	ABQ22280	ABq22280 Oligonuc1	c 565	15	5.1	587	5	ABAI5400	ABa15400 Human ner
c 509	15	5.1	510	6	ABQ22281	ABq22281 Oligonuc1	c 566	15	5.1	590	6	ABQ25857	ABq25857 Oligonuc1
c 510	15	5.1	511	4	AA192763	AA192763 Human pol	c 567	15	5.1	590	6	ABQ25856	ABq25856 Oligonuc1
c 511	15	5.1	514	9	ADD17902	AdD17902 DNA (Seq)	c 568	15	5.1	592	4	ABA62163	ABa62163 Human foe
c 512	15	5.1	515	6	ABQ33939	ABq33939 Oligonuc1	c 569	15	5.1	592	4	AA142117	AA142117 Probe #10
c 513	15	5.1	515	6	ABQ33938	ABq33938 Oligonuc1	c 570	15	5.1	592	4	AAK36383	AAK36383 Human bon
c 514	15	5.1	520	3	AAK39612	AAK39612 Atebldops	c 571	15	5.1	592	4	AAK10484	AAK10484 Human bra
c 515	15	5.1	522	4	AAK62528	AAK62528 Human liv	c 572	15	5.1	592	4	ABX36058	ABx36058 Human gen
c 516	15	5.1	523	6	ABQ50101	ABq50101 Oligonuc1	c 573	15	5.1	592	6	ABQ10424	ABq10424 Human gen
c 517	15	5.1	523	6	ABQ50100	ABq50100 Oligonuc1	c 574	15	5.1	594	6	ABQ24018	ABq24018 Oligonuc1
c 518	15	5.1	525	7	ACA35322	ACa35322 Prokaryot	c 575	15	5.1	594	6	ABQ24019	ABq24019 Oligonuc1
c 519	15	5.1	527	6	ABQ13981	ABq13981 Oligonuc1	c 576	15	5.1	609	6	ABQ43749	ABq43749 Oligonuc1
c 520	15	5.1	527	6	ABQ13980	ABq13980 Oligonuc1	c 577	15	5.1	609	6	ABQ43748	ABq43748 Oligonuc1

578	15	5.1	610	6	ABQ25735	AbQ25735 Oligonucel	c 635	15	5.1	754	4	AAK51627	AAK51627 Human pol
c 579	15	5.1	610	6	ABQ25734	AbQ25734 Oligonucel	c 636	15	5.1	753	3	AAK42653	AAK42653 Arabidops
580	15	5.1	613	6	ABQ6674	AbQ6674 Arabidops	c 637	15	5.1	756	2	AAQ43704	AAQ43704 Sequence
581	15	5.1	614	2	AAZ96182	AAZ96182 S. pneumo	c 638	15	5.1	756	6	ABK84157	ABK84157 Human cDN
c 582	15	5.1	615	6	ABQ27520	AbQ27520 Oligonucel	c 639	15	5.1	760	6	ABE17054	ABE17054 Arabidops
583	15	5.1	615	6	ABQ27521	AbQ27521 Oligonucel	c 640	15	5.1	760	7	ADN69199	ADN69199 Arabidops
584	15	5.1	616	5	ABY51537	AbY51537 Human pro	c 641	15	5.1	772	3	AAZ97291	AAZ97291 Arabidops
585	15	5.1	620	2	AA198607	DNA encod	c 642	15	5.1	774	6	ABQ32213	ABQ32213 Human pro
586	15	5.1	620	7	ADA68382	ADA68382 Arabidops	c 643	15	5.1	774	6	ABQ32212	ABQ32212 Oligonucel
587	15	5.1	621	1	ABE14361	ABE14361 Arabidops	c 644	15	5.1	775	4	AA123383	AA123383 Human bre
588	15	5.1	621	7	ABE24092	ABE24092 Arabidops	c 645	15	5.1	786	4	AA123137	AA123137 Human bre
589	15	5.1	624	6	ABQ77940	AbQ77940 Bacillus	c 646	15	5.1	786	6	ABN69343	ABN69343 Streptoco
590	15	5.1	626	6	ABQ53873	AbQ53873 Oligonucel	c 647	15	5.1	788	6	ABQ47918	ABQ47918 Oligonucel
c 591	15	5.1	626	6	ABQ53872	AbQ53872 Oligonucel	c 648	15	5.1	788	6	ABQ47919	ABQ47919 Oligonucel
c 592	15	5.1	628	6	ABQ25852	AbQ25852 Oligonucel	c 649	15	5.1	793	6	ABQ22881	ABQ22881 Oligonucel
593	15	5.1	628	6	ABQ25953	AbQ25953 Oligonucel	c 650	15	5.1	793	6	ABQ22880	ABQ22880 Oligonucel
c 594	15	5.1	632	3	AAFI0192	AAFI0192 Fusarium	c 651	15	5.1	794	5	ABV24895	ABV24895 Human pro
c 595	15	5.1	632	3	ABK80225	ABK80225 Bacillus	c 652	15	5.1	813	4	AA194687	AA194687 Human neu
c 596	15	5.1	637	7	ABX12499	ABX12499 cDNA encod	c 653	15	5.1	826	6	ABQ37703	ABQ37703 Oligonucel
597	15	5.1	642	6	ABK77841	ABK77841 Bacillus	c 654	15	5.1	826	6	ABQ37702	ABQ37702 Oligonucel
c 598	15	5.1	646	6	ABQ20336	AbQ20336 Oligonucel	c 655	15	5.1	828	2	AA167865	AA167865 H. pylori
599	15	5.1	646	6	ABQ20337	AbQ20337 Oligonucel	c 656	15	5.1	828	4	AA194407	AA194407 Human neu
600	15	5.1	649	4	AA184272	AA184272 Human pol	c 657	15	5.1	835	4	AA195446	AA195446 Human neu
601	15	5.1	657	6	ABQ33195	AbQ33195 Oligonucel	c 658	15	5.1	837	2	AA167694	AA167694 H. pylori
c 602	15	5.1	657	6	ABQ33194	AbQ33194 Oligonucel	c 659	15	5.1	860	6	ABQ52665	ABQ52665 Oligonucel
c 603	15	5.1	658	4	AAE22846	AAE22846 Human pro	c 660	15	5.1	860	6	ABQ52664	ABQ52664 Oligonucel
c 604	15	5.1	664	6	ABQ53676	AbQ53676 Oligonucel	c 661	15	5.1	861	6	ABE25158	ABE25158 H. pylori
605	15	5.1	664	6	ABQ53677	AbQ53677 Oligonucel	c 662	15	5.1	876	7	ACA30332	ACA30332 Protekayot
c 606	15	5.1	674	3	AAQ59543	AAQ59543 Human sec	c 663	15	5.1	876	7	ACA49440	ACA49440 Protekayot
c 607	15	5.1	674	6	ABQ48436	AbQ48436 Oligonucel	c 664	15	5.1	879	4	AA556047	AA556047 Salmonell
608	15	5.1	674	6	ABQ48437	AbQ48437 Oligonucel	c 665	15	5.1	879	7	ACA52000	ACA52000 Protekayot
c 609	15	5.1	682	6	ABN65486	ABN65486 Human can	c 666	15	5.1	899	6	ABQ36688	ABQ36688 Oligonucel
c 610	15	5.1	683	3	AAFI1854	AAFI1854 Aspergill	c 667	15	5.1	899	6	ABQ36687	ABQ36687 Oligonucel
c 611	15	5.1	687	7	ACF73989	ACF73989 Stephyloc	c 668	15	5.1	899	6	ABQ36465	ABQ36465 Oligonucel
c 612	15	5.1	690	7	ACA20358	ACA20358 Protekayot	c 669	15	5.1	899	6	ABQ36689	ABQ36689 Oligonucel
613	15	5.1	693	4	AAK65577	AAK65577 Human imm	c 670	15	5.1	909	6	ABQ28075	ABQ28075 Oligonucel
c 614	15	5.1	694	6	ABQ41430	AbQ41430 Oligonucel	c 671	15	5.1	909	6	ABQ28074	ABQ28074 Oligonucel
c 615	15	5.1	694	6	ABQ41431	AbQ41431 Oligonucel	c 672	15	5.1	930	6	ABQ35481	ABQ35481 Oligonucel
c 616	15	5.1	697	6	ABQ41812	AbQ41812 Oligonucel	c 673	15	5.1	930	6	ABQ35480	ABQ35480 Oligonucel
617	15	5.1	697	6	ABQ41813	AbQ41813 Oligonucel	c 674	15	5.1	943	6	ABQ17438	ABQ17438 Oligonucel
618	15	5.1	699	7	ACA33230	ACA33230 Protekayot	c 675	15	5.1	943	6	ABQ17439	ABQ17439 Oligonucel
619	15	5.1	702	4	AA552908	AA552908 Enterococ	c 676	15	5.1	945	4	AAH32127	AAH32127 Human oif
c 620	15	5.1	706	6	ABQ31819	AbQ31819 Oligonucel	c 677	15	5.1	945	7	ABE27950	ABE27950 Human G P
c 621	15	5.1	706	6	ABQ31818	AbQ31818 Oligonucel	c 678	15	5.1	947	8	AA161111	AA161111 Human T81
c 622	15	5.1	707	6	ABQ48894	AbQ48894 Oligonucel	c 679	15	5.1	949	4	AAH32324	AAH32324 Human oif
c 623	15	5.1	707	6	ABQ48895	AbQ48895 Stephyloc	c 680	15	5.1	954	7	ACF73679	ACF73679 Stephyloc
624	15	5.1	708	6	ABN91859	ABN91859 Stephyloc	c 681	15	5.1	956	9	ADP53698	ADP53698 Human pro
c 625	15	5.1	709	6	ABQ31714	AbQ31714 Oligonucel	c 682	15	5.1	971	6	ABQ16238	ABQ16238 Oligonucel
626	15	5.1	709	6	ABQ31715	AbQ31715 Oligonucel	c 683	15	5.1	971	6	ABQ16239	ABQ16239 Oligonucel
c 627	15	5.1	711	4	AB128355	AB128355 Drosophil	c 684	15	5.1	985	4	AA197659	AA197659 Human neu
628	15	5.1	714	4	AAE22944	AAE22944 Human pro	c 685	15	5.1	993	3	AAZ45340	AAZ45340 DNA encod
629	15	5.1	717	4	AA195196	AA195196 Human neu	c 686	15	5.1	996	4	AAAD12949	AAAD12949 Human G-P
c 630	15	5.1	738	6	ABQ16844	AbQ16844 Oligonucel	c 687	15	5.1	996	5	AA542281	AA542281 Human cDN
c 631	15	5.1	738	6	ABQ17370	AbQ17370 Oligonucel	c 688	15	5.1	996	6	ABQ41998	ABQ41998 Oligonucel
632	15	5.1	738	6	ABQ17371	AbQ17371 Oligonucel	c 689	15	5.1	996	6	ABQ41999	ABQ41999 Oligonucel
633	15	5.1	738	6	ABQ16845	AbQ16845 Oligonucel	c 690	15	5.1	996	6	ABE242987	ABE242987 Human GPC
c 634	15	5.1	747	2	AAV74964	AAV74964 Stephyloc	c 691	15	5.1	996	6	ABK68496	ABK68496 Human DNA

c 692	15	5.1	996	6	ABK37567	Abk37567 DNA encod	748	15	5.1	1380	4	AAH23395	Aah23395 S. aureus
c 693	15	5.1	996	6	ADD18116	Add18116 Human G-P	749	15	5.1	1380	7	ACA46380	Aca46380 Prokaryot
c 694	15	5.1	999	7	ACQ21167	Acq21167 Prokaryot	750	15	5.1	1389	6	AB213533	Ab213533 Arabidops
c 695	15	5.1	1000	8	ADB23173	Adb23173 Envirofome	751	15	5.1	1398	7	ACF74361	Acf74361 Staphyloc
c 696	15	5.1	1003	4	AAD17913	Aad17913 G-protein	752	15	5.1	1401	9	ADC04609	Adc04609 Putative
c 697	15	5.1	1004	4	AAD17914	Aad17914 G-protein	753	15	5.1	1401	9	ADC04609	Adc04609 Putative
c 698	15	5.1	1005	4	AAD17915	Aad17915 G-protein	754	15	5.1	1404	3	AAK47347	Aak47347 Arabidops
c 699	15	5.1	1008	7	ABK81727	Abk81727 Human sec	755	15	5.1	1407	4	AAK51644	Aak51644 Staphyloc
c 700	15	5.1	1008	7	ABK67246	Abk67246 Human sec	756	15	5.1	1407	4	AAK51644	Aak51644 Staphyloc
c 701	15	5.1	1008	7	ABK73652	Abk73652 Secreted	757	15	5.1	1408	3	AAK33658	Aak33658 Arabidops
c 702	15	5.1	1008	7	ADC20294	Adc20294 Human sec	758	15	5.1	1420	4	ABL17629	Ab117629 Drosophi1
c 703	15	5.1	1019	4	AAK59766	Aak59766 Propionib	759	15	5.1	1428	4	AAK51247	Aak51247 Enterococ
c 704	15	5.1	1019	7	ACF64695	Acf64695 Propionib	760	15	5.1	1431	4	AAK53058	Aak53058 Prokaryot
c 705	15	5.1	1031	4	AAK22452	Aak22452 Human cDN	761	15	5.1	1431	4	AAK53058	Aak53058 Prokaryot
c 706	15	5.1	1034	2	AAK21785	Aak21785 Metastasi	762	15	5.1	1443	3	AAK33345	Aak33345 Arabidops
c 707	15	5.1	1047	6	AAK62681	Aak62681 cDNA sequ	763	15	5.1	1443	7	ACA22144	Ac22144 Prokaryot
c 708	15	5.1	1047	8	ADA29215	Ada29215 DNA encod	764	15	5.1	1449	9	ADB31880	Adb31880 DNA encod
c 709	15	5.1	1052	4	AAK22688	Aak22688 Human cDN	765	15	5.1	1455	7	ACA61615	Aca61615 Human fat
c 710	15	5.1	1074	7	ACA47371	Ac447371 Prokaryot	766	15	5.1	1458	2	AAK23672	Aak23672 Gluconoba
c 711	15	5.1	1081	7	ABK95119	Abk95119 DNA sequ	767	15	5.1	1458	3	AAK50516	Aak50516 Arabidops
c 712	15	5.1	1082	7	ABK79296	Abk79296 Rat Biliv	768	15	5.1	1460	3	AAK33457	Aak33457 Arabidops
c 713	15	5.1	1082	7	ADB53527	Adb53527 Primary r	769	15	5.1	1465	3	AAK37393	Aak37393 Arabidops
c 714	15	5.1	1088	6	ABK69005	Abk69005 Listeria	770	15	5.1	1477	2	AAK296342	Aak296342 S. pneumonia
c 715	15	5.1	1096	2	AAK30757	Aak30757 Streptococ	771	15	5.1	1477	2	AAK296342	Aak296342 S. pneumonia
c 716	15	5.1	1099	6	ABK31233	Abk31233 Oligonuc1	772	15	5.1	1491	7	ACF75060	Acf75060 Staphyloc
c 717	15	5.1	1099	6	ABK31232	Abk31232 Oligonuc1	773	15	5.1	1491	7	ACF75060	Acf75060 Staphyloc
c 718	15	5.1	1107	7	ACF70527	Acf70527 Phototrab	774	15	5.1	1494	4	AAK53891	Aak53891 Staphyloc
c 719	15	5.1	1115	6	ABK31973	Abk31973 Oligonuc1	775	15	5.1	1501	2	AAK27424	Aak27424 A. pedicad
c 720	15	5.1	1115	6	ABK31972	Abk31972 Oligonuc1	776	15	5.1	1501	2	AAK27424	Aak27424 A. pedicad
c 721	15	5.1	1128	9	ADC91031	Adc91031 E. faecili	777	15	5.1	1560	6	ABK21446	Abk21446 Arabidops
c 722	15	5.1	1152	6	ABK67997	Abk67997 Listeria	778	15	5.1	1571	3	ADC85922	Adc85922 Human GPC
c 723	15	5.1	1152	6	ABK69985	Abk69985 Listeria	779	15	5.1	1573	3	AAK67654	Aak67654 Human sec
c 724	15	5.1	1188	5	AAK87496	Aak87496 DNA encod	780	15	5.1	1581	5	AAK73187	Aak73187 Human sec
c 725	15	5.1	1188	5	ABK212826	Abk212826 Arabidops	781	15	5.1	1590	6	ABA96173	Ab96173 Human imm
c 726	15	5.1	1200	7	ACA29400	Ac29400 Prokaryot	782	15	5.1	1593	6	ABK13672	Abk13672 Oligonuc1
c 727	15	5.1	1227	6	ABK212662	Abk212662 Arabidops	783	15	5.1	1593	6	ABK13672	Abk13672 Oligonuc1
c 728	15	5.1	1232	4	ABK21161	Abk21161 Drosophi1	784	15	5.1	1594	6	ABK13906	Abk13906 Oligonuc1
c 729	15	5.1	1245	9	ADC91220	Adc91220 E. faecili	785	15	5.1	1671	3	AAK61002	Aak61002 Arabidops
c 730	15	5.1	1282	2	AAK83774	Aak83774 DNA encod	786	15	5.1	1674	6	ABK83552	Abk83552 Human cDN
c 731	15	5.1	1289	4	AAK08693	Aak08693 Rat P2-pu	787	15	5.1	1674	7	ABK71997	Abk71997 Human cDN
c 732	15	5.1	1306	6	ABK33670	Abk33670 Oligonuc1	788	15	5.1	1695	4	AAK330182	Aak330182 DNA encod
c 733	15	5.1	1306	6	ABK33671	Abk33671 Oligonuc1	789	15	5.1	1695	4	AAK330182	Aak330182 DNA encod
c 734	15	5.1	1332	6	AAK40802	Aak40802 Nucleic a	790	15	5.1	1695	7	ACD01437	AcD01437 Human nov
c 735	15	5.1	1332	6	AAK31014	Aak31014 Yeast mev	791	15	5.1	1695	7	ACD01437	AcD01437 Human nov
c 736	15	5.1	1332	6	ABK96800	Abk96800 S. cerevi	792	15	5.1	1716	5	AAH52133	Aah52133 Human sec
c 737	15	5.1	1345	7	ADA71970	Ada71970 Rice gene	793	15	5.1	1729	4	ABL12281	Ab112281 Human AFP
c 738	15	5.1	1350	7	ACA22908	Ac22908 Prokaryot	794	15	5.1	1809	7	ADA52570	Aa52570 Human cod
c 739	15	5.1	1353	4	ABK03857	Abk03857 Drosophi1	795	15	5.1	1845	3	AAK76482	Aak76482 Human sec
c 740	15	5.1	1362	7	ACA21505	Aca21505 Prokaryot	796	15	5.1	1864	3	AAK76482	Aak76482 Human sec
c 741	15	5.1	1366	8	AAK61112	Aak61112 Human T81	797	15	5.1	1890	4	AAK22942	Aak22942 Human ORF
c 742	15	5.1	1367	3	AAK98043	Aak98043 Human col	798	15	5.1	1910	4	AAK16471	Aak16471 Human pro
c 743	15	5.1	1369	7	ABK12305	Abk12305 cDNA encod	799	15	5.1	1936	6	ABL65828	Ab165828 Lung can
c 744	15	5.1	1373	3	AAK42135	Aak42135 Arabidops	800	15	5.1	1946	2	AAZ06736	Aaz06736 Cartilage
c 745	15	5.1	1374	7	ACA22021	Ac22021 Prokaryot	801	15	5.1	1948	6	ABK06181	Abk06181 Listeria
c 746	15	5.1	1379	3	AAK33152	Aak33152 Arabidops	802	15	5.1	1964	8	ABK03066	Abk03066 Mouse Ppp
c 747	15	5.1	1380	4	AAK54968	Aak54968 Stephyloc	803	15	5.1	1964	8	ADA66350	Ada66350 Mouse Ppp
							804	15	5.1	1964	9	ADB72804	Adb72804 Mouse Ppp

805	15	5.1	1968	5	AAH66042	AAH66042	C	glutami
c 806	15	5.1	1974	5	AAH87504	AAH87504	DNA	encod
c 807	15	5.1	1997	6	ABX09818	ABX09818	Promoter	
c 808	15	5.1	2000	6	ABE15616	ABE15616	Arabidops	
809	15	5.1	2000	6	ABE17290	ABE17290	Arabidops	
810	15	5.1	2000	6	ABE17513	ABE17513	Arabidops	
c 811	15	5.1	2000	6	ABE15450	ABE15450	Arabidops	
812	15	5.1	2000	6	ABE17249	ABE17249	Arabidops	
c 813	15	5.1	2000	6	ABE15172	ABE15172	Arabidops	
c 814	15	5.1	2000	6	ABE17176	ABE17176	Arabidops	
815	15	5.1	2000	6	ABE16922	ABE16922	Arabidops	
816	15	5.1	2000	7	ACC61839	ACC61839	Gene sequ	
817	15	5.1	2000	7	ACC60610	ACC60610	Gene sequ	
c 818	15	5.1	2000	7	ADA72965	ADA72965	Rice gene	
c 819	15	5.1	2000	7	ADA69209	ADA69209	Arabidops	
c 820	15	5.1	2000	7	ADA72289	ADA72289	Rice gene	
c 821	15	5.1	2000	7	ADA71503	ADA71503	Rice gene	
c 822	15	5.1	2000	7	ADA72698	ADA72698	Rice gene	
c 823	15	5.1	2000	7	ADA69039	ADA69039	Rice gene	
c 824	15	5.1	2003	4	ABL19153	ABL19153	Drosophill	
c 825	15	5.1	2009	6	ABX09827	ABX09827	Arabidops	
826	15	5.1	2018	6	ABE11954	ABE11954	Human pol	
827	15	5.1	2036	6	ADD69644	ADD69644	Human REM	
c 828	15	5.1	2036	6	ABL29841	ABL29841	Drosophill	
c 829	15	5.1	2136	7	ABX08460	ABX08460	DNA encod	
830	15	5.1	2179	4	AAE58600	AAE58600	Human REC	
831	15	5.1	2183	4	ABL25012	ABL25012	Drosophill	
832	15	5.1	2271	3	AAE39453	AAE39453	Arabidops	
833	15	5.1	2276	4	ABL23704	ABL23704	Drosophill	
834	15	5.1	2286	6	ABL38066	ABL38066	cDNA of n	
835	15	5.1	2246	2	AAE49160	AAE49160	Partial D	
836	15	5.1	2400	6	ABZ32122	ABZ32122	Candida a	
837	15	5.1	2457	4	AAH15791	AAH15791	Human cDN	
838	15	5.1	2457	6	ABJ53519	ABJ53519	Human rec	
839	15	5.1	2457	9	ABA95212	ABA95212	Human mel	
840	15	5.1	2457	9	ACF79543	ACF79543	Human tra	
841	15	5.1	2463	6	ABK75400	ABK75400	Bacillus	
842	15	5.1	2474	4	ABL25010	ABL25010	Drosophill	
c 843	15	5.1	2481	7	AAE25945	AAE25945	Human cDN	
c 844	15	5.1	2481	7	ABK73286	ABK73286	Human nov	
c 845	15	5.1	2497	4	ABL12037	ABL12037	Drosophill	
846	15	5.1	2499	7	ACA29300	ACA29300	Prokaryot	
c 847	15	5.1	2441	4	ABL27442	ABL27442	Drosophill	
848	15	5.1	2570	4	ABL13332	ABL13332	Drosophill	
c 849	15	5.1	2598	4	AAI64886	AAI64886	Korlletia	
c 850	15	5.1	2604	4	AAH15797	AAH15797	Human cDN	
c 851	15	5.1	2631	3	AAV92471	AAV92471	Shewanell	
c 852	15	5.1	2652	3	AAV71573	AAV71573	V. marinu	
853	15	5.1	2672	4	ABL23702	ABL23702	Drosophill	
c 854	15	5.1	2678	9	ADB62602	ADB62602	Human cDN	
855	15	5.1	2680	4	AAH16335	AAH16335	Human cDN	
856	15	5.1	2689	6	ABJ41575	ABJ41575	Human zln	
c 857	15	5.1	2711	3	AAI48642	AAI48642	Rat Mp-10	
c 858	15	5.1	2711	3	AAI48642	AAI48642	Rat Mp-10	
859	15	5.1	2725	6	ABK35276	ABK35276	Drosophill	
860	15	5.1	2742	9	ABK35276	ABK35276	Human cDN	
861	15	5.1	2769	6	ABE11334	ABE11334	Human pol	
862	15	5.1	2776	5	ABA20040	ABA20040	Human ner	
c 863	15	5.1	2840	4	AAH14222	AAH14222	Human cDN	
864	15	5.1	2840	6	ABJ53518	ABJ53518	Human rec	
865	15	5.1	2840	6	ABA95211	ABA95211	Human mel	
866	15	5.1	2840	9	ACF79542	ACF79542	Human tra	
867	15	5.1	2841	2	AAV74488	AAV74488	Staphyloc	
868	15	5.1	2844	4	ABL22730	ABL22730	Drosophill	
869	15	5.1	2853	7	ACA37230	ACA37230	Prokaryot	
870	15	5.1	2860	4	AAH42602	AAH42602	Nucleotid	
871	15	5.1	2872	2	AAQ21001	AAQ21001	Murine re	
872	15	5.1	2872	2	AAE29833	AAE29833	Mouse rec	
873	15	5.1	2881	4	AAE27019	AAE27019	Human enco	
874	15	5.1	2881	4	ADB93197	ADB93197	Human cDN	
875	15	5.1	2942	7	ADA53471	ADA53471	Human cod	
876	15	5.1	2968	4	ABL03856	ABL03856	Drosophill	
877	15	5.1	3021	4	AAH52380	AAH52380	S. epider	
c 878	15	5.1	3034	6	ABQ14764	ABQ14764	Oligonuc	
c 879	15	5.1	3034	6	ABQ14764	ABQ14764	Oligonuc	
880	15	5.1	3081	2	AAE67442	AAE67442	H. pylori	
881	15	5.1	3098	4	ABL28340	ABL28340	Drosophill	
882	15	5.1	3125	9	ADE58074	ADE58074	Human gen	
c 883	15	5.1	3125	9	ADE58070	ADE58070	Human gen	
c 884	15	5.1	3129	7	ACE03435	ACE03435	Mycoplasma	
885	15	5.1	3148	4	AAH54695	AAH54695	S. epider	
886	15	5.1	3148	6	ABQ70799	ABQ70799	Listeria	
887	15	5.1	3162	4	AAE51358	AAE51358	Enterococ	
888	15	5.1	3173	4	AAH54390	AAH54390	S. epider	
c 889	15	5.1	3199	5	AAE87511	AAE87511	DNA encod	
c 890	15	5.1	3213	5	AAE65545	AAE65545	Drosophill	
891	15	5.1	3251	4	ABL03846	ABL03846	Drosophill	
892	15	5.1	3270	4	ABL27736	ABL27736	Drosophill	
893	15	5.1	3278	7	ACC00397	ACC00397	Human cel	
894	15	5.1	3295	4	AAE36186	AAE36186	Human car	
895	15	5.1	3295	4	AAE71764	AAE71764	Human imm	
896	15	5.1	3295	4	AAE71764	AAE71764	Human imm	
897	15	5.1	3295	4	AAE71764	AAE71764	Human imm	
898	15	5.1	3295	4	AAE71764	AAE71764	Human imm	
899	15	5.1	3308	4	AAE91599	AAE91599	Essential	
c 900	15	5.1	3308	4	AAE91599	AAE91599	Staphyloc	
c 901	15	5.1	3308	4	AAE91599	AAE91599	Staphyloc	
c 902	15	5.1	3308	4	AAE91599	AAE91599	Staphyloc	
903	15	5.1	3344	9	AAH54738	AAH54738	Antibacte	
904	15	5.1	3368	5	AAE75563	AAE75563	Mutant ba	
905	15	5.1	3373	6	AAE93388	AAE93388	S. epider	
906	15	5.1	3410	4	ABL18618	ABL18618	Human NOV	
c 907	15	5.1	3440	7	ABE24210	ABE24210	Human NOV	
c 908	15	5.1	3481	7	ABE24207	ABE24207	Human SLC	
c 909	15	5.1	3492	4	AAI06161	AAI06161	Human rep	
910	15	5.1	3526	6	ABQ61182	ABQ61182	FL20047	
c 911	15	5.1	3545	4	AAE25965	AAE25965	Human cDN	
c 912	15	5.1	3545	7	ABX73306	ABX73306	Human nov	
c 913	15	5.1	3562	4	ABL06749	ABL06749	Drosophill	
c 914	15	5.1	3594	7	ACA20853	ACA20853	Prokaryot	
915	15	5.1	3627	4	AAE52893	AAE52893	Enterococ	
916	15	5.1	3639	4	AAE51721	AAE51721	Staphyloc	
917	15	5.1	3651	7	ACA18351	ACA18351	Prokaryot	
918	15	5.1	3651	7	ACF74791	ACF74791	Staphyloc	

919 15 5.1 3652 4 ABL16754 ABL16754 Drosophila
920 15 5.1 3654 4 AAS54788 AAS54788 Stephyloc
921 15 5.1 3654 7 ABT15084 ABT15084 Pathogen
922 15 5.1 3654 7 ACA19742 ACA19742 Prokaryot
923 15 5.1 3658 4 ABL17782 ABL17782 Prokaryot
924 15 5.1 3666 4 AAB54179 AAB54179 S. opider
925 15 5.1 3672 7 ACA46452 ACA46452 Prokaryot
926 15 5.1 3674 6 AAS57736 AAS57736 cDNA enco
927 15 5.1 3754 2 AAV74689 AAV74689 Stephyloc
928 15 5.1 3809 4 ABL10069 ABL10069 Drosophila
929 15 5.1 3870 4 AAK84271 AAK84271 Human imm
930 15 5.1 3934 2 AAT97233 AAT97233 Trlmed e
931 15 5.1 4020 7 ABE24206 ABE24206 Human SLC
932 15 5.1 4034 4 ABL09372 ABL09372 Drosophila
933 15 5.1 4038 4 ABL29090 ABL29090 Drosophila
934 15 5.1 4116 6 ABR24522 ABR24522 EIF-2a1ph
935 15 5.1 4125 4 AAK84260 AAK84260 Human imm
936 15 5.1 4129 4 AAK84261 AAK84261 Human imm
937 15 5.1 4199 6 ABO71077 ABO71077 Listeria
938 15 5.1 4200 4 ABL17628 ABL17628 Drosophila
939 15 5.1 4204 4 ABL21160 ABL21160 Drosophila
940 15 5.1 4327 6 AAS56408 AAS56408 Human DNA
941 15 5.1 4361 5 AAS84867 AAS84867 DNA enco
942 15 5.1 4398 3 ACA3063 ACA3063 Arabidops
943 15 5.1 4409 6 ABR89163 ABR89163 cDNA enco
944 15 5.1 4441 3 AAA47759 AAA47759 KIAA0160
945 15 5.1 4441 6 ABL69961 ABL69961 Pancreas
946 15 5.1 4441 6 ABR89162 ABR89162 cDNA enco
947 15 5.1 4455 4 ABL03329 ABL03329 Drosophila
948 15 5.1 4465 6 AAV77992 AAV77992 Hypoxia-r
949 15 5.1 4465 7 ABX08805 ABX08805 Angiogene
950 15 5.1 4465 8 ACS57774 ACS57774 Human cyc
951 15 5.1 4465 9 ACT9931 ACT9931 Breast ca
952 15 5.1 4496 7 ACA03925 ACA03925 cDNA down
953 15 5.1 4496 7 ABX63478 ABX63478 Human cDN
954 15 5.1 4582 4 AAK72026 AAK72026 Human imm
955 15 5.1 4594 2 AAV74511 AAV74511 Stephyloc
956 15 5.1 4623 4 ABL12280 ABL12280 Drosophila
957 15 5.1 4750 9 ADE25722 ADE25722 Human cDN
958 15 5.1 4802 7 ABE68141 ABE68141 Human sec
959 15 5.1 4802 7 ABE74620 ABE74620 Secreted
960 15 5.1 4802 9 ADC21011 ADC21011 Human sec
961 15 5.1 4910 4 ABL12036 ABL12036 Drosophila
962 15 5.1 4997 7 ACA47636 ACA47636 Prokaryot
963 15 5.1 4998 4 AAK65373 AAK65373 Human imm
964 15 5.1 5082 6 ABQ70953 ABQ70953 Listeria
965 15 5.1 5127 6 ABN80074 ABN80074 Human che
966 15 5.1 5151 4 ABL29840 ABL29840 Drosophila
967 15 5.1 5152 6 ABL49347 ABL49347 Human pol
968 15 5.1 5251 4 ABL15640 ABL15640 Drosophila
969 15 5.1 5251 4 AAS57144 AAS57144 DNA enco
970 15 5.1 5270 6 ABL33039 ABL33039 Human imm
971 15 5.1 5278 6 ABL92238 ABL92238 Chemicall
972 15 5.1 5312 6 ABK39897 ABK39897 Human che
973 15 5.1 5312 6 ABL32842 ABL32842 Human imm
974 15 5.1 5364 6 ABK40005 ABK40005 Human che

976 15 5.1 5373 4 ABL16748 ABL16748 Drosophila
977 15 5.1 5388 6 ABR31344 ABR31344 Signal tr
978 15 5.1 5388 6 ABL70305 ABL70305 Chemicall
979 15 5.1 5388 6 AAS61239 AAS61239 Human gen
980 15 5.1 5556 4 ABL09460 ABL09460 Drosophila
981 15 5.1 5721 6 ABQ71037 ABQ71037 Listeria
982 15 5.1 5740 3 AAA61521 AAA61521 A. vitis
983 15 5.1 5740 3 AAB61522 AAB61522 A. vitis
984 15 5.1 5758 6 ABL32660 ABL32660 Human imm
985 15 5.1 5763 6 ABL32183 ABL32183 Human imm
986 15 5.1 5798 6 ABL33666 ABL33666 Human imm
987 15 5.1 5832 6 ABR80281 ABR80281 Human imm
988 15 5.1 5863 4 ABL28882 ABL28882 Drosophila
989 15 5.1 5966 2 AAV74333 AAV74333 Stephyloc
990 15 5.1 6022 4 AAS46662 AAS46662 Tumour su
991 15 5.1 6042 6 ABL33945 ABL33945 Human imm
992 15 5.1 6056 4 AAS46363 AAS46363 Tumour su
993 15 5.1 6056 6 ABL32780 ABL32780 Human imm
994 15 5.1 6089 6 ABR80235 ABR80235 Human che
995 15 5.1 6101 6 ABL33475 ABL33475 Human imm
996 15 5.1 6114 6 ABL32760 ABL32760 Human imm
997 15 5.1 6117 6 ABL34491 ABL34491 Human met
998 15 5.1 6123 6 ABL33036 ABL33036 Human imm
999 15 5.1 6124 6 ABL32964 ABL32964 Human imm
1000 15 5.1 6124 6 ABL34516 ABL34516 Human met

RESULT 1
AAA68253 standard; DNA; 297 BP.
ID AAA68253; standard; DNA; 297 BP.
AC AAA68253;
XX
XX
DT 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
DE Bacteriophage 77 77ORF182 nucleotide sequence.
XX
XX
KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
XX
OS Staphylococcus aureus; bacteriophage 77.
XX
XX
PN WO2000032825-A2.
PD
XX
XX
XX 08-JUN-2000.
XX
XX
XX 03-DEC-1999; 99WO-1B02040.
XX
XX
XX 03-DEC-1998; 98US-0110992R.
XX 03-JUN-1999; 99US-00326144.
XX 28-SEP-1999; 99US-00407804.
XX 30-SEP-1999; 99US-0157218P.

ALIGNMENTS

01-DEC-1999; 99US-0168777P.
02-DEC-1999; 99US-00434252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Polletier J, Gros P, Dubow M;
XX WPI, 2000-412361/35.
XX P-PSDB; AAB16528.
XX
XX Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
XX inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 163; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
XX coding region encoding a product active on an essential bacterial target.
XX The method comprises identifying a nucleic acid sequence encoding a gene
XX product that provides a bacteria-inhibiting function when an
XX uncharacterised bacteriophage infects a pathogenic bacterium. The
XX compound active on a target of a bacteriophage inhibitor protein in a
XX bacteria is used to treat or prevent a bacterial infection in an animal.
XX AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
XX nucleotide and protein sequences which are used in the exemplification of
XX the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
XX (Updated on 13-SEP-2003 to standardise 05 field.)
XX
SQ Sequence 297 BP; 123 A; 40 C; 57 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 297; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 9,4e-138; Indels 0; Gaps 0;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATATATTAACGAAACGAGGAGTCAAGTATATACAAATAGCGGAATC 60
DB 1 ATGTCATATATTAACGAAACGAGGAGTCAAGTATATAGCAATAGCGGAATC 60
XX
QY 61 ATACGCAAAATATTCATGTTACGATGATTTTAAAGTATTTAAAGTCAAT 120
DB 61 ATACGCAAAATATTCATGTTACGATGATTTTAAAGTATTTAAAGTCAAT 120
XX
QY 121 ATGGGCATATCAATACAAAGTTAAAGATGACACAGTACCAATTAACATGCTATATC 180
DB 121 ATGGGCATATCAATACAAAGTTAAAGATGACACAGTACCAATTAACATGCTATATC 180
XX
QY 181 GTAGATGAGATGACTTGAATGGCATCAAGCTATTTAAACCAAGATGATGATG 240
DB 181 GTAGATGAGATGACTTGAATGGCATCAAGCTATTTAAACCAAGATGATGATG 240
XX
QY 241 ATTGAAGAGACACAGACGACGACGACGACGACGACGACGACGACGACGACG 297
DB 241 ATTGAAGAGACACAGACGACGACGACGACGACGACGACGACGACGACGACG 297
XX

RESULT 2
AAA68247

AAA68247 standard; DNA; 41708 BP.
XX
XX AAA68247;
XX
XX 15-SEP-2003 (revised)
XX 06-AUG-2003 (revised)
XX 27-OCT-2000 (first entry)
XX
XX Bacteriophage 77 complete genome sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
XX bacterial growth inhibition; bacterial infection; ds.
XX
XX Staphylococcus aureus; bacteriophage 77.
XX
XX WO200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-1B002040.
XX
XX 03-DEC-1998; 98US-0110992P.
XX 03-JUN-1999; 99US-00326144.
XX 28-SEP-1999; 99US-00407804.
XX 30-SEP-1999; 99US-0157218P.
XX 01-DEC-1999; 99US-0168777P.
XX 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Polletier J, Gros P, Dubow M;
XX WPI, 2000-412361/35.
XX
XX Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
XX inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Example 3; Page 141-151; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
XX coding region encoding a product active on an essential bacterial target.
XX The method comprises identifying a nucleic acid sequence encoding a gene
XX product that provides a bacteria-inhibiting function when an
XX uncharacterised bacteriophage infects a pathogenic bacterium. The
XX compound active on a target of a bacteriophage inhibitor protein in a
XX bacteria is used to treat or prevent a bacterial infection in an animal.
XX AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
XX nucleotide and protein sequences which are used in the exemplification of
XX the present invention. (Updated on 06-AUG-2003 to correct 05 field.)
XX (Updated on 13-SEP-2003 to standardise 05 field.)
XX
SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;

Query Match 100.0%; Score 297; DB 3; Length 41708;
Best Local Similarity 100.0%; Pred. No. 7.0e-138;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTCAATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACGAAATAGCGAAATC 60
 DB 29268 ATGTTCAATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACGAAATAGCGAAATC 29327
 QY 61 ATACGCAAAAATATTCATGTTACGAGATTCATTTTAAAGTATTCATTTTAAAGGTGAT 120
 DB 29328 ATACGCAAAAATATTCATGTTACGAGATTCATTTTAAAGTATTCATTTTAAAGGTGAT 29387
 QY 121 ATGGGATATCAATACAGTTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 180
 DB 29388 ATGGGATATCAATACAGTTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 29447
 QY 181 GTAGATGAGATGACTAGATATGCGATCGAGCTATTATTACCAAGCAATAGATGATGG 240
 DB 29448 GTAGATGAGATGACTAGATATGCGATCGAGCTATTATTACCAAGCAATAGATGATGG 29507
 QY 241 ATTGAAGAGAACAGACGACAGACGAGACTAATTAACTTACTGATGAATGGTAG 297
 DB 29508 ATTGAAGAGAACAGACGACAGACGAGACTAATTAACTTACTGATGAATGGTAG 29564

RESULT 3
 AAC86106
 ID AAC86106 standard; cDNA; 41708 BP.
 AC AAC86106;
 XX
 AC 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Complete genome of bacteriophage 77.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 RW screening assay; ss.
 OS
 XX Bacteriophage.
 OS
 PN W0200146383-A2.
 XX
 XX 28-JUN-2001.
 PD
 XX 21-DEC-2000; 2000WO-US035180.
 PF
 XX 22-DEC-1999; 99US-00470512.
 PR 12-OCT-2000; 2000US-00689952.
 PA (PHAG-) PHAGE TECH INC.
 PA (WILL-) WILLIAMS K M.
 XX
 PI Pelletier J, Gros P, Dubow M;
 XX
 DR WPI, 2001-418052/44.
 PT Novel DnaI polypeptides useful for treating and diagnosing microbial,
 PT preferably bacterial, diseases such as those caused by Staphylococcus
 PT aureus.

XX
 PS Disclosure; Fig 2; 107bp; English.
 XX
 CC This sequence represents the genome of Bacteriophage 77. The growth
 CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
 CC aureus, to form the basis of a screening assay. DnaI polypeptides and
 CC polynucleotides are useful for treating microbial, preferably bacterial,
 CC especially Staphylococcal, infections. DnaI polypeptides and
 CC polynucleotides are useful for biological, diagnostic, prophylactic,
 CC clinical and therapeutic use, and as components in databases useful for
 CC search analyses as well as in sequence analysis algorithms. (Updated on
 CC 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 41708 BP; 15607 A; 5698 C; 8088 G; 12115 T; 0 U; 0 Other;
 Query Match 100.0%; Score 297; DB 4; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 7.6e-138;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTCAATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACGAAATAGCGAAATC 60
 DB 29268 ATGTTCAATATATTAACGAAAAACGAGAAAGTCAAGATGATATTACGAAATAGCGAAATC 29327
 QY 61 ATACGCAAAAATATTCATGTTACGAGATTCATTTTAAAGTATTCATTTTAAAGGTGAT 120
 DB 29328 ATACGCAAAAATATTCATGTTACGAGATTCATTTTAAAGTATTCATTTTAAAGGTGAT 29387
 QY 121 ATGGGATATCAATACAGTTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 180
 DB 29388 ATGGGATATCAATACAGTTTAAAGATATGACAAAGTACCAATTAAACATGCTTATGTC 29447
 QY 181 GTAGATGAGATGACTAGATATGCGATCGAGCTATTATTACCAAGCAATAGATGATGG 240
 DB 29448 GTAGATGAGATGACTAGATATGCGATCGAGCTATTATTACCAAGCAATAGATGATGG 29507
 QY 241 ATTGAAGAGAACAGACGACAGACGAGACTAATTAACTTACTGATGAATGGTAG 297
 DB 29508 ATTGAAGAGAACAGACGACAGACGAGACTAATTAACTTACTGATGAATGGTAG 29564

RESULT 4
 AAA68250
 ID AAA68250 standard; DNA; 261 BP.
 AC AAA68250;
 XX
 AC 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 77ORF043 nucleotide sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 RW bacterial growth inhibition; bacterial infection; ds.
 OS
 XX Staphylococcus aureus; bacteriophage 77.
 XX

PN WO200032825-A2.
XX
PD 08-JUN-2000.
XX
PF 03-DEC-1999; 99WO-1B002040.
XX
PR 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
PA (PHAG-) PHAGE TECH INC.
XX
PI Polletier J, Gros P, Dubow M;
XX WPI; 2000-412361/35.
DR P-PSDB; AAB16525.
XX
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 157; 456pp; English.
PS
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterized bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAB6243 to AAB69442 and AAB16523 to AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
XX (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
Query Match 87.9%; Score 261; DB 3; Length 261;
Boot Local Similarity 100.0%; Pred. No. 7.7e-120;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 ATGTATTACGAATAGCGCAATCATACGCAAAATATTCTATGTAACGATTCGATTT 96
DB 1 ATGTATTACGAATAGCGCAATCATACGCAAAATATTCTATGTAACGATTCGATTT 60
QY 97 AAGCTATCATTTTAAAGGTCAATGCGCATATCATACAGCTTAAAGATAGAACAC 156
DB 61 AAGCTATCATTTTAAAGGTCAATGCGCATATCATACAGCTTAAAGATAGAACAC 120
QY 157 GTACCAATTAAACATGCTTATGTCGTAGATGAGAAATGAGTAAATGCGATCACTTA 216
DB 121 GTACCAATTAAACATGCTTATGTCGTAGATGAGAAATGAGTAAATGCGATCACTTA 180
QY 217 TTAAACCAAGCATAGATGATGATTGAAGAAACAGACAGACAGACGACTAAT 276

DB 181 TTTAACCAAGCATAGATGATGATTGAAGAAACAGACAGACAGACGACTAAT 240
QY 277 AACTAGTCATGAATGCTAG 297
DB 241 AACTAGTCATGAATGCTAG 261
RESULT 5
ACF72925
ID ACF72925 standard; DNA; 267 BP.
XX
XX ACF72925;
AC
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus DNA #605.
DE
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target; gene; ds.
XX
XX Staphylococcus aureus.
OS
XX WO200294868-A2.
PN
XX 28-NOV-2002.
PD
XX 27-MAR-2002; 2002WO-1B002637.
PF
XX 27-MAR-2001; 2001GB-00007661.
PR
XX (CHIR-) CHIRON SPA.
PA
XX Masignani V, Mora M, Scarselli M;
XX WPI; 2003-120786/11.
DR P-PSDB; ABM71365.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
PS Claim 6; SEQ ID NO 1209; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus genes of the invention
XX
SQ Sequence 267 BP; 108 A; 31 C; 52 G; 76 T; 0 U; 0 Other;

Query Match 9.8%; Score 29; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 ATGATGATGATGAGAGACAGACGAA 261
 ||||||||||||||||||
 DB 206 ATGATGATGATGAGAGACAGACGAA 234

RESULT 6
 AAV75514
 ID AAV75514 standard; DNA; 580 BP.
 XX
 AC AAV75514;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus contig SEQ ID #1203.
 XX
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-00100117.
 XX
 PR 05-JAN-1996; 96US-0009861P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kunach CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
 XX
 DR WPI; 1997-374922/35.
 XX
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
 PT stored on computer readable medium and used in the production of anti-
 PT S.aureus vaccines.
 XX
 PS Claim 1; Page 1876; 3271pp; English.
 XX
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,

CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the computer
 CC readable medium

XX Sequence 580 BP; 255 A; 62 C; 123 G; 135 T; 0 U; 5 Other;
 SQ

Query Match 9.4%; Score 28; DB 2; Length 580;
 Best Local Similarity 100.0%; Pred. No. 0.00061;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 ACTAATTAAGTATGATGAAATGCTAG 297
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 DB 437 ACTAATTAAGTATGATGAAATGCTAG 464

RESULT 7
 AAA68609
 ID AAA68609 standard; DNA; 43576 BP.
 XX
 AC AAA68609;
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 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 96 complete genome sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 XX
 OS Staphylococcus aureus; bacteriophage 96.
 XX
 PN WO200032825-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-IB002040.
 XX
 PR 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1999; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 PI Pelletier J, Gros P, Dubow M;
 XX
 DR WPI; 2000-412361/35.
 XX
 PT Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that

OW nucleic - nucleic search, using SW model

Run on: October 14, 2004, 22:42:59 ; Search time 1388.12 Seconds

(without alignments)
6389.277 Million cell updates/sec

SUMMARIES

28: gb_gsa1: +
29: gb_gsa2: +
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Title:		US-09-407-804A-9
Perfect score:		297
Sequence:		1 atgttcacatataaacgaaa.....actagtcacatgaatggtg 297
Scoring table:		OLIGO_NUC Gapop 60.0 , Gapext 60.0
Searched:		27513289 seqs, 14931090276 residues
Word size :		0
Total number of hits satisfying chosen parameters:		55026578
Minimum DB seq length: 0		
Maximum DB seq length: 2000000000		
Post-processing: Listing first 1000 summaries		
Database :		EST: +
1:	em_estsba: +	
2:	em_estsba: +	
3:	em_estsba: +	
4:	em_estsba: +	
5:	em_estsba: +	
6:	em_estsba: +	
7:	em_estsba: +	
8:	em_estsba: +	
9:	gb_ests1: +	
10:	gb_ests2: +	
11:	gb_ests3: +	
12:	gb_ests3: +	
13:	gb_ests4: +	
14:	gb_ests5: +	
15:	em_estsfun: +	
16:	em_estsfun: +	
17:	em_gsa_hum: +	
18:	em_gsa_inv: +	
19:	em_gsa_pln: +	
20:	em_gsa_vrt: +	
21:	em_gsa_fun: +	
22:	em_gsa_man: +	
23:	em_gsa_mus: +	
24:	em_gsa_pro: +	
25:	em_gsa_rnd: +	
26:	em_gsa_phg: +	
27:	em_gsa_vrt: +	

Result	Score	Query	Match	Length	DB	ID	Description
1	23	7.7	1015	29	CNS07IMP		AL440663 T3 end of
2	20	6.7	571	12	B0618748		B0618748 B0618748
3	20	6.7	736	28	BH514116		BH514116 B06W267F
4	20	6.7	737	29	CE760387		CE760387 t1gr-gsa-
5	19	6.4	121	9	A1951540		A1951540 wv36d07.x
6	19	6.4	188	14	CF856022		CF856022 pMLO06uH
7	19	6.4	423	28	B2920613		B2920613 CH240_70C
8	19	6.4	522	29	CG428882		CG428882 ZMWBB024
9	19	6.4	540	29	BX183031		BX183031 Dantlo_r0r
10	19	6.4	614	28	A2938334		A2938334 ZM0196H21
11	19	6.4	656	14	CB330526		CB330526 SPES7506b
12	19	6.4	663	29	CE786696		CE786696 t1gr-gsa-
13	19	6.4	668	28	AZ466117		AZ466117 1M0278N03
14	19	6.4	672	28	AZ647829		AZ647829 1M0514J06
15	19	6.4	686	28	A0484294		A0484294 RPCI-11-2
16	19	6.4	692	13	BX777633		BX777633 BX777633
17	19	6.4	692	14	CA346528		CA346528 677448 NC
18	19	6.4	738	13	BU482454		BU482454 604129853
19	19	6.4	782	14	CK138726		CK138726 AGNOCOURT
20	19	6.4	828	28	B2422617		B2422617 1D5606.b
21	19	6.4	923	28	AZ539374		AZ539374 ENTGH84TF
22	19	6.4	935	28	AZ549644		AZ549644 ENTGL62TF
23	19	6.4	937	28	BH165826		BH165826 ENTQV67TF
24	19	6.4	968	29	CC976887		CC976887 ZUDH432TH
25	19	6.4	1349	10	BF973749		BF973749 602241818
26	18	6.1	303	28	AF179090		AF179090 AF179090
27	18	6.1	320	9	AA872489		AA872489 g110C03.s
28	18	6.1	347	29	CC859605		CC859605 NDL.101N1
29	18	6.1	349	28	BH825920		BH825920 BACPR2-J
30	18	6.1	354	9	AA282587		AA282587 z59C002.r
31	18	6.1	360	28	A0265943		A0265943 CTRBT-EL-
32	18	6.1	390	28	B37409		B37409 HS-1043-B1-
33	18	6.1	403	29	CE641065		CE641065 t1gr-gsa-
34	18	6.1	408	9	AA088591		AA088591 2K64d07.r
35	18	6.1	409	9	AA630685		AA630685 a665d06.s
36	18	6.1	412	9	AA255702		AA255702 z521C04.r
37	18	6.1	414	10	AW917645		AW917645 EST348949
38	18	6.1	414	13	BY484641		BY484641 BY484641
39	18	6.1	416	28	AZ598867		AZ598867 1M0413H22
40	18	6.1	420	10	AW917612		AW917612 EST348916
41	18	6.1	420	10	AW917643		AW917643 EST348947
42	18	6.1	444	28	BH212049		BH212049 SALX_0070
43	18	6.1	457	29	CE704213		CE704213 t1gr-gsa-
44	18	6.1	458	9	AA047153		AA047153 2K74f07.r
45	18	6.1	461	12	B046548		B046548 B046548

c 46	18	6.1	462	13	BV573081	BV573081	103	18	6.1	699	14	CB466979	CB466979	732693	MA
c 47	18	6.1	463	29	CG989891	CG989891	c 104	18	6.1	705	14	CF795789	CF795789	891982	MA
c 48	18	6.1	468	14	BX93248	T693248	105	18	6.1	706	13	BK488598	BK488598	126586	MA
c 49	18	6.1	486	29	BX124558	BX124558	106	18	6.1	708	12	BG809404	BG809404	mphe0032x	MA
c 50	18	6.1	494	12	BX046014	BX046014	c 107	18	6.1	710	13	BK677557	BK677557	UI-CF-EEO	MA
c 51	18	6.1	495	13	BX872646	BX872646	108	18	6.1	713	29	BK172652	BK172652	Danlo	for
c 52	18	6.1	508	28	AO375859	AO375859	109	18	6.1	715	29	CE217017	CE217017	UI-CF-EEO	MA
c 53	18	6.1	509	9	AM021842	AM021842	c 110	18	6.1	717	29	CG275417	CG275417	OGC1067H	MA
c 54	18	6.1	510	12	B1963093	B1963093	111	18	6.1	720	29	CG275417	CG275417	OGC1067H	MA
c 55	18	6.1	511	9	AA601416	AA601416	112	18	6.1	723	28	B2458710	B2458710	BMF637F	MA
c 56	18	6.1	511	9	AA146950	AA146950	113	18	6.1	725	9	AI1290974	AI1290974	gm15c08.x	MA
c 57	18	6.1	515	10	BB031338	BB031338	114	18	6.1	748	12	B1087876	B1087876	602852679	MA
c 58	18	6.1	518	9	A1958218	A1958218	c 115	18	6.1	749	29	CS024247	CS024247	TEtracdon	MA
c 59	18	6.1	524	12	B0642732	B0642732	c 116	18	6.1	760	14	CA312676	CA312676	UI-CF-FNO	MA
c 60	18	6.1	532	14	CB718807	CB718807	117	18	6.1	779	10	BES19851	BES19851	601061965	MA
c 61	18	6.1	532	29	CE201002	CE201002	c 118	18	6.1	780	28	B2085908	B2085908	11h3Bb01.	MA
c 62	18	6.1	533	28	A2553820	A2553820	119	18	6.1	785	13	B0246775	B0246775	603593512	MA
c 63	18	6.1	533	28	B2518982	B2518982	120	18	6.1	790	28	BH527597	BH527597	BOCZ7307R	MA
c 64	18	6.1	546	13	BU395921	BU395921	121	18	6.1	799	29	BK200998	BK200998	Danlo	for
c 65	18	6.1	547	10	BF34762	BF34762	c 122	18	6.1	804	13	BU620191	BU620191	UI-H-FIL-	MA
c 66	18	6.1	560	12	BU070385	BU070385	123	18	6.1	811	10	BE614108	BE614108	601503850	MA
c 67	18	6.1	563	9	AV590721	AV590721	124	18	6.1	824	9	AU118315	AU118315	10118315	MA
c 68	18	6.1	563	12	BM190058	BM190058	125	18	6.1	830	12	BG784002	BG784002	SEAMC003	MA
c 69	18	6.1	564	28	BH008339	BH008339	c 126	18	6.1	833	28	AZ702636	AZ702636	RPCI-23-2	MA
c 70	18	6.1	573	12	BI444760	BI444760	127	18	6.1	838	28	BH660714	BH660714	BH660714	MA
c 71	18	6.1	575	29	CE495919	CE495919	c 128	18	6.1	841	13	BU116745	BU116745	603139747	MA
c 72	18	6.1	578	14	CA386811	CA386811	c 129	18	6.1	843	29	CG825123	CG825123	SOVACS4TV	MA
c 73	18	6.1	584	14	CD678706	CD678706	c 130	18	6.1	846	14	CA987036	CA987036	AGNOCOURT	MA
c 74	18	6.1	588	14	CA650925	CA650925	131	18	6.1	847	10	BF694081	BF694081	602082686	MA
c 75	18	6.1	590	9	AL704631	AL704631	132	18	6.1	855	13	BK467886	BK467886	BK467886	MA
c 76	18	6.1	592	9	AA818734	AA818734	133	18	6.1	872	12	EG399577	EG399577	602441871	MA
c 77	18	6.1	598	12	BM970383	BM970383	134	18	6.1	891	10	BF618320	BF618320	CHME000	MA
c 78	18	6.1	602	13	BU070239	BU070239	c 135	18	6.1	900	29	CC509879	CC509879	4540	MA
c 79	18	6.1	606	9	AA149491	AA149491	136	18	6.1	910	13	BU201993	BU201993	603951810	MA
c 80	18	6.1	606	14	CA375660	CA375660	137	18	6.1	920	14	CF108627	CF108627	Shu1tzm1	MA
c 81	18	6.1	609	14	CD931537	CD931537	138	18	6.1	937	13	BU481226	BU481226	603469859	MA
c 82	18	6.1	628	12	BM509287	BM509287	139	18	6.1	964	10	BF209546	BF209546	601872730	MA
c 83	18	6.1	632	12	BI492771	BI492771	c 140	18	6.1	998	28	B2466016	B2466016	BONK647F	MA
c 84	18	6.1	645	29	CE511088	CE511088	c 141	18	6.1	1149	28	CC274388	CC274388	CH261-112	MA
c 85	18	6.1	648	12	BU091083	BU091083	142	18	6.1	1183	10	BE875565	BE875565	601487003	MA
c 86	18	6.1	650	14	CA780127	CA780127	143	18	6.1	4693	11	AK081376	AK081376	Mus muscu	MA
c 87	18	6.1	653	28	A2638156	A2638156	144	17	5.7	178	14	CB870415	CB870415	HCI4E06w	MA
c 88	18	6.1	656	29	CG069104	CG069104	c 145	17	5.7	190	14	CB485548	CB485548	otchenh10	MA
c 89	18	6.1	657	13	BU433855	BU433855	146	17	5.7	212	10	BF228723	BF228723	SMOVL3CAN	MA
c 90	18	6.1	658	10	BF637378	BF637378	c 147	17	5.7	213	10	BE009943	BE009943	PM3-RN017	MA
c 91	18	6.1	667	10	BE539553	BE539553	148	17	5.7	214	9	AV020077	AV020077	PFES20ab2	MA
c 92	18	6.1	672	14	CA310990	CA310990	149	17	5.7	227	13	BQ597041	BQ597041	AV020077	MA
c 93	18	6.1	677	13	BQ477501	BQ477501	c 150	17	5.7	229	12	BM027341	BM027341	G1T000068	MA
c 94	18	6.1	681	12	BM491033	BM491033	151	17	5.7	233	28	AZ782938	AZ782938	2M0024P12	MA
c 95	18	6.1	682	14	CF272187	CF272187	152	17	5.7	243	9	AU059887	AU059887	NU059887	MA
c 96	18	6.1	682	28	BH429060	BH429060	153	17	5.7	245	9	AA1715175	AA1715175	AL715175	MA
c 97	18	6.1	682	29	CE721090	CE721090	154	17	5.7	247	9	AA121205	AA121205	zn30b10.f	MA
c 98	18	6.1	684	14	CF273024	CF273024	c 155	17	5.7	260	13	BQ758163	BQ758163	EBEmn10.SQ	MA
c 99	18	6.1	685	14	CD931536	CD931536	c 156	17	5.7	263	14	CD141160	CD141160	MGI-0069T	MA
c 100	18	6.1	688	14	CA367832	CA367832	157	17	5.7	282	10	BF803200	BF803200	CMO-CT013	MA
c 101	18	6.1	688	14	CA775922	CA775922	c 158	17	5.7	287	12	BI703410	BI703410	fs90c04.x	MA
c 102	18	6.1	698	28	AZ702634	AZ702634	159	17	5.7	298	9	AV339529	AV339529	AV339529	MA

c 160	17	5.7	299	14	CD063005	c 217	17	5.7	446	14	CD159741
c 161	17	5.7	301	9	AV428985	c 218	17	5.7	447	13	BX556924
c 162	17	5.7	305	12	BT103411	c 219	17	5.7	449	9	A1384718
c 163	17	5.7	314	14	CF002778	c 220	17	5.7	455	13	BY472564
c 164	17	5.7	321	14	CD159773	c 221	17	5.7	455	14	BY472564
c 165	17	5.7	325	12	BG354250	c 222	17	5.7	455	14	H43732
c 166	17	5.7	338	12	BG354250	c 223	17	5.7	458	9	AJ283752
c 167	17	5.7	340	9	AL501134	c 224	17	5.7	459	9	AA794496
c 168	17	5.7	345	10	AA481192	c 225	17	5.7	460	14	CB737792
c 169	17	5.7	347	13	CA000609	c 226	17	5.7	462	12	BI880146
c 170	17	5.7	348	9	AA487238	c 227	17	5.7	462	29	CE697617
c 171	17	5.7	351	28	AZ417905	c 228	17	5.7	463	14	CF165371
c 172	17	5.7	352	13	BO518498	c 229	17	5.7	463	28	AZ445372
c 173	17	5.7	359	29	CE018865	c 230	17	5.7	465	28	AZ647024
c 174	17	5.7	360	13	CA7083	c 231	17	5.7	476	14	CD151335
c 175	17	5.7	360	14	D76260	c 232	17	5.7	479	28	AZ165551
c 176	17	5.7	360	28	CC428366	c 233	17	5.7	485	13	BY243809
c 177	17	5.7	361	10	AM164055	c 234	17	5.7	485	29	CE629783
c 178	17	5.7	361	12	BT103322	c 235	17	5.7	486	28	BH437709
c 179	17	5.7	364	28	AZ702724	c 236	17	5.7	490	14	CD923032
c 180	17	5.7	365	12	BG380121	c 237	17	5.7	490	28	AQ213527
c 181	17	5.7	378	14	CD171473	c 238	17	5.7	495	9	AA534580
c 182	17	5.7	382	12	BI863990	c 239	17	5.7	495	12	BM737776
c 183	17	5.7	386	13	BU882152	c 240	17	5.7	496	12	BJ461905
c 184	17	5.7	388	12	BI992287	c 241	17	5.7	498	12	BM959014
c 185	17	5.7	394	13	BK492477	c 242	17	5.7	498	12	EM025230
c 186	17	5.7	395	13	BT613376	c 243	17	5.7	500	12	AJ086596
c 187	17	5.7	399	9	AV653367	c 244	17	5.7	501	9	BU462291
c 188	17	5.7	399	9	AV653455	c 245	17	5.7	503	29	CG161066
c 189	17	5.7	403	13	BY510745	c 246	17	5.7	504	10	BF439218
c 190	17	5.7	403	14	CB766715	c 247	17	5.7	509	28	AQ321707
c 191	17	5.7	405	14	CD066383	c 248	17	5.7	510	28	AQ440696
c 192	17	5.7	407	9	AA332691	c 249	17	5.7	513	29	CG865295
c 193	17	5.7	408	10	BE237268	c 250	17	5.7	516	10	BB134753
c 194	17	5.7	410	28	AQ363028	c 251	17	5.7	516	10	BB640566
c 195	17	5.7	411	13	BY623508	c 252	17	5.7	518	28	BH820400
c 196	17	5.7	414	13	BY623508	c 253	17	5.7	518	9	A1732799
c 197	17	5.7	417	14	CD180546	c 254	17	5.7	518	10	AM505521
c 198	17	5.7	417	28	AQ186008	c 255	17	5.7	518	12	BM959057
c 199	17	5.7	419	9	AA487179	c 256	17	5.7	518	14	CA360520
c 200	17	5.7	420	9	AI686161	c 257	17	5.7	519	13	CA000637
c 201	17	5.7	421	13	BQ662116	c 258	17	5.7	520	12	BI864898
c 202	17	5.7	423	29	CC945736	c 259	17	5.7	521	14	CD489268
c 203	17	5.7	424	14	CD179786	c 260	17	5.7	524	14	CD535231
c 204	17	5.7	426	13	BK106841	c 261	17	5.7	524	28	AZ433259
c 205	17	5.7	427	12	BM17861	c 262	17	5.7	526	12	BI350855
c 206	17	5.7	428	29	CE292254	c 263	17	5.7	528	14	CB485130
c 207	17	5.7	434	9	AV792912	c 264	17	5.7	532	13	CA001132
c 208	17	5.7	436	14	CB792209	c 265	17	5.7	532	14	N65371
c 209	17	5.7	439	14	CD071932	c 266	17	5.7	533	28	BH774356
c 210	17	5.7	442	14	CD163698	c 267	17	5.7	535	28	AZ058293
c 211	17	5.7	442	29	DN246167	c 268	17	5.7	535	28	AQ582734
c 212	17	5.7	443	10	BB736326	c 269	17	5.7	536	14	CB223434
c 213	17	5.7	443	10	BB840465	c 270	17	5.7	536	28	BZ130904
c 214	17	5.7	443	28	AQ333975	c 271	17	5.7	537	28	AZ043135
c 215	17	5.7	444	28	AZ664379	c 272	17	5.7	538	13	BY474785
c 216	17	5.7	445	14	N65216	c 273	17	5.7	539	9	AL911728
c 160	17	5.7	299	14	CD063005	c 217	17	5.7	446	14	CD159741
c 161	17	5.7	301	9	AV428985	c 218	17	5.7	447	13	BX556924
c 162	17	5.7	305	12	BT103411	c 219	17	5.7	449	9	A1384718
c 163	17	5.7	314	14	CF002778	c 220	17	5.7	455	13	BY472564
c 164	17	5.7	321	14	CD159773	c 221	17	5.7	455	14	BY472564
c 165	17	5.7	325	12	BG354250	c 222	17	5.7	455	14	H43732
c 166	17	5.7	338	12	BG354250	c 223	17	5.7	458	9	AJ283752
c 167	17	5.7	340	9	AL501134	c 224	17	5.7	459	9	AA794496
c 168	17	5.7	345	10	AA481192	c 225	17	5.7	460	14	CB737792
c 169	17	5.7	347	13	CA000609	c 226	17	5.7	462	12	BI880146
c 170	17	5.7	348	9	AA487238	c 227	17	5.7	462	29	CE697617
c 171	17	5.7	351	28	AZ417905	c 228	17	5.7	463	14	CF165371
c 172	17	5.7	352	13	BO518498	c 229	17	5.7	463	28	AZ445372
c 173	17	5.7	359	29	CE018865	c 230	17	5.7	465	28	AZ647024
c 174	17	5.7	360	13	CA7083	c 231	17	5.7	476	14	CD151335
c 175	17	5.7	360	14	D76260	c 232	17	5.7	479	28	AZ165551
c 176	17	5.7	360	28	CC428366	c 233	17	5.7	485	13	BY243809
c 177	17	5.7	361	10	AM164055	c 234	17	5.7	485	29	CE629783
c 178	17	5.7	361	12	BT103322	c 235	17	5.7	486	28	BH437709
c 179	17	5.7	364	28	AZ702724	c 236	17	5.7	490	14	CD923032
c 180	17	5.7	365	12	BG380121	c 237	17	5.7	490	28	AQ213527
c 181	17	5.7	378	14	CD171473	c 238	17	5.7	495	9	AA534580
c 182	17	5.7	382	12	BI863990	c 239	17	5.7	495	12	BM737776
c 183	17	5.7	386	13	BU882152	c 240	17	5.7	496	12	BJ461905
c 184	17	5.7	388	12	BI992287	c 241	17	5.7	498	12	BM959014
c 185	17	5.7	394	13	BK492477	c 242	17	5.7	498	12	EM025230
c 186	17	5.7	395	13	BT613376	c 243	17	5.7	500	12	AJ086596
c 187	17	5.7	399	9	AV653367	c 244	17	5.7	501	9	BU462291
c 188	17	5.7	399	9	AV653455	c 245	17	5.7	503	29	CG161066
c 189	17	5.7	403	13	BY510745	c 246	17	5.7	504	10	BF439218
c 190	17	5.7	403	14	CB766715	c 247	17	5.7	509	28	AQ321707
c 191	17	5.7	405	14	CD066383	c 248	17	5.7	510	28	AQ440696
c 192	17	5.7	407	9	AA332691	c 249	17	5.7	513	29	CG865295
c 193	17	5.7	408	10	BE237268	c 250	17	5.7	516	10	BB134753
c 194	17	5.7	410	28	AQ363028	c 251	17	5.7	516	10	BB640566
c 195	17	5.7	411	13	BY623508	c 252	17	5.7	518	28	BH820400
c 196	17	5.7	414	13	BY623508	c 253	17	5.7	518	9	A1732799
c 197	17	5.7	417	14	CD180546	c 254	17	5.7	518	10	AM505521
c 198	17	5.7	417	28	AQ186008	c 255	17	5.7	518	12	BM959057
c 199	17	5.7	419	9	AA487179	c 256	17	5.7	518	14	CA360520
c 200	17	5.7	420	9	AI686161	c 257	17	5.7	519	13	CA000637
c 201	17	5.7	421	13	BQ662116	c 258	17	5.7	520	12	BI864898
c 202	17	5.7	423	29	CC945736	c 259	17	5.7	521	14	CD489268
c 203	17	5.7	424	14	CD179786	c 260	17	5.7	524	14	CD535231
c 204	17	5.7	426	13	BK106841	c 261	17	5.7	524	28	AZ433259
c 205	17	5.7	427	12	BM17861	c 262	17	5.7	526	12	BI350855
c 206	17	5.7	428	29	CE292254	c 263	17	5.7	528	14	CB485130
c 207	17	5.7	434	9	AV792912	c 264	17	5.7	532	13	CA001132
c 208	17	5.7	436	14	CB792209	c 265	17	5.7	532	14	N65371
c 209	17	5.7	439	14	CD071932	c 266	17	5.7	533	28	BH774356
c 210	17	5.7	442	14	CD163698	c 267	17	5.7	535	28	AZ058293
c 211	17	5.7	442	29	DN246167	c 268	17	5.7	535	28	AQ582734
c 212	17	5.7	443	10	BB736326	c 269	17	5.7	536	14	CB223434
c 213	17	5.7	443	10	BB840465	c 270	17	5.7	536	28	BZ130904
c 214	17	5.7	443	28	AQ333975	c 271	17	5.7	537	28	AZ043135
c 215	17	5.7	444	28	AZ664379	c 272	17	5.7	538	13	BY474785
c 216	17	5.7	445	14	N65216	c 273	17	5.7	539	9	AL911728
c 160	17	5.7	299	14	CD063005	c 217	17	5.7	446	14	CD159741
c 161	17	5.7	301	9	AV428985	c 218	17	5.7	447	13	BX556924

c 274	17	5.7	539	9	AL925185	AL925185	AL925185	331	17	5.7	592	12	B1429029	B1429029	f71f603.y
c 275	17	5.7	539	12	B0191717	B0191717	B0191717	c 332	17	5.7	597	28	CC393970	CC393970	PUEFLA37D
c 276	17	5.7	541	12	BE082063	H3072A10-	BE082063	333	17	5.7	598	12	BJ497547	BJ497547	B1497547
c 277	17	5.7	541	12	BM160508	EST563031-	BM160508	334	17	5.7	598	13	BQ723941	BQ723941	AGNOCOUNT
c 278	17	5.7	541	14	CF893896	A0128H12-	CF893896	c 335	17	5.7	599	10	AM967305	AM967305	EST379980
c 279	17	5.7	543	28	A2521059	RPCT-11-2	A2521059	c 336	17	5.7	600	12	BG802981	BG802981	01933-45 M
c 280	17	5.7	544	28	AZ043949	RPCT-23-2	AZ043949	c 337	17	5.7	600	13	B0919815	B0919815	6041-11 M
c 281	17	5.7	546	14	AM333189	S18F4 AGS	AM333189	c 338	17	5.7	602	9	AL699109	AL699109	DKE2P686B
c 282	17	5.7	548	14	CA194954	SCG58108	CA194954	c 339	17	5.7	602	9	AL719598	AL719598	AL719598
c 283	17	5.7	548	14	CF532854	UI-M-GH0-	CF532854	c 340	17	5.7	602	12	BJ103294	BJ103294	BU103294
c 284	17	5.7	550	10	AM773600	EST332586	AM773600	c 341	17	5.7	602	13	EX082315	EX082315	BX082315
c 285	17	5.7	551	12	BI429315	BI429315	BI429315	c 342	17	5.7	602	13	CA025081	CA025081	H251C14F
c 286	17	5.7	552	12	BI428471	f7e6a03.y	BI428471	c 343	17	5.7	602	29	CE203399	CE203399	LIgT-gas-
c 287	17	5.7	553	28	A0410320	HS_5111_A	A0410320	c 344	17	5.7	603	13	AM970362	AM970362	EST382443
c 288	17	5.7	554	29	CS134470	LIgT-gas-	CS134470	c 345	17	5.7	604	13	BQ075080	BQ075080	f227a08.x
c 289	17	5.7	556	14	CD185112	MS1-0051T	CD185112	c 346	17	5.7	604	14	CF622008	CF622008	1e111908.
c 290	17	5.7	558	12	BI936043	PFE5T0a2	BI936043	c 347	17	5.7	605	13	BQ913336	BQ913336	QHX7802.Y
c 291	17	5.7	559	14	CB536735	771778 MA	CB536735	c 348	17	5.7	605	28	AZ459386	AZ459386	1M0264L11
c 292	17	5.7	562	10	AM335125	S43B1 AGS	AM335125	c 349	17	5.7	605	28	BZ709988	BZ709988	OGDM0037C
c 293	17	5.7	563	9	AU024507	AU024507	AU024507	c 350	17	5.7	607	12	BI267928	BI267928	NE114H12I
c 294	17	5.7	563	10	BE123231	945039E01	BE123231	c 351	17	5.7	607	14	CB244577	CB244577	UI-M-FY0-
c 295	17	5.7	563	28	AQ923373	RPCT-23-2	AQ923373	c 352	17	5.7	607	29	CE723430	CE723430	LIgT-gas-
c 296	17	5.7	563	28	BZ759503	621_4L_G1	BZ759503	c 353	17	5.7	611	12	EM072582	EM072582	F008B05.Y
c 297	17	5.7	564	12	BM529530	fx64b05.y	BM529530	c 354	17	5.7	611	28	AZ418660	AZ418660	1M0194014
c 298	17	5.7	565	28	AQ720634	HS_5546_B	AQ720634	c 355	17	5.7	612	13	EX621393	EX621393	BX621393
c 299	17	5.7	566	29	CF095411	LIgT-gas-	CF095411	c 356	17	5.7	615	28	BZ423878	BZ423878	1d54d05.y
c 300	17	5.7	567	12	BQ971251	QHE6F15.Y	BQ971251	c 357	17	5.7	617	13	BQ911962	BQ911962	QH149K23.
c 301	17	5.7	569	13	BM275708	PFE5T0a5	BM275708	c 358	17	5.7	618	28	AZ247021	AZ247021	RPCT-23-9
c 302	17	5.7	569	13	BX737918	BX737918	BX737918	c 359	17	5.7	619	12	BJ126743	BJ126743	BU126743
c 303	17	5.7	569	28	BZ679198	PUBB249TD	BZ679198	c 360	17	5.7	620	10	BE605965	BE605965	f124d03.x
c 304	17	5.7	570	12	BM274525	PFE5T0a4	BM274525	c 361	17	5.7	622	12	BJ513713	BJ513713	BU513713
c 305	17	5.7	571	12	BI641775	ft02b09.y	BI641775	c 362	17	5.7	623	14	CB521333	CB521333	UI-M-GH0-
c 306	17	5.7	571	29	CE758952	LIgT-gas-	CE758952	c 363	17	5.7	623	10	BF670958	BF670958	G02150759
c 307	17	5.7	572	12	BM879432	kt95e09.y	BM879432	c 364	17	5.7	625	28	BH082279	BH082279	RPCT-24-3
c 308	17	5.7	574	12	BJ454486	BJ454486	BJ454486	c 365	17	5.7	626	10	BB650326	BB650326	BB650326
c 309	17	5.7	574	14	CF892995	A0117B04-	CF892995	c 366	17	5.7	626	28	BZ106398	BZ106398	CH230-204
c 310	17	5.7	575	13	B0141374	NF01BH07P	B0141374	c 367	17	5.7	628	12	EM079729	EM079729	ME8T98-60
c 311	17	5.7	575	28	BH553505	BOCFPI2TF	BH553505	c 368	17	5.7	628	12	BM079729	BM079729	ME8T98-60
c 312	17	5.7	576	13	B0074286	fz27a08.y	B0074286	c 369	17	5.7	628	28	AZ418043	AZ418043	1M0194A02
c 313	17	5.7	577	12	BI328517	ft39c02.x	BI328517	c 370	17	5.7	629	14	CB249003	CB249003	1M0194A02
c 314	17	5.7	577	12	BI533342	ft80f12.x	BI533342	c 371	17	5.7	631	28	AZ641567	AZ641567	1M0504K07
c 315	17	5.7	578	12	BM275410	PFE5T0a6	BM275410	c 372	17	5.7	632	10	BE413502	BE413502	MO0010.BO
c 316	17	5.7	578	29	CE098477	LIgT-gas-	CE098477	c 373	17	5.7	632	12	EM172610	EM172610	Imagcqc.3
c 317	17	5.7	580	12	BM160962	EST563485	BM160962	c 374	17	5.7	632	28	BH830418	BH830418	BACPE931-B
c 318	17	5.7	581	12	BE226353	kq20e12.y	BE226353	c 375	17	5.7	634	14	CB429663	CB429663	605496 MA
c 319	17	5.7	582	12	BI311979	EST51372	BI311979	c 376	17	5.7	634	28	BH730681	BH730681	BOKAY27R
c 320	17	5.7	583	12	BJ448769	L01e1hant	BJ448769	c 377	17	5.7	635	28	AZ290863	AZ290863	RPCT-23-1
c 321	17	5.7	583	13	BK627326	BK627326	BK627326	c 378	17	5.7	636	12	EM958079	EM958079	f733b09.x
c 322	17	5.7	586	12	BI429187	f74b03.y	BI429187	c 379	17	5.7	636	14	CF746138	CF746138	UI-M-GV0-
c 323	17	5.7	587	12	BI982650	f056c10.y	BI982650	c 380	17	5.7	636	29	CE707246	CE707246	LIgT-gas-
c 324	17	5.7	587	28	AZ846858	2M0147A14	AZ846858	c 381	17	5.7	637	29	CG037889	CG037889	PUM0D6TB
c 325	17	5.7	588	12	BM959194	PLATE_17	BM959194	c 382	17	5.7	638	10	AM970281	AM970281	EST382362
c 326	17	5.7	588	14	CB352383	2F001-P00	CB352383	c 383	17	5.7	638	10	BF295825	BF295825	O28PBG09
c 327	17	5.7	588	14	CB519287	UI-M-GH0-	CB519287	c 384	17	5.7	638	14	CF743537	CF743537	UI-M-GT0-
c 328	17	5.7	588	14	CB519287	UI-M-GH0-	CB519287	c 385	17	5.7	640	13	CA056903	CA056903	98a1g9b52
c 329	17	5.7	590	10	AM281818	fj57d10.x	AM281818	c 386	17	5.7	640	14	CB521158	CB521158	UI-M-GH0-
c 330	17	5.7	590	13	B0180297	UI-M-EX0-	B0180297	c 387	17	5.7	640	28	BH025055	BH025055	RPCT-24-2

388	17	5.7	641	28	B267272	h5t1d09.b	c 445	17	5.7	709	14	CA762859	CA762859
389	17	5.7	642	12	B687372	MEST43-F0	c 446	17	5.7	709	14	CF534097	CF534097
390	17	5.7	643	14	CF532744	UI-M-GH0-	c 447	17	5.7	710	13	BQ180624	BQ180624
391	17	5.7	644	13	BK510120	DKF2P686D	c 448	17	5.7	711	13	BQ201333	BQ201333
392	17	5.7	644	14	CF745029	UI-M-GV0-	c 449	17	5.7	711	13	BK077221	BK077221
393	17	5.7	646	14	CF723748	UI-M-FY0-	c 450	17	5.7	712	10	BG069039	BG069039
394	17	5.7	647	9	AU253519	AU253519	c 451	17	5.7	712	10	CC790062	CC790062
395	17	5.7	649	28	A2912617	RPCT-24-1	c 452	17	5.7	712	29	CG693958	CG693958
396	17	5.7	652	13	CA160894	SCMCR4306	c 453	17	5.7	713	12	BJ540962	BJ540962
397	17	5.7	653	10	BF298122	60PBP01	c 454	17	5.7	713	14	CA132525	CA132525
398	17	5.7	655	29	AG148030	Pan trogl	c 455	17	5.7	713	14	CE182447	CE182447
399	17	5.7	656	28	A2369500	A2369500	c 456	17	5.7	713	29	CE338908	CE338908
400	17	5.7	657	12	BJ509403	BJ509403	c 457	17	5.7	714	13	CF534147	CF534147
401	17	5.7	657	13	BQ480954	Ea62E06.	c 458	17	5.7	714	13	BQ546146	BQ546146
402	17	5.7	663	13	BU715011	SJMBSD01	c 459	17	5.7	717	14	CB249979	CB249979
403	17	5.7	663	14	CB519872	UI-M-GH0-	c 460	17	5.7	717	14	CB526633	CB526633
404	17	5.7	665	13	BY741953	BY741953	c 461	17	5.7	717	28	A2381379	A2381379
405	17	5.7	666	14	CF540041	UI-M-EX0-	c 462	17	5.7	720	12	BJ539515	BJ539515
406	17	5.7	667	10	BB521610	BB521610	c 463	17	5.7	722	14	CA384982	CA384982
407	17	5.7	667	28	A2245826	RPCT-23-4	c 464	17	5.7	723	14	CB248828	CB248828
408	17	5.7	669	12	BI261287	602965018	c 465	17	5.7	723	14	CB289966	CB289966
409	17	5.7	669	28	BH959056	od108604.	c 466	17	5.7	723	14	CB658962	CB658962
410	17	5.7	670	14	CD349458	UI-M-FY0-	c 467	17	5.7	723	29	CE761977	CE761977
411	17	5.7	670	28	A2093842	A2093842	c 468	17	5.7	724	14	CB429306	CB429306
412	17	5.7	671	14	CF744025	UI-M-EX0-	c 469	17	5.7	726	14	CA919348	CA919348
413	17	5.7	672	29	CG829908	SONAUS9TV	c 470	17	5.7	726	14	CF536851	CF536851
414	17	5.7	673	13	BK305022	BK305022	c 471	17	5.7	726	14	BH007589	BH007589
415	17	5.7	675	28	A2468744	1M0281J17	c 472	17	5.7	727	12	BG618564	BG618564
416	17	5.7	676	9	AV653243	AV653243	c 473	17	5.7	728	11	CD348418	CD348418
417	17	5.7	676	29	CG052463	PUMP42TD	c 474	17	5.7	729	14	CNS0807G	CNS0807G
418	17	5.7	678	14	CB214436	CB214436	c 475	17	5.7	730	13	BU347809	BU347809
419	17	5.7	682	28	CC324739	TN332-10C	c 476	17	5.7	730	28	AQ291302	AQ291302
420	17	5.7	683	28	BH824542	BACP20-N	c 477	17	5.7	730	28	B2368356	B2368356
421	17	5.7	689	14	CB519117	UI-M-GH0-	c 478	17	5.7	731	29	CC504377	CC504377
422	17	5.7	690	14	CB248922	UI-M-EX0-	c 479	17	5.7	732	12	BW943819	BW943819
423	17	5.7	690	14	CB248922	UI-M-EX0-	c 480	17	5.7	733	12	CD350082	CD350082
424	17	5.7	690	14	CB447711	701732 MA	c 481	17	5.7	734	14	BI738892	BI738892
425	17	5.7	694	14	CB525130	UI-M-FY0-	c 482	17	5.7	735	14	CB249760	CB249760
426	17	5.7	695	14	CB249774	UI-M-EX0-	c 483	17	5.7	736	29	AG081460	AG081460
427	17	5.7	695	29	CC711044	OG0BD34TV	c 484	17	5.7	738	14	CB520841	CB520841
428	17	5.7	696	28	B2423864	1d54c02.9	c 485	17	5.7	738	29	AG049971	AG049971
429	17	5.7	698	14	CK239312	AGENCOURT	c 486	17	5.7	740	28	BH427301	BH427301
430	17	5.7	699	13	BU722530	SJMAJCO3	c 487	17	5.7	741	13	BQ180496	BQ180496
431	17	5.7	700	12	BP115175	BP115175	c 488	17	5.7	742	14	CA139810	CA139810
432	17	5.7	700	14	CD578408	UI-M-FY0-	c 489	17	5.7	742	14	CB519090	CB519090
433	17	5.7	701	13	BK673897	BK673897	c 490	17	5.7	743	13	CA752208	CA752208
434	17	5.7	701	28	BH054777	RPCT-24-2	c 491	17	5.7	743	14	CA752208	CA752208
435	17	5.7	702	14	CA384914	CA384914	c 492	17	5.7	744	13	BK083166	BK083166
436	17	5.7	702	28	CC072258	665680 NC	c 493	17	5.7	747	14	CE182743	CE182743
437	17	5.7	703	28	BZ012105	o6134d06.	c 494	17	5.7	748	28	CC128622	CC128622
438	17	5.7	704	29	CG924814	MDEKBS1F	c 495	17	5.7	749	28	CC247469	CC247469
439	17	5.7	707	14	BE965957	BE965957	c 496	17	5.7	752	14	CB521168	CB521168
440	17	5.7	707	14	CB528208	UI-M-FY0-	c 497	17	5.7	753	14	CA138569	CA138569
441	17	5.7	708	10	BF362333	PMO-NN004	c 498	17	5.7	754	12	BM167220	BM167220
442	17	5.7	708	12	BJ508392	BJ508392	c 499	17	5.7	754	14	CB519577	CB519577
443	17	5.7	708	13	BQ442269	UI-M-EX0-	c 500	17	5.7	754	14	CF532371	CF532371
444	17	5.7	708	14	CF728091	CF728091	c 501	17	5.7	754	28	CC087704	CC087704

502	17	5.7	755	13	BK082316	BK082316	c 559	17	5.7	904	28	B2176853	B2176853
503	17	5.7	758	13	BK081852	BK081852	c 560	17	5.7	909	29	CG951474	CG951474
504	17	5.7	759	28	BH606187	BH606187	c 561	17	5.7	915	10	BF739615	BF739615
505	17	5.7	760	28	BE709997	BE709997	c 562	17	5.7	921	10	BF689582	BF689582
506	17	5.7	761	13	BK082712	BK082712	c 563	17	5.7	924	29	CGNS04DEL	CGNS04DEL
507	17	5.7	762	12	BM963405	BM963405	c 564	17	5.7	926	29	AG131045	AG131045
508	17	5.7	763	12	BK082712	BK082712	c 565	17	5.7	932	10	BF794648	BF794648
509	17	5.7	763	14	CH027696	CH027696	c 566	17	5.7	938	10	BE986784	BE986784
510	17	5.7	763	28	BZ442109	BZ442109	c 567	17	5.7	944	10	BF104206	BF104206
511	17	5.7	764	29	CG761621	CG761621	c 568	17	5.7	944	28	AZ166857	AZ166857
512	17	5.7	764	29	CG888560	CG888560	c 569	17	5.7	945	29	CG187851	CG187851
513	17	5.7	765	13	BK082712	BK082712	c 570	17	5.7	953	28	CG187851	CG187851
514	17	5.7	766	29	CG952252	CG952252	c 571	17	5.7	953	28	AZ546793	AZ546793
515	17	5.7	766	29	CG952252	CG952252	c 572	17	5.7	962	29	CG864763	CG864763
516	17	5.7	772	28	BH431066	BH431066	c 573	17	5.7	970	13	BQ945847	BQ945847
517	17	5.7	774	14	CG535686	CG535686	c 574	17	5.7	979	12	BM415718	BM415718
518	17	5.7	774	28	BZ502796	BZ502796	c 575	17	5.7	979	29	CG937630	CG937630
519	17	5.7	775	29	CG904137	CG904137	c 576	17	5.7	985	29	CG215171	CG215171
520	17	5.7	776	28	BZ063714	BZ063714	c 577	17	5.7	1001	14	CA471037	CA471037
521	17	5.7	777	14	CF182590	CF182590	c 578	17	5.7	1002	13	BK408717	BK408717
522	17	5.7	782	29	CGNS01KM	CGNS01KM	c 579	17	5.7	1008	12	BG482252	BG482252
523	17	5.7	784	13	BK083167	BK083167	c 580	17	5.7	1015	13	BQ934321	BQ934321
524	17	5.7	785	12	B1851873	B1851873	c 581	17	5.7	1019	28	CG282360	CG282360
525	17	5.7	793	13	BK073840	BK073840	c 582	17	5.7	1024	29	CGNS01579	CGNS01579
526	17	5.7	793	12	BK290678	BK290678	c 583	17	5.7	1028	28	CG304758	CG304758
527	17	5.7	795	13	BK238786	BK238786	c 584	17	5.7	1029	28	CG224470	CG224470
528	17	5.7	796	14	CF550433	CF550433	c 585	17	5.7	1033	29	CG907498	CG907498
529	17	5.7	801	28	BH069243	BH069243	c 586	17	5.7	1033	29	CGNS03D6	CGNS03D6
530	17	5.7	807	13	BK077222	BK077222	c 587	17	5.7	1041	28	CG214449	CG214449
531	17	5.7	808	14	CA969404	CA969404	c 588	17	5.7	1045	12	BG295596	BG295596
532	17	5.7	809	29	CG539302	CG539302	c 589	17	5.7	1092	12	BF342427	BF342427
533	17	5.7	816	28	CC173934	CC173934	c 590	17	5.7	1094	28	CG273432	CG273432
534	17	5.7	818	14	CH027506	CH027506	c 591	17	5.7	1156	12	BG539949	BG539949
535	17	5.7	823	12	B1852870	B1852870	c 592	17	5.7	1167	29	CG746243	CG746243
536	17	5.7	828	28	CC086956	CC086956	c 593	17	5.7	1197	28	CG261180	CG261180
537	17	5.7	831	28	BZ463862	BZ463862	c 594	17	5.7	1201	14	CG082827	CG082827
538	17	5.7	831	28	BZ604705	BZ604705	c 595	17	5.7	1204	29	CG750473	CG750473
539	17	5.7	832	13	BK082517	BK082517	c 596	17	5.7	1212	12	BM549314	BM549314
540	17	5.7	832	14	CG652343	CG652343	c 597	17	5.7	1230	28	CG189151	CG189151
541	17	5.7	836	29	BK169244	BK169244	c 598	17	5.7	1234	12	BF686981	BF686981
542	17	5.7	837	13	BK078183	BK078183	c 599	17	5.7	1253	29	CG748711	CG748711
543	17	5.7	843	29	CG922445	CG922445	c 600	17	5.7	1254	12	BM467495	BM467495
544	17	5.7	844	14	CF662055	CF662055	c 601	17	5.7	1266	29	CG743976	CG743976
545	17	5.7	847	13	BK082517	BK082517	c 602	17	5.7	1277	29	CG746704	CG746704
546	17	5.7	847	29	CG539494	CG539494	c 603	17	5.7	1299	29	CG750474	CG750474
547	17	5.7	861	13	BK081852	BK081852	c 604	17	5.7	1315	29	CG749195	CG749195
548	17	5.7	861	28	AZ197691	AZ197691	c 605	17	5.7	1320	29	CG755797	CG755797
549	17	5.7	867	29	CGNS04EH	CGNS04EH	c 606	17	5.7	1326	11	AY109265	AY109265
550	17	5.7	868	14	CGNS1443	CGNS1443	c 607	17	5.7	1360	29	CG757149	CG757149
551	17	5.7	873	13	BK082068	BK082068	c 608	17	5.7	1370	29	CG757666	CG757666
552	17	5.7	877	13	BK083032	BK083032	c 609	17	5.7	1385	29	CG757667	CG757667
553	17	5.7	883	28	BK0716790	BK0716790	c 610	17	5.7	1464	12	B1758637	B1758637
554	17	5.7	889	14	CGNS1722	CGNS1722	c 611	17	5.7	1812	28	BZ572834	BZ572834
555	17	5.7	893	13	BK081771	BK081771	c 612	17	5.7	2914	11	AK044809	AK044809
556	17	5.7	896	13	BK081771	BK081771	c 613	17	5.7	3404	11	AK046376	AK046376
557	17	5.7	903	29	CG955735	CG955735	c 614	17	5.7	4793	11	AK049003	AK049003
558	17	5.7	904	28	AZ539065	AZ539065	c 615	17	5.7	7886	11	BC034956	BC034956
								16	5.4	113	10	AW493141	AW493141

616	16	5.4	128	28	A2121241	A2121241	RPCI-23-1	673	16	5.4	243	9	AU229087	AU229087
c 617	16	5.4	131	12	BG125723	BG125723	EST471369	c 674	16	5.4	243	9	AA282595	AA282595
618	16	5.4	139	9	AV331698	AV331698	AV331698	c 675	16	5.4	243	10	BB000141	BB000141
619	16	5.4	144	10	BB373750	BB373750	BB373750	c 676	16	5.4	246	28	B58499	B58499
c 620	16	5.4	146	12	BM385843	BM385843	UI-R-DM1-	c 677	16	5.4	247	9	AV244224	AV244224
c 621	16	5.4	148	12	BM196797	BM196797	C0337E11-	c 678	16	5.4	247	10	BB077321	BB077321
622	16	5.4	157	28	CC152863	CC152863	CSU-K34.1	c 679	16	5.4	247	10	BB438388	BB438388
c 623	16	5.4	158	10	BB278128	BB278128	BB278128	c 680	16	5.4	248	10	BF355421	BF355421
c 624	16	5.4	165	13	BY373743	BY373743	BY373743	c 681	16	5.4	249	9	AV244424	AV244424
c 625	16	5.4	166	13	BY461142	BY461142	BY461142	c 682	16	5.4	251	9	AA002435	AA002435
c 626	16	5.4	167	10	BB680644	BB680644	UI-M-AH3-	c 683	16	5.4	253	9	AV221200	AV221200
c 627	16	5.4	170	10	BB349050	BB349050	BB349050	c 684	16	5.4	254	9	AV983111	AV983111
c 628	16	5.4	172	28	BE2475541	BE2475541	BONDV91TR	c 685	16	5.4	254	10	BB428157	BB428157
c 629	16	5.4	174	12	BM974993	BM974993	UI-CF-ECL	c 686	16	5.4	254	14	CD062627	CD062627
c 630	16	5.4	177	9	AT795260	AT795260	RRMCA361	c 687	16	5.4	255	28	A2216346	A2216346
c 631	16	5.4	188	13	BQ311725	BQ311725	MRO-BN007	c 688	16	5.4	255	28	BH859539	BH859539
c 632	16	5.4	190	10	BB569076	BB569076	BB569076	c 689	16	5.4	255	28	BH859542	BH859542
c 633	16	5.4	191	9	AT566420	AT566420	trp9c09.x	c 690	16	5.4	256	13	BX633276	BX633276
c 634	16	5.4	194	14	H31987	H31987	EST106594.R	c 691	16	5.4	260	10	BB384549	BB384549
635	16	5.4	198	29	CE341223	CE341223	tlgr-gas-	c 692	16	5.4	261	12	BG601362	BG601362
636	16	5.4	199	10	BB526321	BB526321	BB526321	c 693	16	5.4	262	13	BU494628	BU494628
637	16	5.4	200	10	AM522327	AM522327	UI-R-B00-	c 694	16	5.4	262	28	B2680871	B2680871
c 638	16	5.4	200	10	BB568419	BB568419	BB568419	c 695	16	5.4	263	10	BF818812	BF818812
c 639	16	5.4	202	9	AT136936	AT136936	UI-R-C2P-	c 696	16	5.4	264	10	BF198277	BF198277
c 640	16	5.4	204	28	A2990332	A2990332	2M0274E05	c 697	16	5.4	265	29	CE103553	CE103553
641	16	5.4	205	10	BF606142	BF606142	273101.NA	c 698	16	5.4	266	12	BG141241	BG141241
642	16	5.4	208	12	BM842177	BM842177	K-EST0119	c 699	16	5.4	266	28	B2364355	B2364355
643	16	5.4	209	14	CA752421	CA752421	UI-M-F00-	c 700	16	5.4	267	13	BQ913747	BQ913747
c 644	16	5.4	213	12	BC382038	BC382038	297756.NA	c 701	16	5.4	268	10	BB066539	BB066539
645	16	5.4	213	28	B2662851	B2662851	SALK_0263	c 702	16	5.4	269	9	AT1289932	AT1289932
646	16	5.4	216	28	B2596216	B2596216	SALK_0922	c 703	16	5.4	270	13	BX557419	BX557419
647	16	5.4	220	28	A2069871	A2069871	RPCI-23-4	c 704	16	5.4	270	29	CE603372	CE603372
c 648	16	5.4	221	14	CB803193	CB803193	UI-M-GV0-	c 705	16	5.4	271	9	AU005947	AU005947
c 649	16	5.4	223	14	F09079	F09079	HSC2WF092.n	c 706	16	5.4	272	9	A1854774	A1854774
c 650	16	5.4	224	10	BB092003	BB092003	BB092003	c 707	16	5.4	274	28	A2492312	A2492312
c 651	16	5.4	224	10	BB473846	BB473846	BB473846	c 708	16	5.4	274	29	CE123258	CE123258
c 652	16	5.4	226	10	BB147843	BB147843	BB147843	c 709	16	5.4	275	10	BB422254	BB422254
c 653	16	5.4	227	9	AT561506	AT561506	w*92a06.x	c 710	16	5.4	275	10	BB413531	BB413531
c 654	16	5.4	227	10	AM524661	AM524661	UI-R-B00-	c 711	16	5.4	276	9	AV011865	AV011865
c 655	16	5.4	227	14	CM090629	CM090629	MC1-0076U	c 712	16	5.4	276	10	BB469644	BB469644
656	16	5.4	227	28	BH848543	BH848543	SALK_0685	c 713	16	5.4	276	12	B1161695	B1161695
657	16	5.4	227	29	CE775871	CE775871	tlgr-gas-	c 714	16	5.4	276	13	BY559776	BY559776
658	16	5.4	228	28	BH482997	BH482997	BQ6J870TF	c 715	16	5.4	278	10	BB348942	BB348942
659	16	5.4	229	10	BH150997	BH150997	BH150997	c 716	16	5.4	278	10	BB528451	BB528451
c 660	16	5.4	229	12	BM284893	BM284893	Kh2c10.Y	c 717	16	5.4	279	10	BF368927	BF368927
c 661	16	5.4	230	13	BY373672	BY373672	BY373672	c 718	16	5.4	279	12	B1283253	B1283253
c 662	16	5.4	230	14	CF539542	CF539542	UI-M-GV0-	c 719	16	5.4	279	29	CG427327	CG427327
663	16	5.4	233	9	AV332643	AV332643	AV332643	c 720	16	5.4	281	10	BB441508	BB441508
c 664	16	5.4	233	10	BB276208	BB276208	BB276208	c 721	16	5.4	282	12	BM999662	BM999662
c 665	16	5.4	235	12	BQ038323	BQ038323	PGM1C.PK0	c 722	16	5.4	283	10	BB143340	BB143340
666	16	5.4	235	14	CA921215	CA921215	EST1638933	c 723	16	5.4	283	10	BB456081	BB456081
667	16	5.4	236	9	AV322814	AV322814	AV322814	c 724	16	5.4	283	12	BJ316370	BJ316370
c 668	16	5.4	237	9	AT1232819	AT1232819	EST229507	c 725	16	5.4	283	28	BH012313	BH012313
c 669	16	5.4	237	9	AV336113	AV336113	AV336113	c 726	16	5.4	284	29	CEB17331	CEB17331
c 670	16	5.4	237	29	CHS07669	CHS07669	tlgr-gas-	c 727	16	5.4	285	14	BH88375	BH88375
c 671	16	5.4	237	29	CHS07669	CHS07669	tlgr-gas-	c 728	16	5.4	287	10	BB472147	BB472147
672	16	5.4	239	9	AV242121	AV242121	AV242121	c 729	16	5.4	287	14	R75424	R75424

730	16	5.4	288	10	BB179748	BB179748	BB179748	787	16	5.4	316	10	BB449185	BB449185
731	16	5.4	288	10	BB181903	BB181903	BB181903	788	16	5.4	317	13	C91101	C91101
732	16	5.4	289	10	AM910708	AM910708	AM910708	789	16	5.4	319	9	A1620600	A1620600
733	16	5.4	289	10	BB071482	BB071482	BB071482	790	16	5.4	320	9	AV169380	AV169380
734	16	5.4	289	10	BB194854	BB194854	BB194854	791	16	5.4	320	29	CE068270	CE068270
735	16	5.4	289	13	BB732670	BB732670	BB732670	792	16	5.4	320	29	CE452881	CE452881
736	16	5.4	289	14	CF631940	CF631940	CF631940	793	16	5.4	321	9	A1542427	A1542427
737	16	5.4	289	28	AA086513	AA086513	AA086513	794	16	5.4	321	10	BB301838	BB301838
738	16	5.4	290	10	BB174457	BB174457	BB174457	795	16	5.4	322	10	BB394532	BB394532
739	16	5.4	290	10	BB298830	BB298830	BB298830	796	16	5.4	322	29	CE681502	CE681502
740	16	5.4	290	10	BB485919	BB485919	BB485919	797	16	5.4	323	28	BB076965	BB076965
741	16	5.4	290	14	HB8389	HB8389	HB8389	798	16	5.4	324	9	AV311754	AV311754
742	16	5.4	290	28	AA882146	AA882146	AA882146	799	16	5.4	325	9	AV311754	AV311754
743	16	5.4	291	10	BB003244	BB003244	BB003244	800	16	5.4	325	14	CB426670	CB426670
744	16	5.4	291	10	BB193034	BB193034	BB193034	801	16	5.4	325	14	CB435945	CB435945
745	16	5.4	291	10	BB245374	BB245374	BB245374	802	16	5.4	327	10	BF756569	BF756569
746	16	5.4	291	10	BB489864	BB489864	BB489864	803	16	5.4	328	10	AM230071	AM230071
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748	16	5.4	292	9	AV242674	AV242674	AV242674	805	16	5.4	329	28	AA200799	AA200799
749	16	5.4	292	10	BB485886	BB485886	BB485886	806	16	5.4	330	9	AA911124	AA911124
750	16	5.4	293	9	A1556095	A1556095	A1556095	807	16	5.4	330	9	AL039771	AL039771
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752	16	5.4	294	10	BF457600	BF457600	BF457600	809	16	5.4	330	9	AV555698	AV555698
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758	16	5.4	297	12	BB393881	BB393881	BB393881	815	16	5.4	335	10	BB678042	BB678042
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760	16	5.4	299	10	BB061758	BB061758	BB061758	817	16	5.4	337	9	A1422429	A1422429
761	16	5.4	300	13	BB368362	BB368362	BB368362	818	16	5.4	337	28	B2919454	B2919454
762	16	5.4	300	28	AA092347	AA092347	AA092347	819	16	5.4	338	9	AA877003	AA877003
763	16	5.4	301	29	CG701034	CG701034	CG701034	820	16	5.4	338	10	BB099450	BB099450
764	16	5.4	303	13	CG20970	CG20970	CG20970	821	16	5.4	339	28	BB810757	BB810757
765	16	5.4	303	28	BZ233559	BZ233559	BZ233559	822	16	5.4	340	9	AT1234909	AT1234909
766	16	5.4	304	10	BB493246	BB493246	BB493246	823	16	5.4	340	10	BB121349	BB121349
767	16	5.4	305	10	BB101640	BB101640	BB101640	824	16	5.4	341	9	AA934653	AA934653
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769	16	5.4	308	9	AA268402	AA268402	AA268402	826	16	5.4	342	10	BB100294	BB100294
770	16	5.4	309	10	BB828214	BB828214	BB828214	827	16	5.4	342	28	AZ560216	AZ560216
771	16	5.4	309	29	CG699293	CG699293	CG699293	828	16	5.4	343	29	AA684914	AA684914
772	16	5.4	309	29	BK532606	BK532606	BK532606	829	16	5.4	344	12	BG372664	BG372664
773	16	5.4	310	10	BB522281	BB522281	BB522281	830	16	5.4	346	12	B1966004	B1966004
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775	16	5.4	311	10	BB333684	BB333684	BB333684	832	16	5.4	346	28	AA022380	AA022380
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777	16	5.4	312	10	AAW242368	AAW242368	AAW242368	834	16	5.4	347	9	AV693524	AV693524
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785	16	5.4	315	9	AV101041	AV101041	AV101041	842	16	5.4	354	28	AZ892139	AZ892139
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 Job time : 1393.12 secs

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OK nucleic - nucleic search, using sw model

Run on: October 14, 2004, 09:12:14 / Search time 1524.57 Seconds

(without alignments)
8443.595 Million cell updates/sec

Title: US-09-407-804A-9

Perfect score: 297
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_bat: +
2: gb_hhg: +
3: gb_in: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
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9: gb_pt: +
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11: gb_ats: +
12: gb_sy: +
13: gb_un: +
14: gb_vl: +
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29: em_vl: +
30: em_hhg_hum: +
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32: em_hhg_other: +
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36: em_hhg_mam: +
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39: em_hhgo_hum: +
40: em_hhgo_mus: +
41: em_hhgo_other: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	297	100.0	41708	6 BD245281	BD245281 Developme
3	297	100.0	41708	6 AR368770	AR368770 Sequence
4	291.2	98.0	41401	7 AB009866	AB009866 Bacteriop
5	284.8	95.9	43081	7 AP001553	AP001553 Bacteriop
6	273	91.9	45366	7 AB044554	AB044554 Staphyloc
7	261	87.9	261	6 BD245277	BD245277 Staphyloc
8	256.2	86.3	42942	7 AB045978	AB045978 Developme
9	256.2	86.3	348527	1 AP003360	AP003360 Staphyloc
10	133	44.8	348550	1 AP003364	AP003364 Staphyloc
11	132.8	44.7	580	6 AR355085	AR355085 Sequence
12	132.8	44.7	43594	6 BD245634	BD245634 Developme
13	132.8	44.7	43594	7 AF424781	AF424781 Staphyloc
14	130.8	44.0	42722	7 AF424783	AF424783 Staphyloc
15	130.8	44.0	272850	1 AP004828	AP004828 Staphyloc
16	128.4	43.2	258	6 AX618548	AX618548 Sequence
17	118.8	40.0	267	6 AX618246	AX618246 Sequence
18	101	34.0	291150	1 AP001335	AP001335 Staphyloc
19	48.2	16.2	82281	8 AC025295	AC025295 Atradiops
20	47.6	16.0	175406	5 BK000522	BK000522 Zebrafish
21	47.4	16.0	192780	9 AL162723	AL162723 Human DNA
22	47	15.8	1496	3 CEY53C12D	CEY53C12D Caenorhab
23	45.8	15.4	1336	3 PFA493427	PFA493427 Plasmodiu
24	45.8	15.4	207726	2 AC024953	AC024953 Homo sapi
25	45.8	15.4	209287	9 AC012077	AC012077 Homo sapi
26	45.6	15.4	250029	3 AE014838	AE014838 Plasmodiu
27	45.2	15.2	200473	2 AC133762	AC133762 Rattus no
28	45.2	15.2	252420	3 AE014841	AE014841 Plasmodiu
29	45.2	15.2	254977	2 AC117353	AC117353 Rattus no
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Db 181 GTAATGAGAAAGCACTTAATGATGGCATCAGAGCTATTTAAACAAGCAATGAATGATGG 240
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QY 241 ATTGAAGAACAACAAGCAAGAAAGCAAGCACTATTTAAGTCTGTCATGAATGGTAG 297
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LOCUS	Development of novel antibiotics based on bacteriophage genomics.				
DEFINITION					
ACCESSION	BD245281				

KEYWORDS	JP 2002531107-A/16.
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 41708)
TITLE	Pelletier, J., Gros, P. and Dubow, M.
JOURNAL	Development of novel antibiotics based on bacteriophage genomics
COMMENT	Patent: JP 2002531107-A 16 24-SEP-2002;
	PHARTECH INC
	OS <i>Staphylococcus aureus</i> bacteriophage 77
	PN JP 2002531107-A/16
	PD 24-SEP-2002

PC	CL2N1/21,CL2Q1/02,CL2Q1/68,G01N33/15,G01N33/50,G01N33/566,PC
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DEFINITION Sequence 3 from patent US 6376652.
ACCESSION AR368770
VERSION AR368770.1 GI:34603077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 41708)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Compositions and methods involving an essential Staphylococcus aureus gene and its encoded protein
JOURNAL Patent: US 6376652-A 3 23-APR-2002;
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VERSION AB009866.2 GI:8051688
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SOURCE Staphylococcus aureus bacteriophage PVL
ORGANISM Staphylococcus aureus bacteriophage PVL
REFERENCE 1 (sites)
AUTHORS Kaneo,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
TITLE Pantone-valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
JOURNAL Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE 9404084
PUBMED
REFERENCE 2 (sites)
AUTHORS Kaneo,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE Complete nucleotide sequence and molecular characterization of the temperate staphylococcal bacteriophage phiPVL carrying Pantone-Valentine leukocidin genes
JOURNAL Gene 215 (1), 57-67 (1998)
MEDLINE 98332719
PUBMED 9666077
REFERENCE 3 (bases 1 to 41401)
AUTHORS Kaneo,J., Kimura,T., Narita,S., Tomita,T. and Kamio,Y.
TITLE Direct Submission
Submitted (17-DEC-1997) Jun Kaneo, Tohoku University, Dept. Appl. Biol. Chem., Faculty of Agriculture; 1-1 Tsutsumi-dori Amamiyama-cho, Aoba-ku, Sendai, Miyagi 981, Japan

(E-mail: j.kaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8761,
Fax: 81-22-717-8780)
On May 24, 2000 this sequence version replaced gi:3341907.
Sequence updated (06-Feb-1998)
Sequence updated (22-May-2000).
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CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

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98.0%; Score 291.2; DB 7; Length 4101;

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DEFINITION Bacteriophage phi ETA DNA, complete genome.
ACCESSION AP001553
VERSION AP001553.1 GI:8918415
KEYWORDS
SOURCE Bacteriophage phi ETA
ORGANISM Bacteriophage phi ETA
Virus; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
REFERENCE
AUTHORS Yamauchi,T., Hayashi,T., Takami,H., Nakasone,K., Ohnishi,M.,
Nakayama,K., Yamada,S., Komatsuze,H. and Sugai,M.
TITLE Phage conversion of enterolysin A production in
Staphylococcus aureus
JOURNAL Mol. Microbiol. 38 (4), 694-705 (2000)
MEDLINE 20566787
PUBMED 1115106
REFERENCE 2 (bases 1 to 43081)
AUTHORS Sugai,M., Yamauchi,T., Hayashi,T., Nakasone,K. and Takami,H.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Motoyuki Sugai, Hiroshima University
Faculty of Dentistry, Microbiology; Kasumi 1-2-3, Hiroshima,
Hiroshima 734-8553, Japan (E-mail:sugai@hiroshima-u.ac.jp,
Tel:81-82-257-5637, Fax:81-82-257-5639)
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Query Match

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6179..6400
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/db_xref="GI:8918762"
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91.9%; Score 273; DB 7; Length 45636;

Best Local Similarity 94.9%; Pred. No. 9e-47;
Matches 282; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGTCAATATATAAACGAAAGAAAGTCAAGATGATTAAGAAATAGCGAATC 60
DB 6999 AAGTTAATTAATCAAAATATACGAGAGTCAAGATGATTAAGAAATAGCGAATC 6998
QY 61 ATACGCAAAATATTCATGTTAACGATTCATTTTAAGCTATTTTAAAGGTGAT 120
DB 6999 ATACGCAAAATATTCATGTTAACGATTCATTTTAAGCTATTTTAAAGGTGAT 7058
QY 121 ATGGGATATCATTAAGTATTAAGATGAACAAGTACATTAACATGCTATGTC 180
DB 7059 ATGGGATATCATTAAGTATTAAGATGAACAAGTACATTAACATGCTATGTC 7118
QY 181 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 7119 GTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7178
QY 241 ATGGAAGAAACAGACGAAACGACGACGATTAATTAAGTATGATGATGATGATG 297
DB 7179 ATGGAAGAAACAGACGAAACGACGACGATTAATTAAGTATGATGATGATGATG 7235
RESULT 7
BD245277
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 261)
Pelletier,J., Gros,P., and Dubow,M.
Development of novel antibiotics based on bacteriophage genomes
Patent: JP 2002531107-A 12 24-SEP-2002;
PHAGETECH INC
OS Staphylococcus aureus bacteriophage 77
PN JP 2002531107-A/12
PD 24-SEP-2002
PR 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/00, A01N63/00, A61K45/00, A61P31/04, C07K14/005,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Coding Sequence
FH Key Location/Qualifiers
FT source 1..261
FT /organism="Staphylococcus
aureus bacteriophage

FEATURES FT 77'
Location/Qualifiers
source 1..261
/organism="unidentified"
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Query Match 87.9%; Score 261; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 4,6e-44;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGATTACGAATAGCGGAATCATACGCAAAATATCATGTTACGATTCGATTT 60
QY 97 AGCTATTCTTTTAAAGGTCAATGCGCATATCATACGATTAAGATGAAAC 156
DB 61 AGCTATTCTTTTAAAGGTCAATGCGCATATCATACGATTAAGATGAAAC 120
QY 157 GTACCAATTAAACATGCTTATGCTAGATGAAATGACTTATGCGCATCA 216
DB 121 GTACCAATTAAACATGCTTATGCTAGATGAAATGACTTATGCGCATCA 180
QY 217 TTAAACCAAGCATAGATGATGATGAAAGCAACAGACAGACAGACATATT 276
DB 181 TTAAACCAAGCATAGATGATGATGAAAGCAACAGACAGACAGACATATT 240
QY 277 AACTAGTCATGAATGGTAG 297
DB 241 AACTAGTCATGAATGGTAG 261

RESULT 8
AB045978 42942 bp DNA linear PHG 26-MAY-2001
LOCUS Staphylococcus aureus temperate phage phiSLT genomic DNA, complete
DEFINITION
AB045978
VERSION
AB045978.1 GI:12697822
KEYWORDS
ORGANISM
Staphylococcus aureus temperate phage phiSLT
Staphylococcus aureus temperate phage phiSLT
Viruses; deDNA viruses; no RNA stage; Caudovirales; Siphoviridae.
REFERENCE
AUTHORS
1 (alters)
Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J.
and Kamio,Y.
TITLE
Phage conversion of Panton-Valentine leukocidin in Staphylococcus
aureus: molecular analysis of a PVL-converting phage, phiSLT
JOURNAL
Gene 266 (1-2), 195-206 (2001)
MEDLINE
21261956
PUBMED
11368915
REFERENCE
2 (bases 1 to 42942)
AUTHORS
Kaneko,J., Narita,S. and Kamio,Y.
TITLE
Direct Submission
JOURNAL
Submitted (12-JUL-2000) Jun Kaneko, Tohoku University, Graduate
school of Agricultural Science, 1-1 Tsutsunodori Azaamiyamachi,

Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel: 81-22-717-8781,
Fax: 81-22-747-8780)
FEATURES
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 4357..4905
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		/translation="KAEQLNLYQKIALDYKRNAGETKDTGKGNESYVSGQLIHIRE KQELHLLVPTTINENWTTTFTRKNGQVEEIVENDADKQKQKSTVSGEFDL HAGQGNDSIQAHGSLTAERYELFMKEFNITDEDADKQKQKSTVSGEFDL TKVENDFIAIKESGEFAEKYQEQINKLEKKNVKNALNQNQINTVROQIKWLGSIHQ"		TITLE	Direct Submission
CDS		8730..9173		JOURNAL	Submitted (28-FEB-2001) Tooshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology; 1-1-1 Ten-nodori, Tsukuba, Ibaraki 305-8577, Japan (E-mail:tohta@tsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-53-3454)
Query Match	86.3%;	Score 256.2;	DB 7;	COMMENT	On May 29, 2001 this sequence version replaced gi:13874937.
Best Local Similarity	98.9%;	Prod. No. 2.6e-43;		FEATURES	Location/Qualifiers
Matches 2589	Conservative 0;	Mismatches 3;	Indels 0;	source	1..348527
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				/mol_type="genomic DNA"	
Db	7273	ATGTATACGAAATAGCGGAATCATACGCAAAAATATTCATGTTACGGATTCGATTT	7332	/strain="Mu50"	
OY	97	AGCATTCATTTTAAAGGTCATATGGCATTCATACAGTTAAAGATAGAACAC	156	/sub_species="aureus Mu50"	
				/db_xref="taxon:138878"	
Db	7333	AGCATTCATTTTAAAGGTCATATGGCATTCATACAGTTAAAGATAGAACAC	7392	/gene="SAV0620"	
OY	157	GTCACATTAACATGCTTATGTGTAGATAGAAATGACTTGAATGGCATCAGACTTA	216	158..718	
				/note="SAV0620"	
Db	7393	GTCACATTAACATGCTTATGTGTAGATAGAAATGACTTGAATGGCATCAGACTTA	7452	/note="similar to flmE recombinase"	
OY	217	TTTACCAAGCAATAGATGAATGGATTGGAAGAACAGACAAACAGACACTAAT	276	/codon_start=1	
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OY	277	AACTTAGCATGAATGCTAG	297	/protein_id="BAB56782.1"	
				/db_xref="GI:14246389"	
Db	7513	AACTTAGCATGAATGCTAG	7533	/translation="MKMKKAIKRNDDIVYKVEALKTKSPRDYLEFKALIHGSLVSEL LRTVSYQKRLIEKTKLSBCKQKHFSLIKRLRPELSELLQYIEDNSLSNEVDLFQ SLRTNQVLSKQKATRIHQASTIAGIDNVGLTLRTKTPYHAYQKGIPIYQRYLDH QSAETLNFTEIGNECHSIVISLQ"	
				737..2761	
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				737..2761	
				/note="SAV0621"	
RESULT 9				/note="similar to NADH dehydrogenase"	
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DEFINITION	Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete			/codon_start=1	
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VERSION	AP003360.2	GI:14246388		/product="hypothetical protein"	
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AUTHORS				/gene="SAV0622"	
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TITLE				/note="similar to NADH dehydrogenase"	
JOURNAL	Lancet 357 (9264), 1225-1240 (2001)				
MEDLINE	21311952				
PubMed	11418146				

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IIYVVLNIGSMFLGIGLLVTVGTINFSLAMRLNDGNRTVTMSILFLVAFS
AKAALVFMMLPKAVAVNTELAALFAALMTKGAVALREFTLFDHNDLHPLLA
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/db_xref="GI:14246397"
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				Gaps 0;

Db	Accession	Sequence
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230674	ATGTATTACGAAATACGGGAATCATACGCAAAATATTCATGTTAAAGATTCGATTTT	
230733		

QY 97 AGCAATTCATTTTAAAGGCATATGGGCATCATCAAGTAAAGATATATACAC 150
|||||
Db 230734 AACATATTCATTTTAAAGGCATATGGGCATCATCAAGTAAAGATATATACAC
230793

Qy	157	GTACCAATTAACATGCTATGCTGAATGATGAAGCTTAAGTATGCGATCAGACTTA	216
Db	230794	GTACCAATTAACATGCTATGCTGAATGATGAAGCTTAAGTATGCGATCAGACTTA	
	230853		

Oy	217	TTTAACACGCAATAGATGAATTGGATTGAAGAACAACGACGAAACGACGACTAAT	276
Dδ	230854	TTCCACACGCAATAGATGAATTGGATTGAAGAACAACGACGAAACGACGACTAAT	
	230913		

Qy	277	A	A	C	T	T	A	G	C	A	T	G	A	A	T	G	T	A	G	297
Db	230914	A	A	C	T	T	A	G	C	A	T	G	A	G	A	T	G	T	A	230934

Search completed: October 14, 2004, 16:00:39
Job time : 1528.57 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 14, 2004, 07:30:59 ; Search time 198 Seconds
(without alignments)
6372.297 Million cell updates/sec

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Title: US-09-407-804A-9
Perfect score: 297
Sequence: 1 atgttcataataaacgaa.....acttagtcatgaatgtag 297
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Scoring table: IDENTITY_NUC

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0% .
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : N_Geneseq_29Jan04:4

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3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002s: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	297	100.0	297	3	AA668253	AA668253 Bacteriophage
2	297	100.0	41708	3	AA668247	AA668247 Bacteriophage
3	297	100.0	41708	4	AA668106	AA668106 Complete
4	261	87.9	261	3	AA668250	AA668250 Bacteriophage
5	132.8	44.7	580	2	AAV75514	AAV75514 Stephi100
6	132.8	44.7	43576	3	AA668609	AA668609 Bacteriophage
7	128.4	43.2	258	7	ACF73076	ACF73076 Stephi100

XX	OS	Staphylococcus aureus; bacteriophage 77.
XX	XX	
XX	XX	WO200032825-A2.
XX	XX	
XX	PD	08-JUN-2000.
XX	XX	
XX	PF	03-DEC-1999; 99MO-IB002040.
XX	XX	
XX	PR	03-DEC-1998; 98US-0110992P.
XX	PR	03-JUN-1999; 99US-00326144.
XX	PR	28-SEP-1999; 99US-00407804.
XX	PR	30-SEP-1999; 99US-0157218P.
XX	PR	01-DEC-1999; 99US-0168777P.
XX	PR	02-DEC-1999; 99US-00454252.
XX	PA	
XX	PA	(PHAG-) PHAGETECH INC.
XX	PI	
XX	PI	Pelletier J, Gros P, Dubow M;
XX	XX	
XX	XX	WPI: 2000-412361/35.
XX	XX	P-PSDB; AAB16528.
XX	XX	
XX	PT	Identifying a bacteriophage coding region for treating bacterial
XX	PT	infections comprises identifying a nucleic acid encoding a product that
XX	PT	inhibits bacteria when a bacteriophage infects a bacterium.
XX	XX	
XX	PS	Disclosure; Page 165; 456pp; English.
XX	XX	
XX	XX	The present invention describes a method for identifying a bacteriophage
XX	XX	coding region encoding a product active on an essential bacterial target.
XX	XX	The method comprises identifying a nucleic acid sequence encoding a gene
XX	XX	product that provides a bacteria-inhibiting function when an
XX	XX	uncharacterised bacteriophage infects a pathogenic bacterium. The
XX	XX	compound active on a target of a bacteriophage inhibitor protein in a
XX	XX	bacteria is used to treat or prevent a bacterial infection in an animal.
XX	XX	AAA69442 and AAB16523 to AAB16954 represent bacteriophage
XX	XX	nucleotide and protein sequences which are used in the exemplification of

XX

[illegible]

DB 121 ATGGGCATATCAATCAAGTTAAAGATGACACAGTACCAATTAACATGCTTATGTC 180
 QY 181 GTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 181 GTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 QY 241 ATTGAAGAGACACAGACAGACAGACAGCTATTAACTTACTGCTGAATGGTAG 297
 DB 241 ATTGAAGAGACACAGACAGACAGACAGCTATTAACTTACTGCTGAATGGTAG 297

RESULT 2
 AAA68247
 ID AAA68247 standard; DNA; 41708 BP.
 AC AAA68247;
 XX
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 27-OCT-2000 (first entry)
 XX
 DE Bacteriophage 77 complete genome sequence.
 XX
 KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
 KW bacterial growth inhibition; bacterial infection; ds.
 OS
 XX Staphylococcus aureus; bacteriophage 77.
 PN WO200032825-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-18002040.
 XX
 PR 03-DEC-1998; 98US-0110992P.
 PR 03-JUN-1999; 99US-00326144.
 PR 28-SEP-1999; 99US-00407804.
 PR 30-SEP-1999; 99US-0157218P.
 PR 01-DEC-1999; 99US-0168777P.
 PR 02-DEC-1999; 99US-00454252.
 XX
 PA (PHAG-) PHAGETECH INC.
 XX
 PI Polietlor J, Gros P, Dubow M;
 XX
 DR WPI; 2000-412361/35.
 XX
 PT Identifying a bacteriophage coding region for treating bacterial
 PT infections comprises identifying a nucleic acid encoding a product that
 PT inhibits bacteria when a bacteriophage infects a bacterium.
 XX
 PS Example 3; Page 141-151; 456pp; English.
 XX
 CC The present invention describes a method for identifying a bacteriophage
 CC coding region encoding a product active on an essential bacterial target.
 CC The method comprises identifying a nucleic acid sequence encoding a gene
 CC product that provides a bacteria-inhibiting function when an

CC uncharacterised bacteriophage infects a pathogenic bacterium. The
 CC compound active on a target of a bacteriophage inhibitor protein in a
 CC bacteria is used to treat or prevent a bacterial infection in an animal.
 CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
 CC nucleotide and protein sequences which are used in the exemplification of
 CC the present invention. (updated on 06-AUG-2003 to correct OS field.)
 CC (updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 other;

Query Match 100.0%; Score 297; DB 3; Length 41708;
 Best Local Similarity 100.0%; Pred. No. 3,1e-64;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATATATTAACGAAACGAGAGAACTCAAGATGATTAAGAAATAGCGAAATC 60
 DB 29268 ATGTCATATATTAACGAAACGAGAGAACTCAAGATGATTAAGAAATAGCGAAATC 29327
 QY 61 ATACGCAAAAATATTCATGTTAACGATTCGATTTTAAAGTATTCATTTAAAAAGTCAAT 120
 DB 29328 ATACGCAAAAATATTCATGTTAACGATTCGATTTTAAAGTATTCATTTAAAAAGTCAAT 29387
 QY 121 ATGGGCATATCAATCAAGTTAAAGATGACACAGTACCAATTAACATGCTTATGTC 180
 DB 29388 ATGGGCATATCAATCAAGTTAAAGATGACACAGTACCAATTAACATGCTTATGTC 29447
 QY 181 GTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 29448 GTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 29507
 QY 241 ATTGAAGAGACACAGACAGACAGACAGCTATTAACTTACTGCTGAATGGTAG 297
 DB 29508 ATTGAAGAGACACAGACAGACAGACAGCTATTAACTTACTGCTGAATGGTAG 29564

RESULT 3
 AAC86106
 ID AAC86106 standard; cDNA; 41708 BP.
 AC AAC86106;
 XX
 DT 06-AUG-2003 (revised)
 DT 29-AUG-2001 (first entry)
 XX
 DE Complete genome of bacteriophage 77.
 XX
 KW DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
 KW screening assay; ss.
 OS Bacteriophage.
 XX
 PN WO200146383-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 21-DEC-2000; 2000WO-US035180.
 XX

PR 22-DEC-1999; 99US-00470512.
PR 12-OCT-2000; 2000US-00689352.
XX
PA (PHAG-) PHAGETECH INC.
PA (WILL/) WILLIAMS K M.
XX
PI Pelletier J, Gros P, Dubow M;
XX WPI, 2001-418052/44.
DR
XX Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT preferably bacterial, diseases such as those caused by Staphylococcus
PT aureus.
XX
XX Disclosure; Fig 2, 107pp; English.
PS
XX This sequence represents the genome of Bacteriophage 77. The growth
CC inhibitory gene product of ORF 104 interacts with DnaI derived from S.
CC aureus, to form the basis of a screening assay. DnaI polypeptides and
CC polynucleotides are useful for treating microbial, preferably bacterial,
CC especially Staphylococcal, infections. DnaI polypeptides and
CC polynucleotides are useful for biological, diagnostic, prophylactic,
CC clinical and therapeutic use, and as components in databases useful for
CC search analyses as well as in sequence analysis algorithms. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX
XX Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 297; DB 4; Length 41708;
Best Local Similarity 100.0%; Prod. No. 3.1e-64;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCATATTAACGAAAAACGAGGAGTCAGATGATTAACGAAAAAGCGAAATC 60
DB 29268 ATGTCATATTAACGAAAAACGAGGAGTCAGATGATTAACGAAAAAGCGAAATC 29327
QY 61 ATACGCAAAATATTCATGTTACGATGCAATTTTAAAGTCTAT 120
DB 29328 ATACGCAAAATATTCATGTTACGATGCAATTTTAAAGTCTAT 29387
QY 121 ATGGCATATCAATACAGTTAAGATATGACAGTACGATTAACATGCTTATGTC 180
DB 29388 ATGGCATATCAATACAGTTAAGATATGACAGTACGATTAACATGCTTATGTC 29447
QY 181 GTACATGAGATGACTAGATATGCGATCACTATTATTAACACCAATAGATGATGG 240
DB 29448 GTACATGAGATGACTAGATATGCGATCACTATTATTAACACCAATAGATGATGG 29507
QY 241 ATTGAAGAGACACAGACAGACGAGCACTAATTAAGTACTGTAATGGTATG 297
DB 29508 ATTGAAGAGACACAGACAGACGAGCACTAATTAAGTACTGTAATGGTATG 29564

RESULT 4
AAA68250
ID AAA68250 standard; DNA; 261 BP.
XX

AC AAA68250;
XX
XX 15-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 27-OCT-2000 (first entry)
XX
XX Bacteriophage 77 77ORF043 nucleotide sequence.
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW bacterial growth inhibition; bacterial infection; ds.
XX
OS Staphylococcus aureus; bacteriophage 77.
XX
XX W0200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-1B002040.
XX
XX 03-DEC-1999; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-) PHAGETECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
PI WPI, 2000-412361/35.
XX
XX P-PSDB; AAB16525.
DR
XX Identifying a bacteriophage coding region for treating bacterial
PT infections comprises identifying a nucleic acid encoding a product that
PT inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX Disclosure; Page 157; 456pp; English.
XX
XX The present invention describes a method for identifying a bacteriophage
CC coding region encoding a product active on an essential bacterial target.
CC The method comprises identifying a nucleic acid sequence encoding a gene
CC product that provides a bacteria-inhibiting function when an
CC uncharacterised bacteriophage infects a pathogenic bacterium. The
CC compound active on a target of a bacteriophage inhibitor protein in a
CC bacteria is used to treat or prevent a bacterial infection in an animal.
CC AAA68243 to AAB169442 and AAB16954 represent bacteriophage
CC nucleotide and protein sequences which are used in the exemplification of
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
CC (Updated on 15-SEP-2003 to standardise OS field)
SQ Sequence 261 BP; 105 A; 36 C; 49 G; 71 T; 0 U; 0 Other;
Query Match 87.9%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Prod. No. 1.1e-55;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ATGATTACGAATAGCGAATCATACCGAATATTCATGTTACGATTCATTT 60
 QY 97 AAGCTATTCATTTAAAGGTCATATGGGCAATCATACAGTTAAAGATGAAAC 156
 |||
 Db 61 AAGCTATTCATTTAAAGGTCATATGGGCAATCATACAGTTAAAGATGAAAC 120
 QY 157 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTAAATGGCATCAACTTA 216
 |||
 Db 121 GTACCAATTAAACATGCTTATGTGCTAGATGAGATGACTTAAATGGCATCAACTTA 180
 QY 217 TTAAACCAAGCAATGATGATGATGAGATGAGACAGACAGACAGACTTA 276
 |||
 Db 181 TTAAACCAAGCAATGATGATGATGAGATGAGACAGACAGACAGACTTA 240
 QY 277 AACTAGTCATGAATGCTAG 297
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 Db 241 AACTAGTCATGAATGCTAG 261

Search completed: October 14, 2004, 12:48:21
 Job time : 200 secs

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 12:03:47 ; Search time 1387.19 Seconds
 (without alignments)
 6393.544 Million cell updates/sec

Title: US-09-407-804A-9

Perfect score: 297
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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22:	em_gss_mam:*
23:	em_gss_nus:*
24:	em_gss_pro:*
25:	em_gss_rtd:*
26:	em_gss_png:*
27:	em_gss_vrl:*

28: gb_ges1:++
29: gb_ges2:++

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	47.2	15.9	1083	29	CNS00970	AL054505 Drosophila
c 4	45.8	15.4	1044	13	BK415231	BK415231 BK415231
5	45.6	15.4	328	28	A2923265	A2923265 4908-8 f20
c 6	44.6	15.0	822	12	BK357887	BK357887 GA Fa000
7	44.4	14.9	954	14	CA788983	CA788983 AGENCOURT
c 8	44.4	14.9	1101	29	CNS00178	AL060732 Drosophila
c 9	44.4	14.9	1198	13	BK395612	BK395612 BK395612
c 10	44.4	14.8	937	28	A2530244	A2530244 ENTBI12TF
c 11	43.6	14.7	700	28	BH371930	BH371930 AG-ND-132
c 12	43.4	14.6	1173	13	BK37986	BK37986 BK37986
13	43.4	14.6	1201	13	BK424465	BK424465 BK424465
14	43	14.5	1164	28	CC261365	CC261365 CH261-72H
15	42.6	14.3	842	10	BF617340	BF617340 HVSNEC001
c 16	42.4	14.3	509	28	B2842685	B2842685 CH240_276
c 17	42.4	14.3	588	29	BK168785	BK168785 Danilo rer
c 18	42.4	14.3	1002	28	B2695524	B2695524 SP_Ba006
19	42.2	14.2	761	14	CF282516	CF282516 AGENCOURT
c 20	42.2	14.2	876	28	BH164960	BH164960 ENTBY63TF
c 21	42.2	14.2	898	28	A2679345	A2679345 ENTKD48TF
c 22	42	14.1	763	10	BF126666	BF126666 601650942
23	42	14.1	1008	13	BK398691	BK398691 BK398691
c 24	42	14.1	1200	13	BK436510	BK436510 BK436510
25	41.8	14.1	519	28	A2525518	A2525518 244PbH11
c 26	41.8	14.1	571	28	A2526884	A2526884 260PB612
27	41.8	14.1	664	28	AE131173	AE131173 OSJNB5010
c 28	41.8	14.1	759	12	BJ375492	BJ375492 BJ375492
c 29	41.8	14.1	899	28	A2531765	A2531765 ENTB221TR
c 30	41.8	14.1	1027	28	A2668237	A2668237 ENTK205TR
31	41.8	14.1	1097	29	CNS01235	AL101650 Drosophila
c 32	41.6	14.0	706	28	BH954338	BH954338 cdb21b04.
33	41.6	14.0	924	28	A2674753	A2674753 ENTHU31TR
34	41.6	14.0	1189	13	BK456444	BK456444 BX456444
35	41.4	13.9	523	28	BH672321	BH672321 BOMH139TF
36	41.4	13.9	668	28	BH592678	BH592678 BOCG049TF
c 37	41.4	13.9	692	28	B2011251	B2011251 oel172a10.
38	41.4	13.9	874	28	A2673257	A2673257 ENTKM68TR
c 39	41.4	13.9	1101	29	CNS00807	AL072991 Drosophila
c 40	41.4	13.9	1234	12	BM911712	BM911712 AGENCOURT
41	41.2	13.9	556	28	BH686139	BH686139 BOMDB03TR
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c 43	41.2	13.9	1101	29	CNS01790	AL108642 Drosophila
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Search completed: October 14, 2004, 18:55:23
Job time : 1390.19 secs